

TChem

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# Chapter 1

## Thermo-chemical software library

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The TChem toolkit is a software library that enables numerical simulations using complex chemistry and facilitates the analysis of detailed kinetic models. The toolkit provide capabilities for thermodynamic properties based on NASA polynomials, kinetic model reaction rates (both for individual reactions and for species). It incorporates methods that can selectively modify reaction parameters for sensitivity analysis and uncertainty quantification. The library contains several functions that provide analytically computed Jacobian matrices necessary for the efficient time advancement and analysis of detailed kinetic models.

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## Chapter 2

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### 2.1 Modules

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## Class Index

### 3.1 Class List

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# Chapter 4

## File Index

### 4.1 File List

Here is a list of all documented files with brief descriptions:

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# Chapter 5

## Module Documentation

### 5.1 Equation of state

#### Functions

- int [TCDND\\_getRhoMixMs](#) (double \*scal, int Nvars, double \*rhomix)  
*Computes density based on temperature and species mass fractions using the equation of state. Input temperature is normalized, output density also normalized before exit.*
- int [TC\\_getRhoMixMs](#) (double \*scal, int Nvars, double \*rhomix)  
*Computes density based on temperature and species mass fractions using the equation of state.*
- int [TCDND\\_getRhoMixMI](#) (double \*scal, int Nvars, double \*rhomix)  
*Computes density based on temperature and species mole fractions using the equation of state. Input temperature is normalized, output density also normalized before exit.*
- int [TC\\_getRhoMixMI](#) (double \*scal, int Nvars, double \*rhomix)  
*Computes density based on temperature and species mole fractions using the equation of state.*
- int [TCDND\\_getTmixMs](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mass fractions using the equation of state. Input density is normalized, output temperature also normalized before exit.*
- int [TC\\_getTmixMs](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mass fractions using the equation of state.*
- int [TCDND\\_getTmixMI](#) (double \*scal, int Nvars, double \*Tmix)

*Computes temperature based on density and species mole fractions using the equation of state. Input density is normalized, output temperature also normalized before exit.*

- int [TC\\_getTmixMI](#) (double \*scal, int Nvars, double \*Tmix)

*Computes temperature based on density and species mole fractions using the equation of state.*

### 5.1.1 Function Documentation

#### 5.1.1.1 int TC\_getRhoMixMI ( double \* scal, int Nvars, double \* rhomix )

Computes density based on temperature and species mole fractions using the equation of state.

##### Parameters

scal	: array of Nspec +1 doubles (T,X <sub>1</sub> ,X <sub>2</sub> ,...,X <sub>Nspec</sub> ), temperature T [K], mole fractions X []
Nvars	: no. of variables = Nspec +1

##### Returns

rhomix : pointer to mixture density [kg/m<sup>3</sup> ]

References [TC\\_errorMSG\(\)](#), [TC\\_Nspec\\_](#), [TC\\_Nvars\\_](#), and [TC\\_sMass\\_](#).

Referenced by [TCDND\\_getRhoMixMI\(\)](#).

#### 5.1.1.2 int TC\_getRhoMixMs ( double \* scal, int Nvars, double \* rhomix )

Computes density based on temperature and species mass fractions using the equation of state.

##### Parameters

scal	: array of Nspec +1 doubles (T,Y <sub>1</sub> ,Y <sub>2</sub> ,...,Y <sub>Nspec</sub> ), temperature T [K], mass fractions Y []
Nvars	: no. of variables = Nspec +1

##### Returns

rhomix : pointer to mixture density [kg/m<sup>3</sup> ]

References [TC\\_errorMSG\(\)](#), [TC\\_Nspec\\_](#), [TC\\_Nvars\\_](#), and [TC\\_sMass\\_](#).

Referenced by TC\_getJacRPTYNanl(), TC\_getJacRPTYNnum(), TC\_getJacTYN(), T-C\_getJacTYNanl(), TC\_getJacTYNm1(), TC\_getJacTYNm1anl(), TC\_getMs2Cc(), TC\_getSrc(), and TCDND\_getRhoMixMs().

#### 5.1.1.3 int TC\_getTmixMI ( double \* *scal*, int *Nvars*, double \* *Tmix* )

Computes temperature based on density and species mole fractions using the equation of state.

##### Parameters

<i>scal</i>	: array of Nspec +1 doubles (rho,X <sub>1</sub> ,X <sub>2</sub> ,...,X <sub>Nspec</sub> ), density rho [kg/m <sup>3</sup> ], mole fractions X []
<i>Nvars</i>	: no. of variables = Nspec +1

##### Returns

*Tmix* : pointer to temperature [K]

References TC\_errorMSG(), TC\_Nspec\_, TC\_Nvars\_, and TC\_sMass\_.

Referenced by TCDND\_getTmixMI().

#### 5.1.1.4 int TC\_getTmixMs ( double \* *scal*, int *Nvars*, double \* *Tmix* )

Computes temperature based on density and species mass fractions using the equation of state.

##### Parameters

<i>scal</i>	: array of Nspec +1 doubles (rho,Y <sub>1</sub> ,Y <sub>2</sub> ,...,Y <sub>Nspec</sub> ), density rho [kg/m <sup>3</sup> ], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

##### Returns

*Tmix* : pointer to temperature [K]

References TC\_errorMSG(), TC\_Nspec\_, TC\_Nvars\_, and TC\_sMass\_.

Referenced by TC\_getSrcCons(), and TCDND\_getTmixMs().

---

**5.1.1.5 int TCDND\_getRhoMixMI ( double \* *scal*, int *Nvars*, double \* *rhomix* )**

Computes density based on temperature and species mole fractions using the equation of state. Input temperature is normalized, output density also normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,X <sub>1</sub> ,X <sub>2</sub> ,...,X <sub>Nspec</sub> ), temperature T [K], mole fractions X []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*rhomix* : pointer to mixture density [kg/m<sup>3</sup> ]

References TC\_errorMSG(), TC\_getRhoMixMI(), and TC\_Nvars\_.

**5.1.1.6 int TCDND\_getRhoMixMs ( double \* *scal*, int *Nvars*, double \* *rhomix* )**

Computes density based on temperature and species mass fractions using the equation of state. Input temperature is normalized, output density also normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,Y <sub>1</sub> ,Y <sub>2</sub> ,...,Y <sub>Nspec</sub> ), temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*rhomix* : pointer to mixture density [kg/m<sup>3</sup> ]

References TC\_errorMSG(), TC\_getRhoMixMs(), and TC\_Nvars\_.

**5.1.1.7 int TCDND\_getTmixMI ( double \* *scal*, int *Nvars*, double \* *Tmix* )**

Computes temperature based on density and species mole fractions using the equation of state. Input density is normalized, output temperature also normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (rho,X <sub>1</sub> ,X <sub>2</sub> ,...,X <sub>Nspec</sub> ), density rho [kg/m <sup>3</sup> ], mole fractions X []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

Tmix : pointer to temperature [K]

References TC\_errorMSG(), TC\_getTmixMI(), and TC\_Nvars\_.

**5.1.1.8 int TCDND\_getTmixMs ( double \* scal, int Nvars, double \* Tmix )**

Computes temperature based on density and species mass fractions using the equation of state. Input density is normalized, output temperature also normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (rho,Y <sub>1</sub> ,Y <sub>2</sub> ...,Y <sub>Nspec</sub> ), density rho [kg/m <sup>3</sup> ], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

Tmix : pointer to temperature [K]

References TC\_errorMSG(), TC\_getTmixMs(), and TC\_Nvars\_.

## 5.2 Thermodynamic properties

### Functions

- int [TCDND\\_getMs2CpMixMs](#) (double \*scal, int Nvars, double \*cpmix)
 

*Computes mixture specific heat at constant pressure based on temperature and species mass fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
- int [TC\\_getMs2CpMixMs](#) (double \*scal, int Nvars, double \*cpmix)
 

*Computes mixture specific heat at constant pressure based on temperature and species mass fractions.*
- int [TCDND\\_getMs2CvMixMs](#) (double \*scal, int Nvars, double \*cvmix)
 

*Computes mixture specific heat at constant volume based on temperature and species mass fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
- int [TC\\_getMs2CvMixMs](#) (double \*scal, int Nvars, double \*cvmix)
 

*Computes mixture specific heat at constant volume based on temperature and species mass fractions.*
- int [TCDND\\_getMI2CpMixMI](#) (double \*scal, int Nvars, double \*cpmix)
 

*Computes mixture heat capacity at constant pressure based on temperature and species mole fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
- int [TC\\_getMI2CpMixMI](#) (double \*scal, int Nvars, double \*cpmix)
 

*Computes mixture specific heat at constant pressure based on temperature and species mole fractions.*
- int [TCDND\\_getCpSpecMs](#) (double t, int Nspec, double \*cpi)
 

*Computes species specific heat at constant pressure based on temperature. Input temperature is normalized, output specific heats are also normalized before exit.*
- int [TC\\_getCpSpecMs](#) (double t, int Nspec, double \*cpi)
 

*Computes species specific heat at constant pressure based on temperature.*
- int [TCDND\\_getCpSpecMI](#) (double t, int Nspec, double \*cpi)
 

*Computes species heat capacities at constant pressure based on temperature. Input temperature is normalized, output heat capacities are also normalized before exit.*
- int [TC\\_getCpSpecMI](#) (double t, int Nspec, double \*cpi)
 

*Computes species heat capacities at constant pressure based on temperature.*
- int [TCDND\\_getMs2HmixMs](#) (double \*scal, int Nvars, double \*hmix)
 

*Computes mixture specific enthalpy based on temperature and species mass fractions. Input temperature is normalized, output enthalpy is normalized before exit.*
- int [TC\\_getMs2HmixMs](#) (double \*scal, int Nvars, double \*hmix)
 

*Computes mixture specific enthalpy based on temperature and species mass fractions.*
- int [TCDND\\_getMI2HmixMI](#) (double \*scal, int Nvars, double \*hmix)
 

*Computes mixture molar enthalpy based on temperature and species mole fractions. Input temperature is normalized, output enthalpy is normalized before exit.*

- int [TC\\_getMI2HmixMI](#) (double \*scal, int Nvars, double \*hmix)  
*Computes mixture molar enthalpy based on temperature and species mole fractions.*
- int [TCDND\\_getHspecMs](#) (double t, int Nspec, double \*hi)  
*Computes species specific enthalpies based on temperature. Input temperature is normalized, output enthalpies are also normalized before exit.*
- int [TC\\_getHspecMs](#) (double t, int Nspec, double \*hi)  
*Computes species specific enthalpies based on temperature.*
- int [TCDND\\_getHspecMI](#) (double t, int Nspec, double \*hi)  
*Computes species molar enthalpies based on temperature. Input temperature is normalized, output enthalpies are also normalized before exit.*
- int [TC\\_getHspecMI](#) (double t, int Nspec, double \*hi)  
*Computes species molar enthalpies based on temperature.*

### 5.2.1 Function Documentation

#### 5.2.1.1 int TC\_getCpSpecMI ( double t, int Nspec, double \* cpi )

Computes species heat capacities at constant pressure based on temperature.

##### Parameters

<i>t</i>	: temperature T [K]
<i>Nspec</i>	: no. of species

##### Returns

cpi : array with species heat capacities at constant pressure [J/(kmol.K)]

References [TC\\_errorMSG\(\)](#), and [TC\\_Nspec\\_](#).

Referenced by [TC\\_getMI2CpMixMI\(\)](#), and [TCDND\\_getCpSpecMI\(\)](#).

#### 5.2.1.2 int TC\_getCpSpecMs ( double t, int Nspec, double \* cpi )

Computes species specific heat at constant pressure based on temperature.

##### Parameters

<i>t</i>	: temperature T [K]
<i>Nspec</i>	: no. of species

**Returns**

cpi : array with species specific heats at constant pressure [J/(kg.K)]

References TC\_errorMSG(), and TC\_Nspec\_.

Referenced by TC\_getJacRPTYNnum(), TC\_getMs2CpMixMs(), and TCDND\_getCpSpecMs().

#### 5.2.1.3 int TC\_getHspecMI ( double *t*, int *Nspec*, double \* *hi* )

Computes species molar enthalpies based on temperature.

**Parameters**

<i>t</i>	: temperature T [K]
<i>Nspec</i>	: no. of species

**Returns**

*hi* : array with species molar enthalpies [J/kmol]

References TC\_errorMSG(), and TC\_Nspec\_.

Referenced by TC\_getMI2HmixMI(), and TCDND\_getHspecMI().

#### 5.2.1.4 int TC\_getHspecMs ( double *t*, int *Nspec*, double \* *hi* )

Computes species specific enthalpies based on temperature.

**Parameters**

<i>t</i>	: temperature T [K]
<i>Nspec</i>	: no. of species

**Returns**

*hi* : array with species specific enthalpies [J/kg]

References TC\_errorMSG(), and TC\_Nspec\_.

Referenced by TC\_getJacRPTYNanl(), TC\_getJacRPTYNnum(), TC\_getMs2HmixMs(), TC\_getSrc(), TC\_getSrcCons(), and TCDND\_getHspecMs().

### 5.2.1.5 int TC\_getMI2CpMixMI ( double \* scal, int Nvars, double \* cpmix )

Computes mixture specific heat at constant pressure based on temperature and species mole fractions.

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, X_1, X_2, \dots, X_{N_{spec}}$ ), temperature $T$ [K], mole fractions $X$ []
<i>Nvars</i>	: no. of variables = $N_{spec} + 1$

#### Returns

*cpmix* : pointer to mixture specific heat at constant pressure [J/(kmol.K)]

References `TC_errorMSG()`, `TC_getCpSpecMI()`, `TC_Nspec_`, and `TC_Nvars_`.

Referenced by `TCDND_getMI2CpMixMI()`.

### 5.2.1.6 int TC\_getMI2HmixMI ( double \* scal, int Nvars, double \* hmix )

Computes mixture molar enthalpy based on temperature and species mole fractions.

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, X_1, X_2, \dots, X_{N_{spec}}$ ), temperature $T$ [K], mole fractions $X$ []
<i>Nvars</i>	: no. of variables = $N_{spec} + 1$

#### Returns

*hmix* : pointer to mixture molar enthalpy [J/kmol]

References `TC_errorMSG()`, `TC_getHspecMI()`, `TC_Nspec_`, and `TC_Nvars_`.

Referenced by `TCDND_getMI2HmixMI()`.

### 5.2.1.7 int TC\_getMs2CpMixMs ( double \* scal, int Nvars, double \* cpmix )

Computes mixture specific heat at constant pressure based on temperature and species mass fractions.

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_{N_{spec}}$ ), temperature $T$ [K], mass fractions $Y$ []
<i>Nvars</i>	: no. of variables = $N_{spec} + 1$

**Returns**

`cpmix` : pointer to mixture specific heat at constant pressure [J/(kg.K)]

References `TC_errorMSG()`, `TC_getCpSpecMs()`, `TC_Nspec_`, and `TC_Nvars_`.

Referenced by `TC_getJacRPTYNanl()`, `TC_getJacRPTYNnum()`, `TC_getMs2CvMixMs()`, `TC_getSrc()`, `TC_getSrcCons()`, and `TCDND_getMs2CpMixMs()`.

#### 5.2.1.8 int `TC_getMs2CvMixMs ( double * scal, int Nvars, double * cvmix )`

Computes mixture specific heat at constant volume based on temperature and species mass fractions.

**Parameters**

<code>scal</code>	: array of <code>Nspec +1</code> doubles ( $T, Y_1, Y_2, \dots, Y_{Nspec}$ ), temperature $T$ [K], mass fractions $Y[]$
<code>Nvars</code>	: no. of variables = <code>Nspec +1</code>

**Returns**

`cvmix` : pointer to mixture specific heat at constant volume [J/(kg.K)]

References `TC_errorMSG()`, `TC_getMs2CpMixMs()`, `TC_Nspec_`, `TC_Nvars_`, and `TC_sMass_`.

Referenced by `TCDND_getMs2CvMixMs()`.

#### 5.2.1.9 int `TC_getMs2HmixMs ( double * scal, int Nvars, double * hmix )`

Computes mixture specific enthalpy based on temperature and species mass fractions.

**Parameters**

<code>scal</code>	: array of <code>Nspec +1</code> doubles ( $T, Y_1, Y_2, \dots, Y_{Nspec}$ ), temperature $T$ [K], mass fractions $Y[]$
<code>Nvars</code>	: no. of variables = <code>Nspec +1</code>

**Returns**

`hmix` : pointer to mixture specific enthalpy [J/kg]

References `TC_errorMSG()`, `TC_getHspecMs()`, `TC_Nspec_`, and `TC_Nvars_`.

Referenced by `TCDND_getMs2HmixMs()`.

### 5.2.1.10 int TCDND\_getCpSpecMI ( double $t$ , int $N_{spec}$ , double \* $cpi$ )

Computes species heat capacities at constant pressure based on temperature. Input temperature is normalized, output heat capacities are also normalized before exit.

#### Parameters

$t$	: temperature T [K]
$N_{spec}$	: no. of species

#### Returns

$cpi$  : array with species heat capacities at constant pressure [J/(kmol.K)]

References TC\_errorMSG(), TC\_getCpSpecMI(), and TC\_Nspec\_.

### 5.2.1.11 int TCDND\_getCpSpecMs ( double $t$ , int $N_{spec}$ , double \* $cpi$ )

Computes species specific heat at constant pressure based on temperature. Input temperature is normalized, output specific heats are also normalized before exit.

#### Parameters

$t$	: temperature T [K]
$N_{spec}$	: no. of species

#### Returns

$cpi$  : array with species specific heats at constant pressure [J/(kg.K)]

References TC\_errorMSG(), TC\_getCpSpecMs(), and TC\_Nspec\_.

### 5.2.1.12 int TCDND\_getHspecMI ( double $t$ , int $N_{spec}$ , double \* $hi$ )

Computes species molar enthalpies based on temperature. Input temperature is normalized, output enthalpies are also normalized before exit.

#### Parameters

$t$	: temperature T [K]
$N_{spec}$	: no. of species

**Returns**

hi : array with species molar enthalpies [J/kmol]

References TC\_errorMSG(), TC\_getHspecMI(), and TC\_Nspec\_.

**5.2.1.13 int TCDND\_getHspecMs ( double t, int Nspec, double \* hi )**

Computes species specific enthalpies based on temperature. Input temperature is normalized, output enthalpies are also normalized before exit.

**Parameters**

<i>t</i>	: temperature T [K]
<i>Nspec</i>	: no. of species

**Returns**

hi : array with species specific enthalpies [J/kg]

References TC\_errorMSG(), TC\_getHspecMs(), and TC\_Nspec\_.

**5.2.1.14 int TCDND\_getMI2CpMixMI ( double \* scal, int Nvars, double \* cpmix )**

Computes mixture heat capacity at constant pressure based on temperature and species mole fractions. Input temperature is normalized, output specific heat is also normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,X <sub>1</sub> ,X <sub>2</sub> ,...,X <sub>Nspec</sub> ), temperature T [K], mole fractions X []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

cpmix : pointer to mixture heat capacity at constant pressure [J/(kmol.K)]

References TC\_errorMSG(), TC\_getMI2CpMixMI(), and TC\_Nvars\_.

**5.2.1.15 int TCDND\_getMI2HmixMI ( double \* scal, int Nvars, double \* hmix )**

Computes mixture molar enthalpy based on temperature and species mole fractions. Input temperature is normalized, output enthalpy is normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,X <sub>1</sub> ,X <sub>2</sub> ,...,X <sub>Nspec</sub> ), temperature T [K], mole fractions X []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*hmix* : pointer to mixture molar enthalpy [J/kmol]

References TC\_errorMSG(), TC\_getMI2HmixMI(), and TC\_Nvars\_.

**5.2.1.16 int TCDND\_getMs2CpMixMs ( double \* *scal*, int *Nvars*, double \* *cpmix* )**

Computes mixture specific heat at constant pressure based on temperature and species mass fractions. Input temperature is normalized, output specific heat is also normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,Y <sub>1</sub> ,Y <sub>2</sub> ,...,Y <sub>Nspec</sub> ), temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*cpmix* : pointer to mixture specific heat at constant pressure [J/(kg.K)]

References TC\_errorMSG(), TC\_getMs2CpMixMs(), and TC\_Nvars\_.

**5.2.1.17 int TCDND\_getMs2CvMixMs ( double \* *scal*, int *Nvars*, double \* *cvmix* )**

Computes mixture specific heat at constant volume based on temperature and species mass fractions. Input temperature is normalized, output specific heat is also normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,Y <sub>1</sub> ,Y <sub>2</sub> ,...,Y <sub>Nspec</sub> ), temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

cpmix : pointer to mixture specific heat at constant volume [J/(kg.K)]

References TC\_errorMSG(), TC\_getMs2CvMixMs(), and TC\_Nvars\_.

**5.2.1.18 int TCDND\_getMs2HmixMs ( double \* scal, int Nvars, double \* hmix )**

Computes mixture specific enthalpy based on temperature and species mass fractions.  
Input temperature is normalized, output enthalpy is normalized before exit.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,Y <sub>1</sub> ,Y <sub>2</sub> ,...,Y <sub>Nspec</sub> ), temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

hmix : pointer to mixture specific enthalpy [J/kg]

References TC\_errorMSG(), TC\_getMs2HmixMs(), and TC\_Nvars\_.

## 5.3 Initialization

### Functions

- int **TC\_initChem** (char \*mechfile, char \*thermofile, int tab, double delT)  
*Initialize library.*
- void **TC\_setRefVal** (double rhoref, double pref, double Tref, double Wref, double Dref, double omgref, double cpref, double href, double timref)  
*Set reference values to the library.*
- void **TC\_setNonDim** ()  
*Set library to function in non-dimensional mode.*
- void **TC\_setDim** ()  
*Set library to function in dimensional mode (default)*
- void **TC\_setThermoPres** (double pressure)  
*Send thermodynamic pressure to the library.*
- int **TC\_makeSpace** ()  
*Allocate internal work arrays for the library. Should not be called by external functions.*
- int **TC\_createTables** (double delT)  
*Create tables for temperature dependent terms. Should not be called by external functions.*
- int **TC\_kmodint\_** (char \*mechfile, int \*lmech, char \*thermofile, int \*lthrm)  
*Kinetic model interpreter.*

#### 5.3.1 Function Documentation

##### 5.3.1.1 int TC\_createTables ( double *delT* )

Create tables for temperature dependent terms. Should not be called by external functions.

###### Parameters

<i>delT</i>	: temperature step size [K]
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References **TC\_Nreac\_**, and **TC\_Nspec\_**.

Referenced by **TC\_initChem()**.

##### 5.3.1.2 int TC\_initChem ( char \* *mechfile*, char \* *thermofile*, int *tab*, double *delT* )

Initialize library.

**Parameters**

<i>mechfile</i>	: name of file containing kinetic model in chemkin format
<i>thermofile</i>	: name of file containing coefficients for NASA polynomials
<i>tab</i>	: flag to tabulate temperature dependent terms (tab=1 -> create tables)
<i>delT</i>	: temperature step size [K] for the tables; used only tab=1

References ATMPA, CALJO, fastIntPow(), LENGTHOFELEMNAME, LENGTHOFSP-ECNAME, RUNIV, TC\_createTables(), TC\_electrIndx\_, TC\_elemcount\_, TC\_eMass\_, TC\_eNames\_, TC\_errorINI(), TC\_kmodint\_(), TC\_makeSpace(), TC\_maxOrdPar\_, T-C\_maxSpecInReac\_, TC\_maxTbinReac\_, TC\_nArhPar\_, TC\_nCpCoef\_, TC\_Nelem\_, TC\_nExcReac\_, TC\_nFallPar\_, TC\_nFallReac\_, TC\_nFit1Par\_, TC\_nFit1Reac\_, -TC\_nHvReac\_, TC\_nIonEspec\_, TC\_nIonSpec\_, TC\_nJanPar\_, TC\_nJanReac\_, T-C\_nLtPar\_, TC\_nLtReac\_, TC\_nMomeReac\_, TC\_nNASAinter\_, TC\_nOrdReac\_, T-C\_Nreac\_, TC\_nRealNuReac\_, TC\_nRevReac\_, TC\_nRltReac\_, TC\_Nspec\_, TC\_nTdepReac\_, TC\_nThbReac\_, TC\_Nvars\_, TC\_Nvjac\_, TC\_nXsmiReac\_, TC\_sCharge\_, TC\_setThermoPres(), TC\_sMass\_, TC\_sNames\_, TC\_sPhase\_, and TC\_sTfit\_.

**5.3.1.3 int TC\_kmodint\_ ( char \* *mechfile*, int \* *lmech*, char \* *thermofile*, int \* *lthrm* )**

Kinetic model interpreter.

**Parameters**

<i>mechfile</i>	: name of file containing kinetic model in chemkin format
<i>lmech</i>	: length of mechfile character string
<i>thermofile</i>	: name of file containing coefficients for NASA polynomials
<i>lthrm</i>	: length of thermofile character string

References checkunits(), cleancharstring(), elimleads(), errmsg(), extractWordLeft(), getelements(), getreactions(), getspecies(), getthermo(), MIN, out\_formatted(), out\_mathem(), out\_unformatted(), rescalereac(), setelementmass(), setperiodictable(), verifyreac(), and wordtoupper().

Referenced by TC\_initChem().

**5.3.1.4 void TC\_setRefVal ( double *rhref*, double *pref*, double *Tref*, double *Wref*, double *Dref*, double *omgref*, double *cpref*, double *href*, double *timref* )**

Set reference values to the library.

**Parameters**

<i>rhref</i>	: density [ $kg/m^3$ ]
<i>pref</i>	: pressure [ $N/m^2$ ]
<i>Tref</i>	: temperature [K]

<i>Wref</i>	: molecular weight [ $kg/kmol$ ]
<i>Daref</i>	: Damkohler number []
<i>omgref</i>	: molar reaction rate [ $kmol/(m^3 \cdot s)$ ]
<i>cpref</i>	: specific heat at constant pressure [ $J/(kg \cdot K)$ ]
<i>href</i>	: specific enthalphy [ $J/kg$ ]
<i>timref</i>	: time [s]

### 5.3.1.5 void TC\_setThermoPres ( double *pressure* )

Send thermodynamic pressure to the library.

#### Parameters

<i>pressure</i>	: thermodynamic pressure [ $N/m^2$ ]
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Referenced by TC\_initChem().

## 5.4 Jacobians

### Functions

- int [TCDND\\_getJacTYNm1anl](#) (double \*scal, int Nspec, double \*jac)
 

*Computes analytical Jacobian (dimensional/non-dimensional) for the system ( $T, Y_1, Y_2, \dots, Y_{N-1}$ ) based on temperature T and species mass fractions Y's.*
- int [TC\\_getJacTYNm1anl](#) (double \*scal, int Nspec, double \*jac)
 

*Computes analytical Jacobian for the system ( $T, Y_1, Y_2, \dots, Y_{N-1}$ ) based on T and Y's.*
- int [TCDND\\_getJacTYNanl](#) (double \*scal, int Nspec, double \*jac)
 

*Computes analytical Jacobian (dimensional/non-dimensional) for the system ( $T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.*
- int [TC\\_getJacTYNanl](#) (double \*scal, int Nspec, double \*jac)
 

*Computes analytical Jacobian for the system ( $T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.*
- int [TCDND\\_getJacTYNm1](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)
 

*Computes (analytical or numerical) Jacobian (dimensional/non-dimensional) for the system ( $T, Y_1, Y_2, \dots, Y_{N-1}$ ) based on temperature T and species mass fractions Y's.*
- int [TC\\_getJacTYNm1](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)
 

*Computes (analytical or numerical) Jacobian for the system ( $T, Y_1, Y_2, \dots, Y_{N-1}$ ) based on T and Y's.*
- int [TCDND\\_getJacTYN](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)
 

*Computes (analytical or numerical) Jacobian for the system ( $T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.*
- int [TC\\_getJacTYN](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)
 

*Computes (analytical or numerical) Jacobian for the system ( $T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.*
- int [TC\\_getJacRPTYN](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)
 

*Computes (analytical) Jacobian for the system ( $\rho, P, T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.*
- int [TC\\_getJacRPTYNanl](#) (double \*scal, int Nspec, double \*jac)
 

*Computes analytical Jacobian for the system ( $\rho, P, T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.*
- int [TC\\_getJacRPTYNnum](#) (double \*scal, int Nspec, double \*jac)
 

*Computes numerical Jacobian for the system ( $\rho, P, T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.*

### 5.4.1 Function Documentation

5.4.1.1 int TC\_getJacRPTYN ( double \* *scal*, int *Nspec*, double \* *jac*, unsigned int *useJacAnl* )

Computes (analytical) Jacobian for the system ( $\rho, P, T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_{N_{spec}}$ ) temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$
<i>useJacAnl</i>	: flag for Jacobian type (1-analytical,other values-numerical)

#### Returns

*jac* : Jacobian array

References TC\_errorMSG(), TC\_getJacRPTYNanl(), TC\_getJacRPTYNnum(), and TC\_Nspec\_.

5.4.1.2 int TC\_getJacRPTYNanl ( double \* *scal*, int *Nspec*, double \* *jac* )

Computes analytical Jacobian for the system ( $\rho, P, T, Y_1, Y_2, \dots, Y_N$ ) based on T and Y's.

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_{N_{spec}}$ ) temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$

#### Returns

*jac* : Jacobian array

References TC\_errorMSG(), TC\_getHspecMs(), TC\_getMs2Cc(), TC\_getMs2CpMixMs(), TC\_getRhoMixMs(), TC\_maxOrdPar\_, TC\_maxSpecInReac\_, TC\_nOrdReac\_, TC\_Nreac\_, TC\_nRealNuReac\_, TC\_Nspec\_, TC\_Nvars\_, TC\_Nvjac\_, and TC\_sMass\_.

Referenced by TC\_getJacRPTYN(), TC\_getJacTYN(), TC\_getJacTYNanl(), TC\_getJacTYNm1(), and TC\_getJacTYNm1anl().

---

#### 5.4.1.3 int TC\_getJacRPTYNnum ( double \* *scal*, int *Nspec*, double \* *jac* )

Computes numerical Jacobian for the system  $(\rho, P, T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.

**Parameters**

<i>scal</i>	: array of $N_{spec} + 1$ doubles $(T, Y_1, Y_2, \dots, Y_{N_{spec}})$ temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$

**Returns**

*jac* : Jacobian array

References TC\_errorMSG(), TC\_getCpSpecMs(), TC\_getHspecMs(), TC\_getMs2Cc(), TC\_getMs2CpMixMs(), TC\_getRhoMixMs(), TC\_getTxC2RRms(), TC\_Nspec\_, TC\_Nvjac\_, and TC\_sMass\_.

Referenced by TC\_getJacRPTYN(), TC\_getJacTYN(), and TC\_getJacTYNm1().

---

#### 5.4.1.4 int TC\_getJacTYN ( double \* *scal*, int *Nspec*, double \* *jac*, unsigned int *useJacAnl* )

Computes (analytical or numerical) Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.

**Parameters**

<i>scal</i>	: array of $N_{spec} + 1$ doubles $(T, Y_1, Y_2, \dots, Y_{N_{spec}})$ temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$
<i>useJacAnl</i>	: flag for Jacobian type (1-analytical,other values-numerical)

**Returns**

*jac* : Jacobian array

References TC\_errorMSG(), TC\_getJacRPTYNanl(), TC\_getJacRPTYNnum(), TC\_getMs2Wmix(), TC\_getRhoMixMs(), TC\_Nspec\_, TC\_Nvars\_, TC\_Nvjac\_, and TC\_sMass\_.

Referenced by TCDND\_getJacTYN().

---

#### 5.4.1.5 int TC\_getJacTYNanl ( double \* *scal*, int *Nspec*, double \* *jac* )

Computes analytical Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.

**Parameters**

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_{N_{spec}}$ ) temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$

**Returns**

jac : Jacobian array

References TC\_errorMSG(), TC\_getJacRPTYNanl(), TC\_getMs2Wmix(), TC\_getRho-MixMs(), TC\_Nspec\_, TC\_Nvars\_, TC\_Nvjac\_, and TC\_sMass\_.

Referenced by TCDND\_getJacTYNanl().

**5.4.1.6 int TC\_getJacTYNm1 ( double \* *scal*, int *Nspec*, double \* *jac*, unsigned int *useJacAnl* )**

Computes (analytical or numerical) Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on T and Y's.

**Parameters**

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_{N_{spec}}$ ) temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$
<i>useJacAnl</i>	: flag for Jacobian type (1-analytical,other values-numerical)

**Returns**

jac : Jacobian array

References TC\_errorMSG(), TC\_getJacRPTYNanl(), TC\_getJacRPTYNnum(), TC\_getMs2Wmix(), TC\_getRhoMixMs(), TC\_Nspec\_, TC\_Nvars\_, TC\_Nvjac\_, and TC\_sMass\_.

Referenced by TCDND\_getJacTYNm1().

**5.4.1.7 int TC\_getJacTYNm1anl ( double \* *scal*, int *Nspec*, double \* *jac* )**

Computes analytical Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on T and Y's.

**Parameters**

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_{N_{spec}}$ ) temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$

**Returns**

`jac` : Jacobian array

References `TC_errorMSG()`, `TC_getJacRPTYNanl()`, `TC_getMs2Wmix()`, `TC_getRho-MixMs()`, `TC_Nspec_`, `TC_Nvars_`, `TC_Nvjac_`, and `TC_sMass_`.

Referenced by `TCDND_getJacTYNm1anl()`.

**5.4.1.8 int TCDND\_getJacTYN ( double \* *scal*, int *Nspec*, double \* *jac*, unsigned int *useJacAnl* )**

Computes (analytical or numerical) Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.

**Parameters**

<code>scal</code>	: array of $N_{spec} + 1$ doubles $(T, Y_1, Y_2, \dots, Y_{N_{spec}})$ temperature T [K], mass fractions Y []
<code>Nspec</code>	: no. of species $N_{spec}$
<code>useJacAnl</code>	: flag for Jacobian type (1-analytical,other values-numerical)

**Returns**

`jac` : Jacobian array

References `TC_errorMSG()`, `TC_getJacTYN()`, and `TC_Nspec_`.

**5.4.1.9 int TCDND\_getJacTYNanl ( double \* *scal*, int *Nspec*, double \* *jac* )**

Computes analytical Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.

**Parameters**

<code>scal</code>	: array of $N_{spec} + 1$ doubles $(T, Y_1, Y_2, \dots, Y_{N_{spec}})$ temperature T [K], mass fractions Y []
<code>Nspec</code>	: no. of species $N_{spec}$

**Returns**

`jac` : Jacobian array

References `TC_errorMSG()`, `TC_getJacTYNanl()`, and `TC_Nspec_`.

---

5.4.1.10 int TCDND\_getJacTYNm1 ( double \* *scal*, int *Nspec*, double \* *jac*, unsigned int *useJacAnl* )

Computes (analytical or numerical) Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on temperature T and species mass fractions Y's.

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles $(T, Y_1, Y_2, \dots, Y_{N_{spec}})$ temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$
<i>useJacAnl</i>	: flag for Jacobian type (1-analytical,other values-numerical)

#### Returns

*jac* : Jacobian array

References TC\_errorMSG(), TC\_getJacTYNm1(), and TC\_Nspec\_.

5.4.1.11 int TCDND\_getJacTYNm1anl ( double \* *scal*, int *Nspec*, double \* *jac* )

Computes analytical Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on temperature T and species mass fractions Y's.

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles $(T, Y_1, Y_2, \dots, Y_{N_{spec}})$ temperature T [K], mass fractions Y []
<i>Nspec</i>	: no. of species $N_{spec}$

#### Returns

*jac* : Jacobian array

References TC\_errorMSG(), TC\_getJacTYNm1anl(), and TC\_Nspec\_.

## 5.5 Source terms

### Functions

- int [TCDND\\_getSrc](#) (double \*scal, int Nvars, double \*omega)

*Returns dimensional/non-dimensional source term for*

$$\frac{\partial T}{\partial t} = \omega_0, \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on temperature T and species mass fractions Y's.*

- int [TC\\_getSrc](#) (double \*scal, int Nvars, double \*omega)

*Returns source term for*

$$\frac{\partial T}{\partial t} = \omega_0, \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on temperature T and species mass fractions Y's.*

- int [TCDND\\_getSrcCons](#) (double \*scal, int Nvars, double \*omega)

*Returns source term (dimensional/non-dimensional) for*

$$\frac{\partial \rho}{\partial t} = \omega_0, \rho \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on  $\rho$  and Y's.*

- int [TC\\_getSrcCons](#) (double \*scal, int Nvars, double \*omega)

*Returns source term for*

$$\frac{\partial \rho}{\partial t} = \omega_0, \rho \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on  $\rho$  and Y's.*

### 5.5.1 Function Documentation

#### 5.5.1.1 int TC\_getSrc ( double \* scal, int Nvars, double \* omega )

*Returns source term for*

$$\frac{\partial T}{\partial t} = \omega_0, \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on temperature T and species mass fractions Y's.*

#### Parameters

<i>scal</i>	: array of Nspec+1 doubles ( $T, Y_1, Y_2, \dots, Y_{N_{spec}}$ ) temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables $N_{vars} = N_{spec} + 1$

**Returns**

omega : array of Nspec +1 source terms for temperature and species mass fractions: omega[0] : [(K/s)], omega[1...Nspec ] : [(1/s)]

References TC\_errorMSG(), TC\_getHspecMs(), TC\_getMs2CpMixMs(), TC\_getRho-MixMs(), TC\_getTY2RRms(), TC\_Nspec\_, and TC\_Nvars\_.

Referenced by TCDND\_getSrc().

**5.5.1.2 int TC\_getSrcCons ( double \* scal, int Nvars, double \* omega )**

Returns source term for

$$\frac{\partial \rho}{\partial t} = \omega_0, \rho \frac{\partial Y_i}{\partial t} = \omega_i,$$

based on  $\rho$  and Y's.

**Parameters**

<i>scal</i>	: array of Nspec+1 doubles ( $\rho, Y_1, Y_2, \dots, Y_N$ ) density [ $kg/m^3$ ], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

omega : array of Nspec +1 source terms for density and species mf conservative formulation: omega[0] : [ $kg/(m^3 \cdot s)$ ], omega[1...Nspec ] : [ $kg/(m^3 \cdot s)$ ]

References TC\_errorMSG(), TC\_getHspecMs(), TC\_getMs2CpMixMs(), TC\_getMs2-Wmix(), TC\_getTmixMs(), TC\_getTY2RRml(), TC\_Nspec\_, TC\_Nvars\_, and TC\_s-Mass\_.

Referenced by TCDND\_getSrcCons().

**5.5.1.3 int TCDND\_getSrc ( double \* scal, int Nvars, double \* omega )**

Returns dimensional/non-dimensional source term for

$$\frac{\partial T}{\partial t} = \omega_0, \frac{\partial Y_i}{\partial t} = \omega_i,$$

based on temperature T and species mass fractions Y's.

**Parameters**

<i>scal</i>	: array of Nspec+1 doubles ( $T, Y_1, Y_2, \dots, Y_{N_{spec}}$ ) temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables $N_{vars} = N_{spec} + 1$

**Returns**

`omega` : array of `Nspec +1` source terms (possibly normalized) for temperature and species mass fractions equations: `omega[0] : [(K/s)], omega[1...Nspec] : [(1/s)]`

References `TC_errorMSG()`, `TC_getSrc()`, `TC_Nspec_`, and `TC_Nvars_`.

#### 5.5.1.4 int TCDND\_getSrcCons ( double \* *scal*, int *Nvars*, double \* *omega* )

Returns source term (dimensional/non-dimensional) for

$$\frac{\partial \rho}{\partial t} = \omega_0, \rho \frac{\partial Y_i}{\partial t} = \omega_i,$$

based on  $\rho$  and  $Y$ 's.

**Parameters**

<code>scal</code>	: array of <code>Nspec+1</code> doubles ( $\rho, Y_1, Y_2, \dots, Y_N$ ) density [ $kg/m^3$ ], mass fractions $Y []$
<code>Nvars</code>	: no. of variables = <code>Nspec +1</code>

**Returns**

`omega` : array of `Nspec +1` source terms for density and species mf conservative formulation: `omega[0] : [kg/(m3 · s)]`, `omega[1...Nspec] : [kg/(m3 · s)]`

References `TC_errorMSG()`, `TC_getSrcCons()`, `TC_Nspec_`, and `TC_Nvars_`.

## 5.6 Max. no. of parameters

### Variables

- static int `TC_maxSpecInReac_`  
*Maximum number of species in a reaction.*
- static int `TC_maxTblInReac_`  
*Max # of third-body efficiencies in a reaction.*
- static int `TC_nNASAinter_`  
*# of temperature regions for thermo fits*
- static int `TC_nCpCoef_`  
*# of polynomial coefficients for thermo fits*
- static int `TC_nArrhPar_`  
*# of Arrhenius parameters*
- static int `TC_nLtPar_`  
*# of parameters for Landau-Teller reactions*
- static int `TC_nFallPar_`  
*# of parameters for pressure-dependent reactions*
- static int `TC_nJanPar_`  
*# of parameters for Jannev-Langer fits (JAN)*
- static int `TC_maxOrdPar_`  
*# of parameters for arbitrary order reactions*
- static int `TC_nFit1Par_`  
*# of parameters for FIT1 fits*

## 5.7 No. of reactions

### Variables

- static int `TC_Nreac_`  
    *# of reactions*
- static int `TC_nRevReac_`  
    *# of reactions with REV given*
- static int `TC_nFallReac_`  
    *# of pressure-dependent reactions*
- static int `TC_nThbReac_`  
    *# of reactions using third-body efficiencies*
- static int `TC_nLtReac_`  
    *# of Landau-Teller reactions*
- static int `TC_nRltReac_`  
    *# of Landau-Teller reactions with RLT given*
- static int `TC_nHvReac_`  
    *# of reactions with HV*
- static int `TC_nJanReac_`  
    *# of reactions with JAN fits*
- static int `TC_nFit1Reac_`  
    *# of reactions with FIT1 fits*
- static int `TC_nExcIReac_`  
    *# of reactions with EXCI*
- static int `TC_nMomeReac_`  
    *# of reactions with MOME*
- static int `TC_nXsmiReac_`  
    *# of reactions with XSMI*
- static int `TC_nTdepReac_`  
    *# of reactions with TDEP*
- static int `TC_nRealNuReac_`  
    *# of reactions with non-int stoichiometric coefficients*
- static int `TC_nOrdReac_`  
    *# of reactions with arbitrary order*

## 5.8 No. of species, variables, etc.

### Variables

- static int **TC\_Nvars\_**  
    # of variables = no. of species + 1
- static int **TC\_Nvjac\_**  
    # of lines/cols in the Jacobian = no. of species + 3
- static int **TC\_Nelem\_**  
    # of chemical elements
- static int **TC\_Nspec\_**  
    # of species
- static int **TC\_nlonSpec\_**  
    # of ion species
- static int **TC\_electrIndx\_**  
    Index of the electron species.
- static int **TC\_nlonEspec\_**  
    # of ion species excluding the electron species



# Chapter 6

## Class Documentation

### 6.1 element Struct Reference

Element data.

```
#include <TC_kmodint.h>
```

#### Public Attributes

- char **name** [LENGTHOFELEMNAME]
- int **hasmass**
- double **mass**

#### 6.1.1 Detailed Description

Element data.

The documentation for this struct was generated from the following file:

- TC\_kmodint.h

### 6.2 elemtable Struct Reference

Entry in the table of periodic elements.

```
#include <TC_kmodint.h>
```

### Public Attributes

- char **name** [LENGTHOFELEMNAME]
- double **mass**

#### 6.2.1 Detailed Description

Entry in the table of periodic elements.

The documentation for this struct was generated from the following file:

- TC\_kmodint.h

## 6.3 reaction Struct Reference

Reaction data.

```
#include <TC_kmodint.h>
```

### Public Attributes

- int **isdup**
- int **isreal**
- int **isrev**
- int **isfall**
- int **specfall**
- int **isthrdb**
- int **nthrdb**
- int **iswl**
- int **isbal**
- int **iscomp**
- int **inreac**
- int **inprod**
- int **ismome**
- int **isxsmi**
- int **isford**
- int **isrord**
- int **islowset**
- int **ishighset**
- int **istroeset**
- int **issriset**
- int **isrevset**

- int **isltset**
- int **isrltset**
- int **ishvset**
- int **istdepset**
- int **isexciset**
- int **isjanset**
- int **isfit1set**
- int **spec** [2 \*NSPECREACMAX]
- int **nuki** [2 \*NSPECREACMAX]
- double **rnuki** [2 \*NSPECREACMAX]
- double **arhenfor** [3]
- double **arhenrev** [3]
- int **ithrdb** [NTHRDBMAX]
- double **rthrdb** [NTHRDBMAX]
- double **fallpar** [8]
- double **ltpar** [2]
- double **rltpar** [2]
- double **hvpar**
- char **aunits** [4]
- char **eunits** [4]
- int **tdeppar**
- double **excipar**
- double **optfit** [9]
- int **arbspec** [4 \*NSPECREACMAX]
- double **arbnuki** [4 \*NSPECREACMAX]

### 6.3.1 Detailed Description

Reaction data.

The documentation for this struct was generated from the following file:

- TC\_kmodint.h

## 6.4 species Struct Reference

Species data.

```
#include <TC_kmodint.h>
```

### Public Attributes

- char **name** [LENGTHOFSPECNAME]
- int **hasthermo**
- int **hasmass**
- double **mass**
- int **charge**
- int **phase**
- int **numofelem**
- int **elemindx** [NUMBEROFELEMINSPEC]
- int **elemcontent** [NUMBEROFELEMINSPEC]
- double **nasapoltemp** [3]
- double **nasapolcoefs** [14]

#### 6.4.1 Detailed Description

Species data.

The documentation for this struct was generated from the following file:

- TC\_kmodint.h

# Chapter 7

## File Documentation

### 7.1 copyright.h File Reference

Copyright 2011 Sandia Corporation. Under the terms of Contract DE-AC04-94AL85000 with Sandia Corporation, the U.S. Government retains certain rights in this software.

#### 7.1.1 Detailed Description

Copyright 2011 Sandia Corporation. Under the terms of Contract DE-AC04-94AL85000 with Sandia Corporation, the U.S. Government retains certain rights in this software. The software is released subject the terms of the GNU Lesser General Public License (<http://www.gnu.org/copyleft/lesser.html>) Please read the license information before downloading the software.

### 7.2 TC\_chg.c File Reference

Functions for changing Arrhenius rate factors.

#### Functions

- int `TC_chgArhenFor` (int ireac, int ipos, double newval)  
*Change parameters for forward rate constants.*
- int `TC_chgArhenForBack` (int ireac, int ipos)  
*Reverse changes for forward rate constants' parameters.*
- int `TC_chgArhenRev` (int ireac, int ipos, double newval)

*Change parameters for reverse rate constants.*

- int [TC\\_chgArhenRevBack](#) (int ireac, int ipos)

*Reverse changes for reverse rate constants' parameters.*

### 7.2.1 Detailed Description

Functions for changing Arrhenius rate factors.

### 7.2.2 Function Documentation

#### 7.2.2.1 int TC\_chgArhenFor ( int *ireac*, int *ipos*, double *newval* )

Change parameters for forward rate constants.

##### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of parameter to be changed (0) pre-exponential factor (1) temperature exponent, (2) activation energy
<i>newval</i>	: new parameter value

References [TC\\_Nreac\\_](#).

#### 7.2.2.2 int TC\_chgArhenForBack ( int *ireac*, int *ipos* )

Reverse changes for forward rate constants' parameters.

##### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of parameter to be changed (0) pre-exponential factor (1) temperature exponent, (2) activation energy

References [TC\\_Nreac\\_](#).

#### 7.2.2.3 int TC\_chgArhenRev ( int *ireac*, int *ipos*, double *newval* )

Change parameters for reverse rate constants.

##### Parameters

<i>ireac</i>	: reaction index
--------------	------------------

<i>ipos</i>	: index of parameter to be changed (0) pre-exponential factor (1) temperature exponent, (2) activation energy
<i>newval</i>	: new parameter value

References [TC\\_nRevReac\\_](#).

#### 7.2.2.4 int TC\_chgArhenRevBack ( int *ireac*, int *ipos* )

Reverse changes for reverse rate constants' parameters.

##### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of parameter to be changed (0) pre-exponential factor (1) temperature exponent, (2) activation energy

References [TC\\_nRevReac\\_](#).

## 7.3 TC\_defs.h File Reference

Definitions of variables names used by the library.

```
#include "copyright.h" #include <stdio.h> #include "TC_params.h"
```

### Defines

- #define **TMAX** 3500.0
- #define **TMIN** 290.0
- #define **DTMID** 10.0

### Functions

- int [TC\\_kmodint\\_](#) (char \*mechfile, int \*lmech, char \*thermofile, int \*lthrm)  
*Kinetic model interpreter.*
- int [TC\\_makeSpace](#) ()  
*Allocate internal work arrays for the library. Should not be called by external functions.*
- int [TC\\_createTables](#) (double delT)  
*Create tables for temperature dependent terms. Should not be called by external functions.*

- void **TC\_errorMSG** (int msgID, char const \*func, int var1, int var2)
 

*Outputs error messages for the library, then exits the execution.*
- void **TC\_errorINI** (FILE \*errfile, char const \*msg)
 

*Outputs error messages generated by TC\_initChem.*
- static double **fastIntPow** (double val, int exponent)
- int **TC\_getRopsLocal** (double \*scal)
- int **TC\_getReacRates** (double \*scal, int Nvars, double \*omega)
 

*Returns molar reaction rates,  $\dot{\omega}_i$ , based on T and molar concentrations XC's (semi-private function)*
- int **TC\_getgk** (double t1, double t\_1, double tln)
- int **TC\_getgkFcn** (double t1, double t\_1, double tln)
- int **TC\_getgkTab** (double t1)
- int **TC\_getgkp** (double t1, double t\_1, double tln)
- int **TC\_getgkpFcn** (double t1, double t\_1, double tln)
- int **TC\_getgkpTab** (double t1)
- double **TC\_getSumNuGk** (int i, double \*gkLoc)
- double **TC\_getSumRealNuGk** (int i, int ir, double \*gkLoc)
- int **TC\_get3rdBdyConc** (double \*concX, double \*concM)
- int **TC\_getkForRev** (double t1, double t\_1, double tln)
- int **TC\_getkForRevFcn** (double t\_1, double tln)
- int **TC\_getkForRevTab** (double t1)
- int **TC\_getkForRevP** (double t1, double t\_1)
- int **TC\_getkForRevPFcn** (double t\_1)
- int **TC\_getkForRevPTab** (double t1)
- int **TC\_getRateofProg** (double \*concX)
- int **TC\_getRateofProgDer** (double \*concX, int ireac, int ispec, double \*qfr)
- int **TC\_getCrnd** (double t1, double t\_1, double tln, double \*concX, double \*concM)
- int **TC\_getCrndDer** (int ireac, int \*itbdy, int \*ipfal, double t1, double t\_1, double tln, double \*concX, double \*concM)
- int **TC\_getCpSpecMsFcn** (double t, double \*cpi)
- int **TC\_getCpSpecMsTab** (double t1, double \*cpi)
- int **TC\_getCpSpecMIFcn** (double t, double \*cpi)
- int **TC\_getCpSpecMITab** (double t1, double \*cpi)
- int **TC\_getCpSpecMs1Fcn** (double t, int i, double \*cpi)
- int **TC\_getCpSpecMI1Fcn** (double t, int i, double \*cpi)
- int **TC\_getCpMixMsP** (double \*scal, int Nvars, double \*cpmix)
- int **TC\_getCpSpecMsP** (double t, int Nspec, double \*cpi)
- int **TC\_getCpSpecMsPFcn** (double t, double \*cpi)
- int **TC\_getCpSpecMsPtab** (double t1, double \*cpi)
- int **TC\_getCpSpecMs1PFCn** (double t, int i, double \*cpi)
- int **TC\_getHspecMsFcn** (double t, double \*hi)
- int **TC\_getHspecMsTab** (double t1, double \*hi)
- int **TC\_getHspecMIFcn** (double t, double \*hi)
- int **TC\_getHspecMITab** (double t1, double \*hi)

## Variables

- static int `TC_maxSpecInReac_`  
*Maximum number of species in a reaction.*
- static int `TC_maxTblInReac_`  
*Max # of third-body efficiencies in a reaction.*
- static int `TC_nNASAinter_`  
*# of temperature regions for thermo fits*
- static int `TC_nCpCoef_`  
*# of polynomial coefficients for thermo fits*
- static int `TC_nArrhPar_`  
*# of Arrhenius parameters*
- static int `TC_nLtPar_`  
*# of parameters for Landau-Teller reactions*
- static int `TC_nFallPar_`  
*# of parameters for pressure-dependent reactions*
- static int `TC_nJanPar_`  
*# of parameters for Jannev-Langer fits (JAN)*
- static int `TC_maxOrdPar_`  
*# of parameters for arbitrary order reactions*
- static int `TC_nFit1Par_`  
*# of parameters for FIT1 fits*
- static int `TC_Nvars_`  
*# of variables = no. of species + 1*
- static int `TC_Njac_`  
*# of lines/cols in the Jacobian = no. of species + 3*
- static int `TC_Nelem_`  
*# of chemical elements*
- static int `TC_Nspec_`  
*# of species*
- static int `TC_nIonSpec_`  
*# of ion species*
- static int `TC_electrIndx_`  
*Index of the electron species.*
- static int `TC_nIonEspec_`  
*# of ion species excluding the electron species*
- static int `TC_Nreac_`  
*# of reactions*
- static int `TC_nRevReac_`  
*# of reactions with REV given*

- static int **TC\_nFallReac\_**  
    # of pressure-dependent reactions
- static int **TC\_nThbReac\_**  
    # of reactions using third-body efficiencies
- static int **TC\_nLtReac\_**  
    # of Landau-Teller reactions
- static int **TC\_nRltReac\_**  
    # of Landau-Teller reactions with RLT given
- static int **TC\_nHvReac\_**  
    # of reactions with HV
- static int **TC\_nJanReac\_**  
    # of reactions with JAN fits
- static int **TC\_nFit1Reac\_**  
    # of reactions with FIT1 fits
- static int **TC\_nExcIReac\_**  
    # of reactions with EXCI
- static int **TC\_nMomeReac\_**  
    # of reactions with MOME
- static int **TC\_nXsmiReac\_**  
    # of reactions with XSMI
- static int **TC\_nTdepReac\_**  
    # of reactions with TDEP
- static int **TC\_nRealNuReac\_**  
    # of reactions with non-int stoichiometric coefficients
- static int **TC\_nOrdReac\_**  
    # of reactions with arbitrary order
- static char \* **TC\_sNames\_**  
    species names, name of species *i* stored at LENGTHOFSPECNAME\*i
- static char \* **TC\_eNames\_**  
    species names, name of species *i* stored at LENGTHOFELEMNAME\*i
- static double \* **TC\_sMass\_**  
    array of species molar masses
- static double \* **TC\_eMass\_**  
    array of element molar masses
- static int \* **TC\_elemcnt\_**  
    no. of atoms of element *j* in each species *i* at (*i*\*TC\_Nelem\_+*j*)
- static int \* **TC\_sCharge\_**  
    species electrical charges
- static int \* **TC\_sTfit\_**

*no. of temperature fits for thermodynamic properties*

- static int \* **TC\_sPhase\_**  
*species phase id*
- static double \* **TC\_Tlo\_**
- static double \* **TC\_Tmi\_**
- static double \* **TC\_Thi\_**
- static double \* **TC\_cpol\_**
- static int \* **TC\_sNion\_**
- static int \* **TC\_isRev\_**
- static int \* **TC\_reacNrp\_**
- static int \* **TC\_reacNreact\_**
- static int \* **TC\_reacNprod\_**
- static int \* **TC\_reacScoef\_**
- static int \* **TC\_reacNuki\_**
- static int \* **TC\_reacSidx\_**
- static double \* **TC\_reacNukiDbl\_**
- static int \* **TC\_reacRnu\_**
- static double \* **TC\_reacRealNuki\_**
- static int \* **TC\_reacRev\_**
- static double \* **TC\_reacArhenFor\_**
- static double \* **TC\_reacArhenRev\_**
- static int \* **TC\_reacPfai\_**
- static int \* **TC\_reacPtype\_**
- static int \* **TC\_reacPlohi\_**
- static int \* **TC\_reacPspec\_**
- static double \* **TC\_reacPpar\_**
- static int \* **TC\_reacTbdy\_**
- static int \* **TC\_reacTbno\_**
- static int \* **TC\_specTbdIdx\_**
- static double \* **TC\_specTbdEff\_**
- static int \* **TC\_reacAOnd\_**
- static int \* **TC\_specAOidx\_**
- static double \* **TC\_specAOval\_**
- static int \* **TC\_reachVIdx\_**
- static double \* **TC\_reachVPar\_**
- static double \* **TC\_kfor**
- static double \* **TC\_krev**
- static double \* **TC\_kforP**
- static double \* **TC\_krevP**
- static double \* **TC\_ropFor**
- static double \* **TC\_ropRev**
- static double \* **TC\_rop**

- static double \* **TC\_cpks**
- static double \* **TC\_hks**
- static double \* **TC\_gk**
- static double \* **TC\_gkp**
- static double \* **TC\_PrDer**
- static double \* **TC\_Crnd**
- static double \* **TC\_CrndDer**
- static double \* **TC\_dFFac**
- static double \* **TC\_omg**
- static double \* **TC\_omgP**
- static double \* **TC\_jacFull**
- static double \* **TC\_Xconc**
- static double \* **TC\_scalln**
- static double \* **TC\_Mconc**
- static int \* **TC\_sigNu**
- static int \* **TC\_NulJ**
- static double \* **TC\_sigRealNu**
- static double \* **TC\_RealNuJ**
- static double \* **qfr**
- static double **TC\_reltol**
- static double **TC\_abstol**
- static double **TC\_rhoref\_**
- static double **TC\_pref\_**
- static double **TC\_Tref\_**
- static double **TC\_Wref\_**
- static double **TC\_Daref\_**
- static double **TC\_omgref\_**
- static double **TC\_cpref\_**
- static double **TC\_href\_**
- static double **TC\_timref\_**
- static int **TC\_isInit\_**
- static int **TC\_tab\_**
- static int **TC\_nonDim\_**
- static int **TC\_RVset\_**
- static int **TC\_Ntab\_**
- static double **TC\_deiT\_**
- static double **TC\_odelT\_**
- static double \* **TC\_cptab**
- static double \* **TC\_cpPtab**
- static double \* **TC\_htab**
- static double \* **TC\_gktab**
- static double \* **TC\_gkPtab**
- static double \* **TC\_kfortab**

- static double \* **TC\_krevtab**
- static double \* **TC\_kforPtab**
- static double \* **TC\_krevPtab**
- static double **TC\_pressure\_**
- static double **TC\_prescgs\_**
- static double **TC\_Runiv\_**
- static double **TC\_Rcal\_**
- static double **TC\_Rcgs\_**
- static int **TC\_ArhenForChg\_**
- static int **TC\_ArhenRevChg\_**
- static double \* **TC\_reacArhenForSave\_**
- static double \* **TC\_reacArhenRevSave\_**
- static double \* **TC\_kc\_coeff**
- static int **TC\_initRemoved**
- static int **TC\_NreactBackup\_**
- static int **TC\_NrevBackup\_**
- static int **TC\_NfalBackup\_**
- static int **TC\_NthbBackup\_**
- static int **TC\_nRealNuReacBackup\_**
- static int **TC\_nOrdReacBackup\_**
- static int \* **TC\_isRevBackup\_**
- static int \* **TC\_reacNrpBackup\_**
- static int \* **TC\_reacNreacBackup\_**
- static int \* **TC\_reacNprodBackup\_**
- static int \* **TC\_reacNukiBackup\_**
- static int \* **TC\_reacSidxBackup\_**
- static int \* **TC\_reacScoefBackup\_**
- static double \* **TC\_reacArhenForBackup\_**
- static double \* **TC\_reacArhenRevBackup\_**
- static double \* **TC\_reacNukiDblBackup\_**
- static int \* **TC\_reacPfalBackup\_**
- static int \* **TC\_reacPtypeBackup\_**
- static int \* **TC\_reacPlohiBackup\_**
- static int \* **TC\_reacPspecBackup\_**
- static int \* **TC\_reacTbdyBackup\_**
- static int \* **TC\_reacTbnoBackup\_**
- static int \* **TC\_specTbdIdxBackup\_**
- static double \* **TC\_reacPparBackup\_**
- static double \* **TC\_specTbdEffBackup\_**
- static int \* **TC\_reacRnuBackup\_**
- static int \* **TC\_reacAOrdBackup\_**
- static int \* **TC\_specAOidxBackup\_**
- static double \* **TC\_reacRealNukiBackup\_**

- static double \* **TC\_sigRealNuBackup**
- static double \* **TC\_RealNuJBackup**
- static double \* **TC\_specAOvalBackup\_**
- static double \* **TC\_kc\_coeffBackup**
- static int \* **TC\_sigNuBackup**
- static int \* **TC\_NuJBackup**

### 7.3.1 Detailed Description

Definitions of variables names used by the library. #

### 7.3.2 Function Documentation

#### 7.3.2.1 void TC\_errorINI ( FILE \* *errfile*, char const \* *msg* )

Outputs error messages generated by TC\_initChem.

##### Parameters

<i>errfile</i>	: file pointer for output
<i>msg</i>	: error message

Referenced by TC\_initChem().

#### 7.3.2.2 void TC\_errorMSG ( int *msgID*, char const \* *func*, int *var1*, int *var2* )

Outputs error messages for the library, then exits the execution.

##### Parameters

<i>msgID</i>	: message ID
<i>func</i>	: name of function calling this error function
<i>var1</i>	: value #1 to be printed in the message
<i>var2</i>	: value #2 to be printed in the message

Referenced by TC\_getCpSpecMI(), TC\_getCpSpecMs(), TC\_getHspecMI(), TC\_getHspecMs(), TC\_getJacRPTYN(), TC\_getJacRPTYNanl(), TC\_getJacRPTYNnum(), TC\_getJacTYN(), TC\_getJacTYNanl(), TC\_getJacTYNm1(), TC\_getJacTYNm1anl(), TC\_getMI2CpMixMI(), TC\_getMI2HmixMI(), TC\_getMs2CpMixMs(), TC\_getMs2CvMixMs(), TC\_getMs2HmixMs(), TC\_getRfrb(), TC\_getRhoMixMI(), TC\_getRhoMixMs(), TC\_getRops(), TC\_getSrc(), TC\_getSrcCons(), TC\_getStoiCoef(), TC\_getStoiCoefReac(), TC\_getTmixMI(), TC\_getTmixMs(), TC\_getTXC2RRml(), TC\_getTXC2RRms(), TC\_getTY2RRml(), TC\_getTY2RRms(), TCDND\_getCpSpecMI(), TCDND\_getCp-

SpecMs(), TCDND\_getHspecMI(), TCDND\_getHspecMs(), TCDND\_getJacTYN(), TCDND\_getJacTYNanl(), TCDND\_getJacTYNm1(), TCDND\_getJacTYNm1anl(), TCDND\_getMI2CpMixMI(), TCDND\_getMI2HmixMI(), TCDND\_getMs2CpMixMs(), TCDND\_getMs2CvMixMs(), TCDND\_getMs2HmixMs(), TCDND\_getRhoMixMI(), TCDND\_getRhoMixMs(), TCDND\_getSrc(), TCDND\_getSrcCons(), TCDND\_getTmixMI(), TCDND\_getTmixMs(), TCDND\_getTXC2RRml(), TCDND\_getTXC2RRms(), TCDND\_getTY2RRml(), and TCDND\_getTY2RRms().

### 7.3.2.3 int TC\_getReacRates ( double \* scal, int Nvars, double \* omega )

Returns molar reaction rates,  $\dot{\omega}_i$ , based on T and molar concentrations XC's (semi-private function)

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles (( $T, XC_1, XC_2, \dots, XC_N$ ): temperature T [K], molar concentrations XC [ $kmol/m^3$ ])
<i>Nvars</i>	: no. of variables $N_{vars} = N_{spec} + 1$

#### Returns

*omega* : array of  $N_{spec}$  molar reaction rates  $\dot{\omega}_i$  [ $kmol/(m^3 \cdot s)$ ]

References TC\_maxSpecInReac\_, TC\_Nreac\_, TC\_nRealNuReac\_, and TC\_Nspec\_.

Referenced by TC\_getTXC2RRml(), TC\_getTXC2RRms(), TC\_getTY2RRml(), and TC\_getTY2RRms().

## 7.4 TC\_init.c File Reference

Initialize chemical library.

### Functions

- int [TC\\_initChem](#) (char \*mechfile, char \*thermofile, int tab, double delT)
 

*Initialize library.*
- void [TC\\_setRefVal](#) (double rhoref, double pref, double Tref, double Wref, double Dref, double omgref, double cpref, double href, double timref)
 

*Set reference values to the library.*
- void [TC\\_setNonDim](#) ()
 

*Set library to function in non-dimensional mode.*
- void [TC\\_setDim](#) ()

- Set library to function in dimensional mode (default)
- void **TC\_setThermoPres** (double pressure)
 

Send thermodynamic pressure to the library.
- int **TC\_makeSpace** ()
 

Allocate internal work arrays for the library. Should not be called by external functions.
- int **TC\_createTables** (double delT)
 

Create tables for temperature dependent terms. Should not be called by external functions.
- void **TC\_errorMSG** (int msgID, char const \*func, int var1, int var2)
 

Outputs error messages for the library, then exits the execution.
- void **TC\_errorINI** (FILE \*errfile, char const \*msg)
 

Outputs error messages generated by TC\_initChem.

#### 7.4.1 Detailed Description

Initialize chemical library.

#### 7.4.2 Function Documentation

##### 7.4.2.1 void **TC\_errorINI** ( FILE \* *errfile*, char const \* *msg* )

Outputs error messages generated by TC\_initChem.

###### Parameters

<i>errfile</i>	: file pointer for output
<i>msg</i>	: error message

Referenced by TC\_initChem().

##### 7.4.2.2 void **TC\_errorMSG** ( int *msgID*, char const \* *func*, int *var1*, int *var2* )

Outputs error messages for the library, then exits the execution.

###### Parameters

<i>msgID</i>	: message ID
<i>func</i>	: name of function calling this error function
<i>var1</i>	: value #1 to be printed in the message
<i>var2</i>	: value #2 to be printed in the message

Referenced by `TC_getCpSpecMI()`, `TC_getCpSpecMs()`, `TC_getHspecMI()`, `TC_getHspecMs()`, `TC_getJacRPTYN()`, `TC_getJacRPTYNani()`, `TC_getJacRPTYNnum()`, `TC_getJacTYN()`, `TC_getJacTYNani()`, `TC_getJacTYNm1()`, `TC_getJacTYNm1ani()`, `TC_getMI2CpMixMI()`, `TC_getMI2HmixMI()`, `TC_getMs2CpMixMs()`, `TC_getMs2CvMixMs()`, `TC_getMs2HmixMs()`, `TC_getRfrb()`, `TC_getRhoMixMI()`, `TC_getRhoMixMs()`, `TC_getRops()`, `TC_getSrc()`, `TC_getSrcCons()`, `TC_getStoiCoef()`, `TC_getStoiCoefReac()`, `TC_getTmixMI()`, `TC_getTmixMs()`, `TC_getTXC2RRml()`, `TC_getTXC2RRrms()`, `TC_getTY2RRml()`, `TC_getTY2RRrms()`, `TCDND_getCpSpecMI()`, `TCDND_getCpSpecMs()`, `TCDND_getHspecMI()`, `TCDND_getHspecMs()`, `TCDND_getJacTYN()`, `TCDND_getJacTYNani()`, `TCDND_getJacTYNm1()`, `TCDND_getJacTYNm1ani()`, `TCDND_getMI2CpMixMI()`, `TCDND_getMI2HmixMI()`, `TCDND_getMs2CpMixMs()`, `TCDND_getMs2CvMixMs()`, `TCDND_getMs2HmixMs()`, `TCDND_getRhoMixMI()`, `TCDND_getRhoMixMs()`, `TCDND_getSrc()`, `TCDND_getSrcCons()`, `TCDND_getTmixMI()`, `TCDND_getTmixMs()`, `TCDND_getTXC2RRml()`, `TCDND_getTXC2RRrms()`, `TCDND_getTY2RRml()`, and `TCDND_getTY2RRrms()`.

## 7.5 TC\_interface.h File Reference

Header file to be included in user's code. Contains function definitions.

```
#include "copyright.h"
```

### Defines

- `#define TCSMALL 1.e-30`

### Functions

- int `TC_chgArhenFor` (int ireac, int ipos, double newval)  
*Change parameters for forward rate constants.*
- int `TC_chgArhenRev` (int ireac, int ipos, double newval)  
*Change parameters for reverse rate constants.*
- int `TC_chgArhenForBack` (int ireac, int ipos)  
*Reverse changes for forward rate constants' parameters.*
- int `TC_chgArhenRevBack` (int ireac, int ipos)  
*Reverse changes for reverse rate constants' parameters.*
- int `TC_getArhenRev` (int ireac, int ipos, double \*val)  
*Return current value of the Arrhenius parameters for reverse rate constants. Return -1 if no data available, otherwise return 0 and store value in val.*
- int `TC_getArhenFor` (int ireac, int ipos, double \*val)

- Return current value of the Arrhenius parameters for forward rate constants. Return -1 if no data available, otherwise return 0 and store value in val.*
- void **TC\_reset ()**

*Frees all memory and sets variables to 0 so that TC\_initChem can be called again without a memory leak. Not designed for use with tables.*
  - void **TC\_removeReaction (int \*reacArr, int numRemoveReacs, int revOnly)**

*Removes a reaction from the mechanism. Not designed for use with tables.*
  - void **TC\_restoreReactions ()**

*Restores reaction mechanism to original state. Any changes from TC\_chgArhenFor and TC\_chgArhenRev are also reset.*
  - int **TC\_initChem (char \*mechfile, char \*thermofile, int tab, double delT)**

*Initialize library.*
  - void **TC\_setRefVal (double rhoref, double pref, double Tref, double Wref, double Dref, double omgref, double cpref, double href, double timref)**

*Set reference values to the library.*
  - void **TC\_setNonDim ()**

*Set library to function in non-dimensional mode.*
  - void **TC\_setDim ()**

*Set library to function in dimensional mode (default)*
  - void **TC\_setThermoPres (double pressure)**

*Send thermodynamic pressure to the library.*
  - int **TC\_getNspec ()**

*Returns no. of species  $N_{spec}$*
  - int **TC\_getNelem ()**

*Returns no. of elements  $N_{elem}$*
  - int **TC\_getNvars ()**

*Returns no. of variables ( $N_{spec} + 1$ )*
  - double **TC\_getThermoPres ()**
  - int **TC\_getSnames (int Nspec, char \*snames)**

*Returns species names.*
  - int **TC\_getSpos (const char \*sname, const int slen)**

*Returns position a species in the list of species.*
  - int **TC\_getSmass (int Nspec, double \*Wi)**

*Returns species molar weights.*
  - int **TC\_getSnameLen ()**

*Returns length of species names.*
  - int **TC\_getNreac ()**

*Returns number of reactions  $N_{reac}$ .*
  - int **TC\_getStoicCoef (int Nspec, int Nreac, double \*stoicoef)**

*Returns stoichiometric coefficients' matrix. The stoichiometric coefficient for species "j" in reaction "i" is stored at position  $i \cdot N_{spec} + j$ . It assumes that stoicoef was dimensioned to at least  $N_{reac} \cdot N_{spec}$ .*

- int [TC\\_getStoCoefReac](#) (int Nspec, int Nreac, int ireac, int idx, double \*stoicoef)

*Returns stoichiometric coefficients' array for reaction 'ireac' for either reactants (idx=0) or products (idx=1) The stoichiometric coefficient for species "j" in reaction "ireac" is stored at position  $j$ . It assumes that stoicoef was dimensioned to at least  $N_{spec}$ .*

- int [TCDND\\_getTY2RRml](#) (double \*scal, int Nvars, double \*omega)

*Returns non-dimensional molar reaction rates,  $\dot{\omega}_i \cdot t_{ref} \frac{W_{ref}}{P_{ref}}$ , based on T and Y's.*

- int [TC\\_getTY2RRml](#) (double \*scal, int Nvars, double \*omega)

*Returns molar reaction rates,  $\dot{\omega}_i$ , based on T and Y's.*

- int [TCDND\\_getTY2RRms](#) (double \*scal, int Nvars, double \*omega)

*Returns non-dimensional mass reaction rates based on T and Y's.*

- int [TC\\_getTY2RRms](#) (double \*scal, int Nvars, double \*omega)

*Returns mass reaction rates based on T and Y's.*

- int [TCDND\\_getTxC2RRml](#) (double \*scal, int Nvars, double \*omega)

*Returns non-dimensional molar reaction rates based on temperature T and molar concentrations XC.*

- int [TC\\_getTxC2RRml](#) (double \*scal, int Nvars, double \*omega)

*Returns molar reaction rates based on temperature T and molar concentrations XC.*

- int [TCDND\\_getTxC2RRms](#) (double \*scal, int Nvars, double \*omega)

*Returns non-dimensional mass reaction rates based on T and molar concentrations.*

- int [TC\\_getTxC2RRms](#) (double \*scal, int Nvars, double \*omega)

*Returns mass reaction rates based on T and molar concentrations.*

- int [TC\\_getRops](#) (double \*scal, int Nvars, double \*datarop)

*Returns rate-of-progress variables based on temperature T and species mass fractions Y's.*

- int [TC\\_getRfrb](#) (double \*scal, int Nvars, double \*datarop)

*Returns forward and reverse rate-of-progress variables based on T and Y's.*

- int [TCDND\\_getRhoMixMs](#) (double \*scal, int Nvars, double \*rhomix)

*Computes density based on temperature and species mass fractions using the equation of state. Input temperature is normalized, output density also normalized before exit.*

- int [TC\\_getRhoMixMs](#) (double \*scal, int Nvars, double \*rhomix)

*Computes density based on temperature and species mass fractions using the equation of state.*

- int [TCDND\\_getRhoMixMI](#) (double \*scal, int Nvars, double \*rhomix)

*Computes density based on temperature and species mole fractions using the equation of state. Input temperature is normalized, output density also normalized before exit.*

- int [TC\\_getRhoMixMI](#) (double \*scal, int Nvars, double \*rhomix)

- Computes density based on temperature and species mole fractions using the equation of state.*
- int [TCDND\\_getTmixMs](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mass fractions using the equation of state. Input density is normalized, output temperature also normalized before exit.*
  - int [TC\\_getTmixMs](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mass fractions using the equation of state.*
  - int [TCDND\\_getTmixMI](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mole fractions using the equation of state. Input density is normalized, output temperature also normalized before exit.*
  - int [TC\\_getTmixMI](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mole fractions using the equation of state.*
  - int [TCDND\\_getMs2CpMixMs](#) (double \*scal, int Nvars, double \*cpmix)  
*Computes mixture specific heat at constant pressure based on temperature and species mass fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
  - int [TC\\_getMs2CpMixMs](#) (double \*scal, int Nvars, double \*cpmix)  
*Computes mixture specific heat at constant pressure based on temperature and species mass fractions.*
  - int [TCDND\\_getMs2CvMixMs](#) (double \*scal, int Nvars, double \*cvmix)  
*Computes mixture specific heat at constant volume based on temperature and species mass fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
  - int [TC\\_getMs2CvMixMs](#) (double \*scal, int Nvars, double \*cvmix)  
*Computes mixture specific heat at constant volume based on temperature and species mass fractions.*
  - int [TCDND\\_getMI2CpMixMI](#) (double \*scal, int Nvars, double \*cpmix)  
*Computes mixture heat capacity at constant pressure based on temperature and species mole fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
  - int [TC\\_getMI2CpMixMI](#) (double \*scal, int Nvars, double \*cpmix)  
*Computes mixture specific heat at constant pressure based on temperature and species mole fractions.*
  - int [TCDND\\_getCpSpecMs](#) (double t, int Nspec, double \*cpi)  
*Computes species specific heat at constant pressure based on temperature. Input temperature is normalized, output specific heats are also normalized before exit.*
  - int [TC\\_getCpSpecMs](#) (double t, int Nspec, double \*cpi)  
*Computes species specific heat at constant pressure based on temperature.*
  - int [TCDND\\_getCpSpecMI](#) (double t, int Nspec, double \*cpi)

*Computes species heat capacities at constant pressure based on temperature. Input temperature is normalized, output heat capacities are also normalized before exit.*

- int [TC\\_getCpSpecMI](#) (double t, int Nspec, double \*cpi)

*Computes species heat capacities at constant pressure based on temperature.*

- int [TCDND\\_getMs2HmixMs](#) (double \*scal, int Nvars, double \*hmix)

*Computes mixture specific enthalpy based on temperature and species mass fractions. Input temperature is normalized, output enthalpy is normalized before exit.*

- int [TC\\_getMs2HmixMs](#) (double \*scal, int Nvars, double \*hmix)

*Computes mixture specific enthalpy based on temperature and species mass fractions.*

- int [TCDND\\_getMI2HmixMI](#) (double \*scal, int Nvars, double \*hmix)

*Computes mixture molar enthalpy based on temperature and species mole fractions. Input temperature is normalized, output enthalpy is normalized before exit.*

- int [TC\\_getMI2HmixMI](#) (double \*scal, int Nvars, double \*hmix)

*Computes mixture molar enthalpy based on temperature and species mole fractions.*

- int [TCDND\\_getHspecMs](#) (double t, int Nspec, double \*hi)

*Computes species specific enthalpies based on temperature. Input temperature is normalized, output enthalpies are also normalized before exit.*

- int [TC\\_getHspecMs](#) (double t, int Nspec, double \*hi)

*Computes species specific enthalpies based on temperature.*

- int [TCDND\\_getHspecMI](#) (double t, int Nspec, double \*hi)

*Computes species molar enthalpies based on temperature. Input temperature is normalized, output enthalpies are also normalized before exit.*

- int [TC\\_getHspecMI](#) (double t, int Nspec, double \*hi)

*Computes species molar enthalpies based on temperature.*

- int [TCDND\\_getMs2Cc](#) (double \*scal, int Nvars, double \*concX)

*Computes molar concentrations based on temperature and species mass fractions. Input temperature is normalized, output concentrations are also normalized before exit.*

$$\overline{[X_k]} = [X_k] \cdot \frac{W_{ref}}{\rho_{ref}} = Y_k \cdot \frac{\rho}{W_k} \cdot \frac{W_{ref}}{\rho_{ref}}$$

- int [TC\\_getMs2Cc](#) (double \*scal, int Nvars, double \*concX)

*Computes molar concentrations based on temperature and species mass fractions.*

$$[X_k] = Y_k \cdot \rho / W_k$$

- int [TCDND\\_getMI2Ms](#) (double \*Xspec, int Nspec, double \*Yspec)

*Transforms mole fractions to mass fractions (same as [TC\\_getMI2Ms\(\)](#)).*

$$Y_k = X_k \cdot W_k / W_{mix}$$

- int [TC\\_getMI2Ms](#) (double \*Xspec, int Nspec, double \*Yspec)

*Transforms mole fractions to mass fractions.*

$$Y_k = X_k \cdot W_k / W_{mix}$$

- int [TCDND\\_getMs2MI](#) (double \*Yspec, int Nspec, double \*Xspec)

*Transforms mass fractions to mole fractions (same as [TC\\_getMs2MI\(\)](#))*

$$X_k = Y_k \cdot W_{mix} / W_k$$

- int [TC\\_getMs2MI](#) (double \*Yspec, int Nspec, double \*Xspec)

*Transforms mass fractions to mole fractions.*

$$X_k = Y_k \cdot W_{mix} / W_k$$

- int [TCDND\\_getMs2Wmix](#) (double \*Yspec, int Nspec, double \*Wmix)

*Computes mixture molecular weight based on species mass fractions. The molecular weight ([kg/kmol]=[g/mol]) is normalized before output.*

$$\bar{W}_{mix} = \frac{W_{mix}}{W_{ref}} = \frac{1}{W_{ref}} \left( \sum_{k=1}^{N_{spec}} Y_k / W_k \right)^{-1}$$

- int [TC\\_getMs2Wmix](#) (double \*Yspec, int Nspec, double \*Wmix)

*Computes mixture molecular weight based on species mass fractions.*

$$W_{mix} = \left( \sum_{k=1}^{N_{spec}} Y_k / W_k \right)^{-1}$$

- int [TCDND\\_getMI2Wmix](#) (double \*Xspec, int Nspec, double \*Wmix)

*Computes mixture molecular weight based on species mole fractions. The molecular weight ([kg/kmol]=[g/mol]) is normalized before output.*

$$\bar{W}_{mix} = \frac{W_{mix}}{W_{ref}} = \frac{1}{W_{ref}} \sum_{k=1}^{N_{spec}} X_k W_k$$

- int [TC\\_getMI2Wmix](#) (double \*Xspec, int Nspec, double \*Wmix)

*Computes mixture molecular weight based on species mole fractions.*

$$W_{mix} = \sum_{k=1}^{N_{spec}} X_k W_k$$

- int [TCDND\\_getSrc](#) (double \*scal, int Nvars, double \*omega)

*Returns dimensional/non-dimensional source term for*

$$\frac{\partial T}{\partial t} = \omega_0, \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on temperature T and species mass fractions Y's.*

- int [TC\\_getSrc](#) (double \*scal, int Nvars, double \*omega)

*Returns source term for*

$$\frac{\partial T}{\partial t} = \omega_0, \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on temperature T and species mass fractions Y's.*

- int [TCDND\\_getSrcCons](#) (double \*scal, int Nvars, double \*omega)

*Returns source term (dimensional/non-dimensional) for*

$$\frac{\partial \rho}{\partial t} = \omega_0, \rho \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on  $\rho$  and Y's.*

- int [TC\\_getSrcCons](#) (double \*scal, int Nvars, double \*omega)

*Returns source term for*

$$\frac{\partial \rho}{\partial t} = \omega_0, \rho \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on  $\rho$  and Y's.*

- int [TCDND\\_getJacTYNm1anl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on temperature T and species mass fractions Y's.*

- int [TC\\_getJacTYNm1anl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on T and Y's.*

- int [TCDND\\_getJacTYNm1](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical or numerical) Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on temperature T and species mass fractions Y's.*

- int [TC\\_getJacTYNm1](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical or numerical) Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on T and Y's.*

- int [TCDND\\_getJacTYNanl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.*

- int [TC\\_getJacTYNanl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.*

- int [TCDND\\_getJacTYN](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical or numerical) Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.*

- int [TC\\_getJacTYN](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical or numerical) Jacobian for the system ( $T, Y_1, Y_2, \dots, Y_N$ ) based on  $T$  and  $Y$ 's.*

- int [TC\\_getJacRPTYN](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical) Jacobian for the system ( $\rho, P, T, Y_1, Y_2, \dots, Y_N$ ) based on  $T$  and  $Y$ 's.*

- int [TC\\_getJacRPTYNanl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian for the system ( $\rho, P, T, Y_1, Y_2, \dots, Y_N$ ) based on  $T$  and  $Y$ 's.*

- int [TC\\_getJacRPTYNnum](#) (double \*scal, int Nspec, double \*jac)

*Computes numerical Jacobian for the system ( $\rho, P, T, Y_1, Y_2, \dots, Y_N$ ) based on  $T$  and  $Y$ 's.*

### 7.5.1 Detailed Description

Header file to be included in user's code. Contains function definitions.

### 7.5.2 Function Documentation

#### 7.5.2.1 int TC\_chgArhenFor ( int ireac, int ipos, double newval )

Change parameters for forward rate constants.

##### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of parameter to be changed (0) pre-exponential factor (1) temperature exponent, (2) activation energy
<i>newval</i>	: new parameter value

References [TC\\_Nreac\\_](#).

#### 7.5.2.2 int TC\_chgArhenForBack ( int ireac, int ipos )

Reverse changes for forward rate constants' parameters.

##### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of parameter to be changed (0) pre-exponential factor (1) temperature exponent, (2) activation energy

References [TC\\_Nreac\\_](#).

### 7.5.2.3 int TC\_chgArhenRev ( int *ireac*, int *ipos*, double *newval* )

Change parameters for reverse rate constants.

#### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of parameter to be changed (0) pre-exponential factor (1) temperature exponent, (2) activation energy
<i>newval</i>	: new parameter value

References TC\_nRevReac\_.

### 7.5.2.4 int TC\_chgArhenRevBack ( int *ireac*, int *ipos* )

Reverse changes for reverse rate constants' parameters.

#### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of parameter to be changed (0) pre-exponential factor (1) temperature exponent, (2) activation energy

References TC\_nRevReac\_.

### 7.5.2.5 int TC\_getArhenFor ( int *ireac*, int *ipos*, double \* *val* )

Return current value of the Arrhenius parameters for forward rate constants. Return -1 if no data available, otherwise return 0 and store value in val.

#### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of Arrhenius parameter (0) pre-exponential factor (1) temperature exponent, (2) activation energy
* <i>val</i>	: value of Arrhenius parameter

References TC\_Nreac\_.

### 7.5.2.6 int TC\_getArhenRev ( int *ireac*, int *ipos*, double \* *val* )

Return current value of the Arrhenius parameters for reverse rate constants. Return -1 if no data available, otherwise return 0 and store value in val.

**Parameters**

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of Arrhenius parameter (0) pre-exponential factor (1) temperature exponent, (2) activation energy
<i>*val</i>	: value of Arrhenius parameter

References TC\_nRevReac\_.

**7.5.2.7 int TC\_getMI2Ms ( double \* Xspec, int Nspec, double \* Yspec )**

Transforms mole fractions to mass fractions.

$$Y_k = X_k \cdot W_k / W_{mix}$$

**Parameters**

<i>Xspec</i>	: array of <i>Nspec</i> mole fractions
<i>Nspec</i>	: no. of species

**Returns***Yspec* : array of *Nspec* mass fractions

References TC\_getMI2Wmix(), TC\_Nspec\_, and TC\_sMass\_.

Referenced by TCDND\_getMI2Ms().

**7.5.2.8 int TC\_getMI2Wmix ( double \* Xspec, int Nspec, double \* Wmix )**

Computes mixture molecular weight based on species mole fractions.

$$W_{mix} = \sum_{k=1}^{N_{spec}} X_k W_k$$

**Parameters**

<i>Xspec</i>	: array of <i>Nspec</i> mole fractions
<i>Nspec</i>	: no. of species

**Returns**

`Wmix` : pointer to mixture molecular weight [kg/kmol]=[g/mol]

References `TC_Nspec_`, and `TC_sMass_`.

Referenced by `TC_getMl2Ms()`.

**7.5.2.9 int TC\_getMs2Cc ( double \* *scal*, int *Nvars*, double \* *concX* )**

Computes molar concentrations based on temperature and species mass fractions.

$$[X_k] = Y_k \cdot \rho / W_k$$

**Parameters**

<code>scal</code>	: array of <code>Nspec +1</code> doubles ( <code>T, Y<sub>1</sub>, Y<sub>2</sub>, ..., Y<sub>Nspec</sub></code> ), temperature <code>T</code> [K], mass fractions <code>Y</code> []
<code>Nvars</code>	: no. of variables = <code>Nspec +1</code>

**Returns**

`concX` : array of doubles containing species molar concentrations [kmol/m<sup>3</sup> ]

References `TC_getRhoMixMs()`, `TC_Nspec_`, `TC_Nvars_`, and `TC_sMass_`.

Referenced by `TC_getJacRPTYNani()`, `TC_getJacRPTYNnum()`, `TC_getRfrb()`, `TC_getRops()`, `TC_getTY2RRml()`, `TC_getTY2RRms()`, and `TCDND_getMs2Cc()`.

**7.5.2.10 int TC\_getMs2MI ( double \* *Yspec*, int *Nspec*, double \* *Xspec* )**

Transforms mass fractions to mole fractions.

$$X_k = Y_k \cdot W_{mix} / W_k$$

**Parameters**

<code>Yspec</code>	: array of <code>Nspec</code> mass fractions
<code>Nspec</code>	: no. of species

**Returns**

Xspec : array of Nspec mole fractions

References TC\_getMs2Wmix(), TC\_Nspec\_, and TC\_sMass\_.

Referenced by TCDND\_getMs2MI().

#### 7.5.2.11 int TC\_getMs2Wmix ( double \* Yspec, int Nspec, double \* Wmix )

Computes mixture molecular weight based on species mass fractions.

$$W_{mix} = \left( \sum_{k=1}^{N_{spec}} Y_k / W_k \right)^{-1}$$

**Parameters**

<i>Yspec</i>	: array of Nspec mass fractions
<i>Nspec</i>	: no. of species

**Returns**

Wmix : pointer to mixture molecular weight [kg/kmol]=[g/mol]

References TC\_Nspec\_, and TC\_sMass\_.

Referenced by TC\_getJacTYN(), TC\_getJacTYNanl(), TC\_getJacTYNm1(), TC\_getJacTYNm1anl(), TC\_getMs2MI(), TC\_getSrcCons(), TCDND\_getMI2Wmix(), and TCDND\_getMs2Wmix().

#### 7.5.2.12 int TC\_getRfrb ( double \* scal, int Nvars, double \* datarop )

Returns forward and reverse rate-of-progress variables based on T and Y's.

**Parameters**

<i>scal</i>	: array of Nspec+1 doubles (T,Y_1,Y_2,...,Y_N) temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

datarop : array of Nreac forward rate-of-progress variables and Nreac reverse rate-of-progress variables [kmol/(m3.s)]

References `TC_errorMSG()`, `TC_getMs2Cc()`, `TC_Nreac_`, `TC_Nspec_`, and `TC_Nvars_`.

#### 7.5.2.13 int `TC_getRops` ( `double * scal`, `int Nvars`, `double * datarop` )

Returns rate-of-progress variables based on temperature T and species mass fractions Y's.

##### Parameters

<code>scal</code>	: array of <code>Nreac +1</code> doubles ( <code>T,Y_1,Y_2,...,Y_N</code> ) temperature <code>T [K]</code> , mass fractions <code>Y []</code>
<code>Nvars</code>	: no. of variables = <code>Nspec +1</code>

##### Returns

`datarop` : array of `Nreac` rate-of-progress variables [`kmol/(m3.s)`]

References `TC_errorMSG()`, `TC_getMs2Cc()`, `TC_Nreac_`, `TC_Nspec_`, and `TC_Nvars_`.

#### 7.5.2.14 int `TC_getSmass` ( `int Nspec`, `double * Wi` )

Returns species molar weights.

##### Parameters

<code>Nspec</code>	: no. of species
--------------------	------------------

##### Returns

`Wi` : array of species molar weights [`kg/kmol`]=[`g/mol`]

References `TC_Nspec_`, and `TC_sMass_`.

#### 7.5.2.15 int `TC_getSnames` ( `int Nspec`, `char * snames` )

Returns species names.

##### Parameters

<code>Nspec</code>	: no. of species
--------------------	------------------

**Returns**

snames: array of characters containing species names, each name is LENGTHOFSPECNAME characters

References LENGTHOFSPECNAME, TC\_Nspec\_, and TC\_sNames\_.

**7.5.2.16 int TC\_getSpos ( const char \* *sname*, const int *slen* )**

Returns position a species in the list of species.

**Parameters**

<i>sname</i>	: string containing the name of the species
<i>slen</i>	: length of species "sname" name

**Returns**

position of species sname in the list of species, 0...(Nspec -1)

References LENGTHOFSPECNAME, TC\_Nspec\_, and TC\_sNames\_.

**7.5.2.17 int TC\_getStoCoef ( int *Nspec*, int *Nreac*, double \* *stoicoef* )**

Returns stoichiometric coefficients' matrix. The stoichiometric coefficient for species "j" in reaction "i" is stored at position  $i \cdot N_{spec} + j$ . It assumes that stoicoef was dimentioned to at least  $N_{reac} \cdot N_{spec}$ .

**Parameters**

<i>Nspec</i>	: no. of species
<i>Nreac</i>	: no. of reactions

**Returns**

*stoicoef* : array of stoichiometric coefficients

References TC\_errorMSG(), TC\_maxSpecInReac\_, TC\_Nreac\_, TC\_nRealNuReac\_, and TC\_Nspec\_.

**7.5.2.18 int TC\_getStoCoefReac ( int *Nspec*, int *Nreac*, int *ireac*, int *idx*, double \* *stoicoef* )**

Returns stoichiometric coefficients' array for reaction 'ireac' for either reactants (idx=0) or products (idx=1) The stoichiometric coefficient for species "j" in reaction "ireac" is

stored at position  $j$ . It assumes that stoicoef was dimentioned to at least  $N_{spec}$ .

#### Parameters

$N_{spec}$	: no. of species
$N_{reac}$	: no. of reactions
$i_{reac}$	: reaction index
$idx$	: 0-reactants, 1-products

#### Returns

stoicoef : array of stoichiometric coefficients

References TC\_errorMSG(), TC\_maxSpecInReac\_, TC\_Nreac\_, TC\_nRealNuReac\_, and TC\_Nspec\_.

#### 7.5.2.19 int TC\_getTXC2RRml ( double \* scal, int Nvars, double \* omega )

Returns molar reaction rates based on temperature T and molar concentrations XC.

#### Parameters

$scal$	: array of $N_{spec} + 1$ doubles (T,XC_1,XC_2,...,XC_N) temperature T [K], molar concentrations XC [kmol/m3]
$N_{vars}$	: no. of variables = $N_{spec} + 1$

#### Returns

omega : array of  $N_{spec}$  (molar) reaction rates [kmol/(m3.s)]

References TC\_errorMSG(), TC\_getReacRates(), TC\_Nspec\_, and TC\_Nvars\_.

Referenced by TCDND\_getTXC2RRml().

#### 7.5.2.20 int TC\_getTXC2RRms ( double \* scal, int Nvars, double \* omega )

Returns mass reaction rates based on T and molar concentrations.

#### Parameters

$scal$	: array of $N_{spec} + 1$ doubles (T,XC_1,XC_2,...,XC_N) temperature T [K], molar concentrations XC [kmol/m3]
$N_{vars}$	: no. of variables = $N_{spec} + 1$

**Returns**

`omega` : array of  $N_{spec}$  (mass) reaction rates [kg/(m<sup>3</sup>.s)]

References `TC_errorMSG()`, `TC_getReacRates()`, `TC_Nspec_`, `TC_Nvars_`, and `TC_sMass_`.

Referenced by `TC_getJacRPTYNnum()`, and `TCDND_getTXC2RRms()`.

#### 7.5.2.21 int `TC_getTY2RRml` ( `double * scal`, `int Nvars`, `double * omega` )

Returns molar reaction rates,  $\dot{\omega}_i$ , based on T and Y's.

**Parameters**

<code>scal</code>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_N$ ): temperature T [K], mass fractions Y []
<code>Nvars</code>	: no. of variables $N_{vars} = N_{spec} + 1$

**Returns**

`omega` : array of  $N_{spec}$  molar reaction rates  $\dot{\omega}_i$  [ $kmol/(m^3 \cdot s)$ ]

References `TC_errorMSG()`, `TC_getMs2Cc()`, `TC_getReacRates()`, `TC_Nspec_`, and `TC_Nvars_`.

Referenced by `TC_getSrcCons()`, and `TCDND_getTY2RRml()`.

#### 7.5.2.22 int `TC_getTY2RRms` ( `double * scal`, `int Nvars`, `double * omega` )

Returns mass reaction rates based on T and Y's.

**Parameters**

<code>scal</code>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_N$ ) temperature T [K], mass fractions Y []
<code>Nvars</code>	: no. of variables = $N_{spec} + 1$

**Returns**

`omega` : array of  $N_{spec}$  mass reaction rates [kg/(m<sup>3</sup>.s)]

References `TC_errorMSG()`, `TC_getMs2Cc()`, `TC_getReacRates()`, `TC_Nspec_`, `TC_Nvars_`, and `TC_sMass_`.

Referenced by `TC_getSrc()`, and `TCDND_getTY2RRms()`.

### 7.5.2.23 void TC\_removeReaction ( int \* *reacArr*, int *numRemoveReacs*, int *revOnly* )

Removes a reaction from the mechanism. Not designed for use with tables.

#### Parameters

<i>reacArr</i>	: 0-based reaction indices in ascending order.
<i>num-</i> <i>Remove-</i> <i>Reacs</i>	: length of rearArr array.
<i>revOnly</i>	: set to 1 to remove reverse only, 0 to remove forward and reverse.

References `TC_maxOrdPar_`, `TC_maxSpecInReac_`, `TC_maxTblInReac_`, `TC_nFallPar_`, `TC_nFallReac_`, `TC_nOrdReac_`, `TC_Nreac_`, `TC_nRealNuReac_`, `TC_nRevReac_`, `TC_Nspec_`, `TC_nThbReac_`, and `TC_removeReaction()`.

Referenced by `TC_removeReaction()`.

### 7.5.2.24 int TCDND\_getMI2Ms ( double \* *Xspec*, int *Nspec*, double \* *Yspec* )

Transforms mole fractions to mass fractions (same as [TC\\_getMI2Ms\(\)](#)).

$$Y_k = X_k \cdot W_k / W_{mix}$$

#### Parameters

<i>Xspec</i>	: array of <i>Nspec</i> mole fractions
<i>Nspec</i>	: no. of species

#### Returns

*Yspec* : array of *Nspec* mass fractions

References `TC_getMI2Ms()`, and `TC_Nspec_`.

### 7.5.2.25 int TCDND\_getMI2Wmix ( double \* *Xspec*, int *Nspec*, double \* *Wmix* )

Computes mixture molecular weight based on species mole fractions. The molecular weight ([kg/kmol]=[g/mol]) is normalized before output.

$$\bar{W}_{mix} = \frac{W_{mix}}{W_{ref}} = \frac{1}{W_{ref}} \sum_{k=1}^{N_{spec}} X_k W_k$$

**Parameters**

<i>Xspec</i>	: array of <i>Nspec</i> mole fractions
<i>Nspec</i>	: no. of species

**Returns**

*Wmix* : pointer to normalized mixture molecular weight

References [TC\\_getMs2Wmix\(\)](#), and [TC\\_Nspec\\_](#).

**7.5.2.26 int TCDND\_getMs2Cc ( double \* *scal*, int *Nvars*, double \* *concX* )**

Computes molar concentrations based on temperature and species mass fractions. - Input temperature is normalized, output concentrations are also normalized before exit.

$$\overline{[X_k]} = [X_k] \cdot \frac{W_{ref}}{\rho_{ref}} = Y_k \cdot \frac{\rho}{W_k} \cdot \frac{W_{ref}}{\rho_{ref}}$$

**Parameters**

<i>scal</i>	: array of <i>Nspec</i> +1 doubles ( <i>T</i> , <i>Y</i> <sub>1</sub> , <i>Y</i> <sub>2</sub> ..., <i>Y</i> <sub><i>Nspec</i></sub> ), temperature <i>T</i> [K], mass fractions <i>Y</i> []
<i>Nvars</i>	: no. of variables = <i>Nspec</i> +1

**Returns**

*concX* : array of doubles containing species molar concentrations [kmol/m<sup>3</sup> ]

References [TC\\_getMs2Cc\(\)](#), [TC\\_Nspec\\_](#), and [TC\\_Nvars\\_](#).

**7.5.2.27 int TCDND\_getMs2MI ( double \* *Yspec*, int *Nspec*, double \* *Xspec* )**

Transforms mass fractions to mole fractions (same as [TC\\_getMs2MI\(\)](#))

$$X_k = Y_k \cdot W_{mix}/W_k$$

**Parameters**

<i>Yspec</i>	: array of <i>Nspec</i> mass fractions
<i>Nspec</i>	: no. of species

**Returns**

Xspec : array of Nspec mole fractions

References TC\_getMs2MI(), and TC\_Nspec\_.

**7.5.2.28 int TCDND\_getMs2Wmix ( double \* Yspec, int Nspec, double \* Wmix )**

Computes mixture molecular weight based on species mass fractions. The molecular weight ([kg/kmol]=[g/mol]) is normalized before output.

$$\bar{W}_{mix} = \frac{W_{mix}}{W_{ref}} = \frac{1}{W_{ref}} \left( \sum_{k=1}^{N_{spec}} Y_k / W_k \right)^{-1}$$

**Parameters**

<i>Yspec</i>	: array of Nspec mass fractions
<i>Nspec</i>	: no. of species

**Returns**

Wmix : pointer to normalized mixture molecular weight

References TC\_getMs2Wmix(), and TC\_Nspec\_.

**7.5.2.29 int TCDND\_getTxC2RRml ( double \* scal, int Nvars, double \* omega )**

Returns non-dimensional molar reaction rates based on temperature T and molar concentrations XC.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,XC_1,XC_2,...,XC_N) temperature T [K], molar concentrations XC [kmol/m3] (but non-dimensional)
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*omega* : array of Nspec (molar) reaction rates [kmol/(m3.s)] (but non-dimensional)

References TC\_errorMSG(), TC\_getTxC2RRml(), TC\_Nspec\_, and TC\_Nvars\_.

---

**7.5.2.30 int TCDND\_getTxC2RRms ( double \* *scal*, int *Nvars*, double \* *omega* )**

Returns non-dimensional mass reaction rates based on T and molar concentrations.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,XC_1,XC_2,...,XC_N) temperature T [K], molar concentrations XC [kmol/m3] (but non-dimensional)
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*omega* : array of Nspec (mass) reaction rates [kg/(m3.s)] (but non-dimensional)

References TC\_errorMSG(), TC\_getTxC2RRms(), TC\_Nspec\_, and TC\_Nvars\_.

**7.5.2.31 int TCDND\_getTY2RRml ( double \* *scal*, int *Nvars*, double \* *omega* )**

Returns non-dimensional molar reaction rates,  $\dot{\omega}_i \cdot t_{ref} \frac{W_{ref}}{\rho_{ref}}$ , based on T and Y's.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,Y_1,Y_2,...,Y_N) temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*omega* : array of Nspec molar reaction rates [kmol/(m3.s)] (but non-dimensional)

References TC\_errorMSG(), TC\_getTY2RRml(), TC\_Nspec\_, and TC\_Nvars\_.

**7.5.2.32 int TCDND\_getTY2RRms ( double \* *scal*, int *Nvars*, double \* *omega* )**

Returns non-dimensional mass reaction rates based on T and Y's.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,Y_1,Y_2,...,Y_N) temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

omega : array of Nspec mass reaction rates [kg/(m<sup>3</sup>.s)] (but non-dimensional)

References TC\_errorMSG(), TC\_getTY2RRms(), TC\_Nspec\_, and TC\_Nvars\_.

## 7.6 TC\_kmodint.c File Reference

Collection of functions used to parse kinetic models from files.

```
#include <stdio.h> #include <stdlib.h> #include <math.h>
#include <string.h> #include <ctype.h> #include <assert.h>
#include "TC_params.h" #include "TC_kmodint.h"
```

### Functions

- int **TC\_kmodint\_** (char \*mechfile, int \*lmech, char \*thermofile, int \*lthrm)  
*Kinetic model interpreter.*
- void **setperiodictable** (elemtable \*periodictable, int \*Natoms, int iflag)  
*Read periodic table.*
- void **checkelemminlist** (char \*elemname, element \*listelem, int \*Nelem, int \*ipos)  
*Returns index of an element in the list of elements:*
- int **getelements** (char \*linein, char \*singleword, element \*\*listelemaddr, int \*Nelem, int \*Nelemax, int \*iread, int \*ierror)  
*Interprets a character string containing element names and possible their mass.*
- void **resetelemdata** (element \*currentelem)  
*Reset data for an element.*
- int **setelementmass** (element \*listelem, int \*Nelem, elemtable \*periodictable, int \*Natoms, int \*ierror)  
*Set the mass for all entries in the list of elements based on the values found in the periodic table.*
- int **getspecies** (char \*linein, char \*singleword, species \*\*listspeccaddr, int \*Nspecc, int \*Nspeccmax, int \*iread, int \*ierror)  
*Interprets a character string containing species names.*
- void **resetspeccdata** (species \*currentspecc)  
*Reset data for a species.*
- int **setspeccmass** (element \*listelem, int \*Nelem, species \*listspecc, int \*Nspecc, int \*ierror)  
*Set the mass for all entries in the list of elements based on the values found in the periodic table.*
- void **checkspecinlist** (char \*specname, species \*listspecc, int \*Nspecc, int \*ipos)

- int **checkthermo** (*species* \*listspec, int \*Nspec)
 

Returns position of a species in the list of species The index goes from 0 to (Nspec-1); if the species is not found the value of Nspec is returned.
- int **getthermo** (char \*linein, char \*singleword, FILE \*mechin, FILE \*thermoin, *element* \*listelem, int \*Nelem, *species* \*listspec, int \*Nspec, double \*Tglobal, int \*ithermo, int \*iread, int \*ierror)
 

Returns 1 if all species have thermodynamic properties set, 0 otherwise.
- int **getreactionline** (char \*linein, char \*singleword, *species* \*listspec, int \*Nspec, *reaction* \*listreac, int \*Nreac, int \*ierror)
 

Reads thermodynamic properties (NASA polynomials) from the mechanism input file or from a separate file.
- void **resetreacdata** (*reaction* \*currentreac, char \*aunits, char \*eunits)
 

Resets the current entry in the list of reactions.
- void **checkunits** (char \*linein, char \*singleword, char \*aunits, char \*eunits)
 

Sets units for the pre-exponential factor and for the activation energy.
- int **getreacauxl** (char \*linein, char \*singleword, *species* \*listspec, int \*Nspec, *reaction* \*listreac, int \*Nreac, int \*ierror)
 

Interprets a character string containing reaction description (equation + forward - Arrhenius parameters)
- int **getreactions** (char \*linein, char \*singleword, *species* \*listspec, int \*Nspec, *reaction* \*listreac, int \*Nreac, char \*aunits, char \*eunits, int \*ierror)
 

Interprets a character string containing reaction description (auxiliary information)
- int **verifyreac** (*element* \*listelem, int \*Nelem, *species* \*listspec, int \*Nspec, *reaction* \*listreac, int \*Nreac, int \*ierror)
 

Verifies correctness and completeness for all reactions in the list.
- int **rescalereac** (*reaction* \*listreac, int \*Nreac)
 

Verifies correctness and completeness for all reactions in the list.
- int **out\_formatted** (*element* \*listelem, int \*Nelem, *species* \*listspec, int \*Nspec, *reaction* \*listreac, int \*Nreac, char \*aunits, char \*eunits, FILE \*fileascii)
 

Outputs reaction data to ascii file.
- int **out\_unformatted** (*element* \*listelem, int \*Nelem, *species* \*listspec, int \*Nspec, *reaction* \*listreac, int \*Nreac, char \*aunits, char \*eunits, FILE \*filelist, int \*ierror)
 

Outputs reaction data to an unformatted ascii file.
- void **errormsg** (int ierror)
 

Outputs error messages.
- int **elimleads** (char \*linein)
 

Checks if a string of characters contains leading spaces Then shifts the string left over the leading spaces, and marks the remaining space at the right with null characters.
- int **elimends** (char \*linein)
 

Checks if a string of characters contains trailing spaces Marks all those positions with null characters.

- int **elimspace** (char \*linein)
 

*Eliminates space characters from a string.*
- int **elimcomm** (char \*linein)
 

*Eliminate comments: advances through a line of characters, determines the first occurrence of "!" (if any), then nulls out all the positions downstream (including the "!")*
- int **tab2space** (char \*linein)
 

*Replaces all horizontal tab, vertical tab, line feed, and carriage return characters in a line with spaces.*
- int **extractWordLeft** (char \*linein, char \*oneword)
 

*Extracts the left most word from a character string.*
- int **extractWordLeftauxline** (char \*linein, char \*oneword, char \*twoword, int \*inum, int \*ierror)
 

*Extracts two strings from a character strings.*
- int **extractWordLeftNoslash** (char \*linein, char \*oneword)
 

*The only difference between this method and "extractWordLeft" is the absence of "/" as delimiter.*
- int **extractWordRight** (char \*linein, char \*oneword)
 

*Extracts last word from a character strings: (1) assumes the word is separated from the rest of the string by at least a space; (2) the corresponding positions in the initial string are filled with null characters.*
- int **extractdouble** (char \*wordval, double \*dvalues, int \*inum, int \*ierror)
 

*Extracts a double number from a character string: (1) the number is assumed to be the left most word in the string; (2) words are separated by spaces.*
- void **wordtoupper** (char \*linein, char \*oneword, int Npos)
 

*Converts all letters in a character string to uppercase.*
- void **cleancharstring** (char \*linein, int \*len1)
 

*Performs various operations on a character strings (see explanations for individual methods)*
- int **charfixespc** (char \*singleword, int \*len1)
 

*Checks if all components of a character string are valid number characters (as described by the f or e formats)*
- int **checkstrnum** (char \*singleword, int \*len1, int \*ierror)
 

*Identifies the first position in the character string that does not correspond to a positive f format. (in other words, finds the first position that is not a digit or a decimal point)*
- int **kmodsum** (**element** \*listelem, int \*Nelem, **species** \*listspec, int \*Nspec, **reaction** \*listreac, int \*Nreact, int \*nlonEspec, int \*electrlIdx, int \*nlonSpec, int \*maxSpecInReact, int \*maxTbInReact, int \*maxOrdPar, int \*nFallPar, int \*maxTpRange, int \*nLtReact, int \*nRltReact, int \*nFallReact, int \*nThbReact, int \*nRevReact, int \*nHvReact, int \*nTdepReact, int \*nJanReact, int \*nFit1React, int \*nExcReact, int \*nMomeReact, int \*nXsmiReact, int \*nRealNuReact, int \*nOrdReact, int \*nNASAinter, int \*nCpCoef, int \*nNASAf, int \*nArhPar, int \*nLtPar, int \*nJanPar, int \*nFit1Par)

*kinetic model summary*

- int **out\_mathem** (**element** \*listelem, int \*Nelem, **species** \*listspec, int \*Nspec, **reaction** \*listreac, int \*Nreact, char \*aunits, char \*eunits)

*Outputs reaction data to ascii file.*

### 7.6.1 Detailed Description

Collection of functions used to parse kinetic models from files. TC\_kmodint - utility used to parse kinetic models -----

Usage: **TC\_kmodint\_(char \*mechfile,int \*lmech,char \*thermofile,int \*lthrm)**

- mechfile: file containing the kinetic model
- lmech: length of the character string above (introduced to enable passing of character strings from Fortran to C)
- thermofile: file containing thermodynamic properties (NASA polynomials)
- lmech: length of the character string thermofile (introduced to enable passing of character strings from Fortran to C)

Output:

- kmod.out - ascii file containing kinetic model info formatted for visual inspection
- kmod.list - ascii file containing unformatted data for tchem

**Brief description of kinetic model input format** ( For a detailed description of the kinetic model format and keywords see: Robert J. Kee, Fran M. Rupley, Ellen Meeks, and James A. Miller "CHEMKIN-III:A Fortran Chemical Kinetics Package for the Analysis of Gas-phase Chemical and Plasma Kinetics", Sandia Report, SAND96-8216, (1996) )

#### Elements :

- Number of elements is "unlimited"
- Elements not present in file periodictable.dat must be followed by their atomic weight, e.g. N+ /14.0010/
- Element names are one or two characters long
- Any duplicate listing of an element is ignored

#### Species :

- Number of species is "unlimited"

- Species need to be formed only of elements declared in the list of elements
- Species names are "LENGTHOFSPECNAME" characters long
- Any duplicate listing of a species is ignored
- A species can contain at most "NUMBEROFELEMINSPEC" distinct elements

**Thermodynamic data :**

- Data can be provided in the kinetic model file and/or the thermodynamic file;
- Currently, only NASA polynomials are accepted; two (2) temperature intervals
- Data needs to be provided for all species

**Reactions :**

- Number of reactions is "unlimited"
- Pre-exponential factor units MOLES or MOLECULES; default is MOLES
- Activation energy units: CAL/MOLE, KCAL/MOLE, JOULES/MOLE, KJOULES/-MOLE, KELVINS, eVOLTS ; default is CAL/MOLE. Units are converted to KELVINS if necessary; conversion factors are based on NIST data as of July 2007
- maximum number of reactants or products is "NSPECREACMAX"
- reactants and products are separated by "<=>" or "=" (reversible reactions) or "=>" (irreversible reactions)
- species are separated by "+"
- three Arrhenius parameters should be given for each reaction in the order : pre-exponential factor, temperature exponent, activation energy
- reaction lines that are too long can be split on several lines using the character "&" at the end of each line

**Auxiliary reaction info :**

- Auxiliary data needs to be provided immediately following the reaction to which it corresponds to
- Any keywords except DUPLICATE,MOME, and XSMI need to be followed by numerical values enclosed between "/"
- Duplicate reactions

**DUPLICATE**

- third-body efficiencies for reactions containing "+M" (not "(+M)" ) as a reactant and/or product:

speciesname /value/ the maximum number of third-body efficiencies is given by "NTHRDBMAX"

- pressure-dependent reaction are signaled by the inclusion of "(+M)" as a reactant and/or product or by the inclusion of a particular species, e.g. "(+H2)" as a reactant and/or product. Some of the following parameters are required to describe the pressure dependency:

**LOW** /value1 value2 value3/

**HIGH** /value1 value2 value3/

**TROE** /value1 value2 value3 value4/ (if value4 is omitted then the corresponding term is omitted in the corresponding Troe formulation)

**SRI** /value1 value2 value3 value4 value5/ (if value4 and value5 are omitted then value4=1.0, value5=0.0)

- Landau-Teller reactions

**LT** /value1 value2/ for the forward rate

**RLT** /value1 value2/ for the reverse rate. If REV is given then RLT is mandatory; if not then RLT is optional

- Additional rate fit expressions:

**JAN** /value1 value2 ... value9/

**FIT1** /value1 value2 value3 value4/

- Radiation wavelength for reactions containing HV as a reactant and/or product

**HV** /value1/

- Reaction rate dependence on a particular species temperature

**TDEP** /speciename/

– Energy loss parameter

**EXCI** /value1/

- Plasma (Ion) momentum-transfer collision frequency

**MOME (XSMI)**

- Reverse reaction Arrhenius parameters

**REV** /value1 value2 value3/

- Change reaction order parameters

**FORD** /specname value1/ (for forward rate)

**RORD** /specname value1/ (for reverse rate)

- Reaction units for reactions with units different than most of the other reactions

**UNITS** /unit1 unit2/

(the number of keywords between "//" can be one if only one set of units is changed or two if both pre-exponential factor and activation energy are to be modified)

## 7.6.2 Function Documentation

**7.6.2.1 void checkelemelist ( char \* elemname, element \* listelem, int \* Nelem, int \* ipos )**

Returns index of an element in the list of elements:

- the index goes from 0 to (Nelem-1);
- the value of Nelem is returned if the element is not found

Referenced by getthermo().

**7.6.2.2 int extractWordLeft ( char \* linein, char \* oneword )**

Extracts the left most word from a character string.

- this function assumes words are separated by spaces or "/"
- the initial character string is shifted to the left starting with the separation character
- the corresponding positions left at the right are filled with null characters

References elimleads().

Referenced by getelements(), getspecies(), getthermo(), and TC\_kmodint\_().

**7.6.2.3 int extractWordLeftauxline ( char \* linein, char \* oneword, char \* twoword, int \* inum, int \* ierror )**

Extracts two strings from a character strings.

- the first string starts from the first position until a space or a "/"
- the second string starts after the first slash and ends at the second "/"
  - the initial character string is shifted to the left starting with the first character after the second "/"

- the corresponding positions left at the right are filled with null characters

References `elimleads()`.

Referenced by `getreacauxl()`.

**7.6.2.4 int getreactions ( *char \* linein, char \* singleword, species \* listspec, int \* Nspec, reaction \* listreac, int \* Nreac, char \* aunits, char \* eunits, int \* ierror* )**

Interprets a character string containing reaction description.

- decides if the character string describes a reaction or the auxiliary information associated with one

References `getreacauxl()`, `getreacline()`, and `resetreacdata()`.

Referenced by `TC_kmodint_()`.

**7.6.2.5 void setperiodictable ( *elemtable \* periodictable, int \* Natoms, int iflag* )**

Read periodic table.

- First line contains two integer values: the total number of elements and the number of elements listed on each of the following lines
- The following lines (an even number) contain lists of elements names (two characters separated by one or more spaces, and elemental masses (separated by spaces):
  1. S1 S2 ... S(Nline)
  2. M1 M2 ... M(Nline)
  3. S(Nline+1) S(Nline+2) ....
  4. M(Nline+1) M(Nline+2) ....

Referenced by `TC_kmodint_()`.

**7.6.2.6 int tab2space ( *char \* linein* )**

Replaces all horizontal tab, vertical tab, line feed, and carriage return characters in a line with spaces.

- ASCII code for a horizontal TAB is 9

- ASCII code for a vertical TAB is 11
- ASCII code for a SPACE is 32
- ASCII code for line feed (new line) is 10
- ASCII code for carriage return is 15

Referenced by cleancharstring().

## 7.7 TC\_mlms.c File Reference

Mass fractions - Mole fractions - Molar concentrations - Molecular weight.

### Functions

- int [TCDND\\_getMs2Cc](#) (double \*scal, int Nvars, double \*concX)

*Computes molar concentrations based on temperature and species mass fractions.  
Input temperature is normalized, output concentrations are also normalized before exit.*

$$\overline{[X_k]} = [X_k] \cdot \frac{W_{ref}}{\rho_{ref}} = Y_k \cdot \frac{\rho}{W_k} \cdot \frac{W_{ref}}{\rho_{ref}}$$

- int [TC\\_getMs2Cc](#) (double \*scal, int Nvars, double \*concX)

*Computes molar concentrations based on temperature and species mass fractions.*

$$[X_k] = Y_k \cdot \rho / W_k$$

- int [TCDND\\_getMI2Ms](#) (double \*Xspec, int Nspec, double \*Yspec)

*Transforms mole fractions to mass fractions (same as [TC\\_getMI2Ms\(\)](#)).*

$$Y_k = X_k \cdot W_k / W_{mix}$$

- int [TC\\_getMI2Ms](#) (double \*Xspec, int Nspec, double \*Yspec)

*Transforms mole fractions to mass fractions.*

$$Y_k = X_k \cdot W_k / W_{mix}$$

- int [TCDND\\_getMs2MI](#) (double \*Yspec, int Nspec, double \*Xspec)

*Transforms mass fractions to mole fractions (same as [TC\\_getMs2MI\(\)](#))*

$$X_k = Y_k \cdot W_{mix} / W_k$$

- int [TC\\_getMs2MI](#) (double \*Yspec, int Nspec, double \*Xspec)

*Transforms mass fractions to mole fractions.*

$$X_k = Y_k \cdot W_{mix}/W_k$$

- int [TCDND\\_getMs2Wmix](#) (double \*Yspec, int Nspec, double \*Wmix)

*Computes mixture molecular weight based on species mass fractions. The molecular weight ([kg/kmol]=[g/mol]) is normalized before output.*

$$\bar{W}_{mix} = \frac{W_{mix}}{W_{ref}} = \frac{1}{W_{ref}} \left( \sum_{k=1}^{N_{spec}} Y_k/W_k \right)^{-1}$$

- int [TC\\_getMs2Wmix](#) (double \*Yspec, int Nspec, double \*Wmix)

*Computes mixture molecular weight based on species mass fractions.*

$$W_{mix} = \left( \sum_{k=1}^{N_{spec}} Y_k/W_k \right)^{-1}$$

- int [TCDND\\_getMI2Wmix](#) (double \*Xspec, int Nspec, double \*Wmix)

*Computes mixture molecular weight based on species mole fractions. The molecular weight ([kg/kmol]=[g/mol]) is normalized before output.*

$$\bar{W}_{mix} = \frac{W_{mix}}{W_{ref}} = \frac{1}{W_{ref}} \sum_{k=1}^{N_{spec}} X_k W_k$$

- int [TC\\_getMI2Wmix](#) (double \*Xspec, int Nspec, double \*Wmix)

*Computes mixture molecular weight based on species mole fractions.*

$$W_{mix} = \sum_{k=1}^{N_{spec}} X_k W_k$$

### 7.7.1 Detailed Description

Mass fractions - Mole fractions - Molar concentrations - Molecular weight.

### 7.7.2 Function Documentation

#### 7.7.2.1 int [TC\\_getMI2Ms](#) ( double \* Xspec, int Nspec, double \* Yspec )

Transforms mole fractions to mass fractions.

$$Y_k = X_k \cdot W_k/W_{mix}$$

**Parameters**

<i>Xspec</i>	: array of <i>Nspec</i> mole fractions
<i>Nspec</i>	: no. of species

**Returns**

*Yspec* : array of *Nspec* mass fractions

References TC\_getMI2Wmix(), TC\_Nspec\_, and TC\_sMass\_.

Referenced by TCDND\_getMI2Ms().

**7.7.2.2 int TC\_getMI2Wmix ( double \* *Xspec*, int *Nspec*, double \* *Wmix* )**

Computes mixture molecular weight based on species mole fractions.

$$W_{mix} = \sum_{k=1}^{N_{spec}} X_k W_k$$

**Parameters**

<i>Xspec</i>	: array of <i>Nspec</i> mole fractions
<i>Nspec</i>	: no. of species

**Returns**

*Wmix* : pointer to mixture molecular weight [kg/kmol]=[g/mol]

References TC\_Nspec\_, and TC\_sMass\_.

Referenced by TC\_getMI2Ms().

**7.7.2.3 int TC\_getMs2Cc ( double \* *scal*, int *Nvars*, double \* *concX* )**

Computes molar concentrations based on temperature and species mass fractions.

$$[X_k] = Y_k \cdot \rho / W_k$$

**Parameters**

<i>scal</i>	: array of <i>Nspec</i> +1 doubles (T,Y <sub>1</sub> ,Y <sub>2</sub> ,...,Y <sub>Nspec</sub> ), temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = <i>Nspec</i> +1

**Returns**

`concX` : array of doubles containing species molar concentrations [kmol/m<sup>3</sup> ]

References `TC_getRhoMixMs()`, `TC_Nspec_`, `TC_Nvars_`, and `TC_sMass_`.

Referenced by `TC_getJacRPTYNanl()`, `TC_getJacRPTYNnum()`, `TC_getRfrb()`, `TC_getRops()`, `TC_getTY2RRml()`, `TC_getTY2RRms()`, and `TCDND_getMs2Cc()`.

#### 7.7.2.4 int `TC_getMs2MI` ( double \* *Yspec*, int *Nspec*, double \* *Xspec* )

Transforms mass fractions to mole fractions.

$$X_k = Y_k \cdot W_{mix}/W_k$$

**Parameters**

<code>Yspec</code>	: array of <i>Nspec</i> mass fractions
<code>Nspec</code>	: no. of species

**Returns**

`Xspec` : array of *Nspec* mole fractions

References `TC_getMs2Wmix()`, `TC_Nspec_`, and `TC_sMass_`.

Referenced by `TCDND_getMs2MI()`.

#### 7.7.2.5 int `TC_getMs2Wmix` ( double \* *Yspec*, int *Nspec*, double \* *Wmix* )

Computes mixture molecular weight based on species mass fractions.

$$W_{mix} = \left( \sum_{k=1}^{N_{spec}} Y_k/W_k \right)^{-1}$$

**Parameters**

<code>Yspec</code>	: array of <i>Nspec</i> mass fractions
<code>Nspec</code>	: no. of species

**Returns**

`Wmix` : pointer to mixture molecular weight [kg/kmol]=[g/mol]

References `TC_Nspec_`, and `TC_sMass_`.

Referenced by `TC_getJacTYN()`, `TC_getJacTYNanl()`, `TC_getJacTYNm1()`, `TC_getJacTYNm1anl()`, `TC_getMs2MI()`, `TC_getSrcCons()`, `TCDND_getMI2Wmix()`, and `TCDND_getMs2Wmix()`.

#### 7.7.2.6 int TCDND\_getMI2Ms ( double \* *Xspec*, int *Nspec*, double \* *Yspec* )

Transforms mole fractions to mass fractions (same as [TC\\_getMI2Ms\(\)](#)).

$$Y_k = X_k \cdot W_k / W_{mix}$$

**Parameters**

<code>Xspec</code>	: array of <code>Nspec</code> mole fractions
<code>Nspec</code>	: no. of species

**Returns**

`Yspec` : array of `Nspec` mass fractions

References `TC_getMI2Ms()`, and `TC_Nspec_`.

#### 7.7.2.7 int TCDND\_getMI2Wmix ( double \* *Xspec*, int *Nspec*, double \* *Wmix* )

Computes mixture molecular weight based on species mole fractions. The molecular weight ([kg/kmol]=[g/mol]) is normalized before output.

$$\bar{W}_{mix} = \frac{W_{mix}}{W_{ref}} = \frac{1}{W_{ref}} \sum_{k=1}^{N_{spec}} X_k W_k$$

**Parameters**

<code>Xspec</code>	: array of <code>Nspec</code> mole fractions
<code>Nspec</code>	: no. of species

**Returns**

Wmix : pointer to normalized mixture molecular weight

References [TC\\_getMs2Wmix\(\)](#), and [TC\\_Nspec\\_](#).

**7.7.2.8 int TCDND\_getMs2Cc ( double \* scal, int Nvars, double \* concX )**

Computes molar concentrations based on temperature and species mass fractions. - Input temperature is normalized, output concentrations are also normalized before exit.

$$\overline{[X_k]} = [X_k] \cdot \frac{W_{ref}}{\rho_{ref}} = Y_k \cdot \frac{\rho}{W_k} \cdot \frac{W_{ref}}{\rho_{ref}}$$

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,Y <sub>1</sub> ,Y <sub>2</sub> ,...,Y <sub>Nspec</sub> ), temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

concX : array of doubles containing species molar concentrations [kmol/m<sup>3</sup> ]

References [TC\\_getMs2Cc\(\)](#), [TC\\_Nspec\\_](#), and [TC\\_Nvars\\_](#).

**7.7.2.9 int TCDND\_getMs2MI ( double \* Yspec, int Nspec, double \* Xspec )**

Transforms mass fractions to mole fractions (same as [TC\\_getMs2MI\(\)](#))

$$X_k = Y_k \cdot W_{mix}/W_k$$

**Parameters**

<i>Yspec</i>	: array of Nspec mass fractions
<i>Nspec</i>	: no. of species

**Returns**

Xspec : array of Nspec mole fractions

References [TC\\_getMs2MI\(\)](#), and [TC\\_Nspec\\_](#).

### 7.7.2.10 int TCDND\_getMs2Wmix ( double \* Yspec, int Nspec, double \* Wmix )

Computes mixture molecular weight based on species mass fractions. The molecular weight ([kg/kmol]=[g/mol]) is normalized before output.

$$\bar{W}_{mix} = \frac{W_{mix}}{W_{ref}} = \frac{1}{W_{ref}} \left( \sum_{k=1}^{N_{spec}} Y_k / W_k \right)^{-1}$$

#### Parameters

<code>Yspec</code>	: array of <code>Nspec</code> mass fractions
<code>Nspec</code>	: no. of species

#### Returns

`Wmix` : pointer to normalized mixture molecular weight

References `TC_getMs2Wmix()`, and `TC_Nspec_`.

## 7.8 TC\_params.h File Reference

Definitions of parameters and constants.

```
#include "copyright.h"
```

#### Defines

- #define `MAX(A, B)` ( ((A) > (B)) ? (A) : (B) )
- #define `MIN(A, B)` ( ((A) < (B)) ? (A) : (B) )
- #define `LENGTHOFELEMNAME` 3
- #define `LENGTHOFSPECNAME` 18
- #define `NUMBEROFELEMINSPEC` 5
- #define `NTHRDBMAX` 10
- #define `NSPECREACMAX` 6
- #define `REACBALANCE` 1.e-4
- #define `RUNIV` 8.314472
- #define `NAVOG` 6.02214179E23
- #define `ATMPA` 101325.0
- #define `CALJO` 4.184
- #define `KBOLT` 1.3806504E-23
- #define `EVOLT` 1.60217653E-19

### 7.8.1 Detailed Description

Definitions of parameters and constants.

### 7.8.2 Define Documentation

#### 7.8.2.1 #define ATMPA 101325.0

Standard atmospheric pressure [ $Pa$ ]

Referenced by TC\_initChem().

#### 7.8.2.2 #define CALJO 4.184

Conversion from calories to Joule

Referenced by rescalereac(), and TC\_initChem().

#### 7.8.2.3 #define EVOLT 1.60217653E-19

electron volt (eV) unit [ $J$ ]

Referenced by rescalereac().

#### 7.8.2.4 #define KBOLT 1.3806504E-23

Boltzmann's constant ( $k_B$ ) [ $JK^{-1}$ ]

Referenced by rescalereac().

#### 7.8.2.5 #define LENGTHOFELEMNAME 3

Maximum number of characters for element names

Referenced by TC\_initChem().

#### 7.8.2.6 #define LENGTHOFSPECNAME 18

Maximum number of characters for species names

Referenced by getreacline(), getspecies(), TC\_getSnameLen(), TC\_getSnames(), TC\_getSpos(), and TC\_initChem().

7.8.2.7 `#define MAX( A, B )( ((A) > (B)) ? (A) : (B) )`

Maximum of two expressions

Referenced by `kmodsum()`.

7.8.2.8 `#define MIN( A, B )( ((A) < (B)) ? (A) : (B) )`

Minimum of two expressions

Referenced by `TC_kmodint_()`.

7.8.2.9 `#define NAVOG 6.02214179E23`

Avogadro's number

Referenced by `rescalereac()`.

7.8.2.10 `#define NSPECREACMAX 6`

Maximum number of reactant or product species in a reaction

Referenced by `getreacauxl()`, `getreacline()`, `out_formatted()`, `out_mathem()`, `out_unformatted()`, `rescalereac()`, `resetreacdata()`, and `verifyreac()`.

7.8.2.11 `#define NTHRDBMAX 10`

Maximum number of third body efficiencies

Referenced by `getreacauxl()`, and `resetreacdata()`.

7.8.2.12 `#define NUMBEROFELEMINSPEC 5`

Maximum number of (different) elements that compose a species

Referenced by `resetspecdata()`.

7.8.2.13 `#define REACBALANCE 1.e-4`

Threshold for checking reaction balance with real stoichiometric coefficients

Referenced by `out_formatted()`, `out_unformatted()`, and `verifyreac()`.

---

### 7.8.2.14 #define RUNIV 8.314472

Universal gas constant  $J/(mol \cdot K)$

Referenced by rescalereac(), and TC\_initChem().

## 7.9 TC\_rr.c File Reference

Reaction rate functions.

### Functions

- int [TC\\_getNreac \(\)](#)  
*Returns number of reactions  $N_{reac}$ .*
- int [TC\\_getStoCoef \(int Nspec, int Nreac, double \\*stoicoef\)](#)  
*Returns stoichiometric coefficients' matrix. The stoichiometric coefficient for species "j" in reaction "i" is stored at position  $i \cdot N_{spec} + j$ . It assumes that stoicoef was dimensioned to at least  $N_{reac} \cdot N_{spec}$ .*
- int [TC\\_getStoCoefReac \(int Nspec, int Nreac, int ireac, int idx, double \\*stoicoef\)](#)  
*Returns stoichiometric coefficients' array for reaction 'ireac' for either reactants (idx=0) or products (idx=1). The stoichiometric coefficient for species "j" in reaction "ireac" is stored at position  $j$ . It assumes that stoicoef was dimensioned to at least  $N_{spec}$ .*
- int [TC\\_getArhenFor \(int ireac, int ipos, double \\*val\)](#)  
*Return current value of the Arrhenius parameters for forward rate constants. Return -1 if no data available, otherwise return 0 and store value in val.*
- int [TC\\_getArhenRev \(int ireac, int ipos, double \\*val\)](#)  
*Return current value of the Arrhenius parameters for reverse rate constants. Return -1 if no data available, otherwise return 0 and store value in val.*
- int [TCDND\\_getTY2RRml \(double \\*scal, int Nvars, double \\*omega\)](#)  
*Returns non-dimensional molar reaction rates,  $\dot{\omega}_i \cdot t_{ref} \frac{W_{ref}}{\rho_{ref}}$ , based on T and Y's.*
- int [TC\\_getTY2RRml \(double \\*scal, int Nvars, double \\*omega\)](#)  
*Returns molar reaction rates,  $\dot{\omega}_i$ , based on T and Y's.*
- int [TCDND\\_getTY2RRms \(double \\*scal, int Nvars, double \\*omega\)](#)  
*Returns non-dimensional mass reaction rates based on T and Y's.*
- int [TC\\_getTY2RRms \(double \\*scal, int Nvars, double \\*omega\)](#)  
*Returns mass reaction rates based on T and Y's.*
- int [TCDND\\_getTxC2RRml \(double \\*scal, int Nvars, double \\*omega\)](#)  
*Returns non-dimensional molar reaction rates based on temperature T and molar concentrations XC.*
- int [TC\\_getTxC2RRml \(double \\*scal, int Nvars, double \\*omega\)](#)  
*Returns non-dimensional molar reaction rates based on temperature T and molar concentrations XC.*

*Returns molar reaction rates based on temperature T and molar concentrations XC.*

- int **TCDND\_getTC2RRms** (double \*scal, int Nvars, double \*omega)

*Returns non-dimensional mass reaction rates based on T and molar concentrations.*

- int **TC\_getTC2RRms** (double \*scal, int Nvars, double \*omega)

*Returns mass reaction rates based on T and molar concentrations.*

- int **TC\_getRops** (double \*scal, int Nvars, double \*datarop)

*Returns rate-of-progress variables based on temperature T and species mass fractions Y's.*

- int **TC\_getRfrb** (double \*scal, int Nvars, double \*dataRfrb)

*Returns forward and reverse rate-of-progress variables based on T and Y's.*

- int **TC\_getRopsLocal** (double \*scal)

- int **TC\_getReacRates** (double \*scal, int Nvars, double \*omega)

*Returns molar reaction rates,  $\dot{\omega}_i$ , based on T and molar concentrations XC's (semi-private function)*

- int **TC\_getgk** (double t1, double t\_1, double tln)

- int **TC\_getgkFcn** (double t1, double t\_1, double tln)

- int **TC\_getgkTab** (double t1)

- int **TC\_getgkp** (double t1, double t\_1, double tln)

- int **TC\_getgkpFcn** (double t1, double t\_1, double tln)

- int **TC\_getgkpTab** (double t1)

- double **TC\_getSumNuGk** (int i, double \*gkLoc)

- double **TC\_getSumRealNuGk** (int i, int ir, double \*gkLoc)

- int **TC\_get3rdBdyConc** (double \*concX, double \*concM)

- int **TC\_getkForRev** (double t1, double t\_1, double tln)

- int **TC\_getkForRevFcn** (double t\_1, double tln)

- int **TC\_getkForRevTab** (double t1)

- int **TC\_getkForRevP** (double t1, double t\_1)

- int **TC\_getkForRevPFcn** (double t\_1)

- int **TC\_getkForRevPTab** (double t1)

- int **TC\_getRateofProg** (double \*concX)

- int **TC\_getRateofProgDer** (double \*concX, int ireac, int ispec, double \*qfr)

- int **TC\_getCrnd** (double t1, double t\_1, double tln, double \*concX, double \*concM)

- int **TC\_getCrndDer** (int ireac, int \*itbdy, int \*ipfal, double t1, double t\_1, double tln, double \*concX, double \*concM)

### 7.9.1 Detailed Description

Reaction rate functions.

## 7.9.2 Function Documentation

### 7.9.2.1 int TC\_getArhenFor ( int ireac, int ipos, double \* val )

Return current value of the Arrhenius parameters for forward rate constants. Return -1 if no data available, otherwise return 0 and store value in val.

#### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of Arrhenius parameter (0) pre-exponential factor (1) temperature exponent, (2) activation energy
<i>*val</i>	: value of Arrhenius parameter

References TC\_Nreac\_.

### 7.9.2.2 int TC\_getArhenRev ( int ireac, int ipos, double \* val )

Return current value of the Arrhenius parameters for reverse rate constants. Return -1 if no data available, otherwise return 0 and store value in val.

#### Parameters

<i>ireac</i>	: reaction index
<i>ipos</i>	: index of Arrhenius parameter (0) pre-exponential factor (1) temperature exponent, (2) activation energy
<i>*val</i>	: value of Arrhenius parameter

References TC\_nRevReac\_.

### 7.9.2.3 int TC\_getReacRates ( double \* scal, int Nvars, double \* omega )

Returns molar reaction rates,  $\omega_i$ , based on T and molar concentrations XC's (semi-private function)

#### Parameters

<i>scal</i>	: array of $N_{spec} + 1$ doubles (( $T, XC_1, XC_2, \dots, XC_N$ ): temperature T [K], molar concentrations XC [ $kmol/m^3$ ])
<i>Nvars</i>	: no. of variables $N_{vars} = N_{spec} + 1$

**Returns**

`omega` : array of  $N_{spec}$  molar reaction rates  $\dot{\omega}_i$  [ $kmol/(m^3 \cdot s)$ ]

References `TC_maxSpecInReac_`, `TC_Nreac_`, `TC_nRealNuReac_`, and `TC_Nspec_`.

Referenced by `TC_getTxC2RRml()`, `TC_getTxC2RRms()`, `TC_getTY2RRml()`, and `T-C_getTY2RRms()`.

**7.9.2.4 int TC\_getRfrb ( double \* scal, int Nvars, double \* dataRfrb )**

Returns forward and reverse rate-of-progress variables based on T and Y's.

**Parameters**

<code>scal</code>	: array of $N_{spec}+1$ doubles ( $T, Y_1, Y_2, \dots, Y_N$ ) temperature T [K], mass fractions Y []
<code>Nvars</code>	: no. of variables = $N_{spec} + 1$

**Returns**

`datarop` : array of  $N_{reac}$  forward rate-of-progress variables and  $N_{reac}$  reverse rate-of-progress variables [ $kmol/(m^3.s)$ ]

References `TC_errorMSG()`, `TC_getMs2Cc()`, `TC_Nreac_`, `TC_Nspec_`, and `TC_Nvars_`.

**7.9.2.5 int TC\_getRops ( double \* scal, int Nvars, double \* datarop )**

Returns rate-of-progress variables based on temperature T and species mass fractions Y's.

**Parameters**

<code>scal</code>	: array of $N_{reac} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_N$ ) temperature T [K], mass fractions Y []
<code>Nvars</code>	: no. of variables = $N_{spec} + 1$

**Returns**

`datarop` : array of  $N_{reac}$  rate-of-progress variables [ $kmol/(m^3.s)$ ]

References `TC_errorMSG()`, `TC_getMs2Cc()`, `TC_Nreac_`, `TC_Nspec_`, and `TC_Nvars_`.

---

**7.9.2.6 int TC\_getStoCoef ( int *Nspec*, int *Nreac*, double \* *stoicoef* )**

Returns stoichiometric coefficients' matrix. The stoichiometric coefficient for species "j" in reaction "i" is stored at position  $i \cdot N_{spec} + j$ . It assumes that stoicoef was dimentioned to at least  $N_{reac} \cdot N_{spec}$ .

**Parameters**

<i>Nspec</i>	: no. of species
<i>Nreac</i>	: no. of reactions

**Returns**

*stoicoef* : array of stoichiometric coefficients

References `TC_errorMSG()`, `TC_maxSpecInReac_`, `TC_Nreac_`, `TC_nRealNuReac_`, and `TC_Nspec_`.

**7.9.2.7 int TC\_getStoCoefReac ( int *Nspec*, int *Nreac*, int *ireac*, int *idx*, double \* *stoicoef* )**

Returns stoichiometric coefficients' array for reaction 'ireac' for either reactants (*idx*=0) or products (*idx*=1). The stoichiometric coefficient for species "j" in reaction "ireac" is stored at position *j*. It assumes that stoicoef was dimentioned to at least  $N_{spec}$ .

**Parameters**

<i>Nspec</i>	: no. of species
<i>Nreac</i>	: no. of reactions
<i>ireac</i>	: reaction index
<i>idx</i>	: 0-reactants, 1-products

**Returns**

*stoicoef* : array of stoichiometric coefficients

References `TC_errorMSG()`, `TC_maxSpecInReac_`, `TC_Nreac_`, `TC_nRealNuReac_`, and `TC_Nspec_`.

**7.9.2.8 int TC\_getTxC2RRml ( double \* *scal*, int *Nvars*, double \* *omega* )**

Returns molar reaction rates based on temperature T and molar concentrations XC.

**Parameters**

<i>scal</i>	: array of Nspec +1 doubles (T,XC_1,XC_2,...,XC_N) temperature T [K], molar concentrations XC [kmol/m3]
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*omega* : array of Nspec (molar) reaction rates [kmol/(m3.s)]

References TC\_errorMSG(), TC\_getReacRates(), TC\_Nspec\_, and TC\_Nvars\_.

Referenced by TCDND\_getTXC2RRml().

**7.9.2.9 int TC\_getTXC2RRms ( double \* *scal*, int *Nvars*, double \* *omega* )**

Returns mass reaction rates based on T and molar concentrations.

**Parameters**

<i>scal</i>	: array of Nspec+1 doubles (T,XC_1,XC_2,...,XC_N) temperature T [K], molar concentrations XC [kmol/m3]
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

*omega* : array of Nspec (mass) reaction rates [kg/(m3.s)]

References TC\_errorMSG(), TC\_getReacRates(), TC\_Nspec\_, TC\_Nvars\_, and TC\_s-Mass\_.

Referenced by TC\_getJacRPTYNnum(), and TCDND\_getTXC2RRms().

**7.9.2.10 int TC\_getTY2RRml ( double \* *scal*, int *Nvars*, double \* *omega* )**

Returns molar reaction rates,  $\dot{\omega}_i$ , based on T and Y's.

**Parameters**

<i>scal</i>	: array of $N_{spec} + 1$ doubles ( $T, Y_1, Y_2, \dots, Y_N$ ): temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables $N_{vars} = N_{spec} + 1$

**Returns**

`omega` : array of  $N_{spec}$  molar reaction rates  $\dot{\omega}_i$  [ $kmol/(m^3 \cdot s)$ ]

References `TC_errorMSG()`, `TC_getMs2Cc()`, `TC_getReacRates()`, `TC_Nspec_`, and `TC_Nvars_`.

Referenced by `TC_getSrcCons()`, and `TCDND_getTY2RRml()`.

#### 7.9.2.11 int `TC_getTY2RRms` ( `double * scal`, `int Nvars`, `double * omega` )

Returns mass reaction rates based on T and Y's.

**Parameters**

<code>scal</code>	: array of $N_{spec} + 1$ doubles (T,Y_1,Y_2,...,Y_N) temperature T [K], mass fractions Y []
<code>Nvars</code>	: no. of variables = $N_{spec} + 1$

**Returns**

`omega` : array of  $N_{spec}$  mass reaction rates [kg/(m3.s)]

References `TC_errorMSG()`, `TC_getMs2Cc()`, `TC_getReacRates()`, `TC_Nspec_`, `TC_Nvars_`, and `TC_sMass_`.

Referenced by `TC_getSrc()`, and `TCDND_getTY2RRms()`.

#### 7.9.2.12 int `TCDND_getTXC2RRml` ( `double * scal`, `int Nvars`, `double * omega` )

Returns non-dimensional molar reaction rates based on temperature T and molar concentrations XC.

**Parameters**

<code>scal</code>	: array of $N_{spec} + 1$ doubles (T,XC_1,XC_2,...,XC_N) temperature T [K], molar concentrations XC [kmol/m3] (but non-dimensional)
<code>Nvars</code>	: no. of variables = $N_{spec} + 1$

**Returns**

`omega` : array of  $N_{spec}$  (molar) reaction rates [kmol/(m3.s)] (but non-dimensional)

References `TC_errorMSG()`, `TC_getTXC2RRml()`, `TC_Nspec_`, and `TC_Nvars_`.

#### 7.9.2.13 int TCDND\_getTXC2RRms ( double \* *scal*, int *Nvars*, double \* *omega* )

Returns non-dimensional mass reaction rates based on T and molar concentrations.

##### Parameters

<i>scal</i>	: array of Nspec +1 doubles (T,XC_1,XC_2,...,XC_N) temperature T [K], molar concentrations XC [kmol/m3] (but non-dimensional)
<i>Nvars</i>	: no. of variables = Nspec +1

##### Returns

*omega* : array of Nspec (mass) reaction rates [kg/(m3.s)] (but non-dimensional)

References TC\_errorMSG(), TC\_getTXC2RRms(), TC\_Nspec\_, and TC\_Nvars\_.

#### 7.9.2.14 int TCDND\_getTY2RRml ( double \* *scal*, int *Nvars*, double \* *omega* )

Returns non-dimensional molar reaction rates,  $\dot{\omega}_i \cdot t_{ref} \frac{W_{ref}}{\rho_{ref}}$ , based on T and Y's.

##### Parameters

<i>scal</i>	: array of Nspec +1 doubles (T,Y_1,Y_2,...,Y_N) temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

##### Returns

*omega* : array of Nspec molar reaction rates [kmol/(m3.s)] (but non-dimensional)

References TC\_errorMSG(), TC\_getTY2RRml(), TC\_Nspec\_, and TC\_Nvars\_.

#### 7.9.2.15 int TCDND\_getTY2RRms ( double \* *scal*, int *Nvars*, double \* *omega* )

Returns non-dimensional mass reaction rates based on T and Y's.

##### Parameters

<i>scal</i>	: array of Nspec +1 doubles (T,Y_1,Y_2,...,Y_N) temperature T [K], mass fractions Y []
<i>Nvars</i>	: no. of variables = Nspec +1

**Returns**

`omega` : array of `Nspec` mass reaction rates [kg/(m<sup>3</sup>.s)] (but non-dimensional)

References `TC_errorMSG()`, `TC_getTY2RRms()`, `TC_Nspec_`, and `TC_Nvars_`.

## 7.10 TC\_spec.c File Reference

Species info.

### Functions

- int `TC_getNspec ()`  
*Returns no. of species `Nspec`*
- int `TC_getNelem ()`  
*Returns no. of elements `Nelem`*
- int `TC_getNvars ()`  
*Returns no. of variables (`Nspec +1`)*
- int `TC_getSnames (int Nspec, char *snames)`  
*Returns species names.*
- int `TC_getSnameLen ()`  
*Returns length of species names.*
- int `TC_getSpos (const char *sname, const int slen)`  
*Returns position a species in the list of species.*
- int `TC_getSmass (int Nspec, double *Wi)`  
*Returns species molar weights.*

### 7.10.1 Detailed Description

Species info.

### 7.10.2 Function Documentation

#### 7.10.2.1 int `TC_getSmass ( int Nspec, double * Wi )`

Returns species molar weights.

##### Parameters

<code>Nspec</code>	: no. of species
--------------------	------------------

**Returns**

Wi : array of species molar weights [kg/kmol]=[g/mol]

References TC\_Nspec\_, and TC\_sMass\_.

**7.10.2.2 int TC\_getSnames ( int Nspec, char \* snames )**

Returns species names.

**Parameters**

Nspec	: no. of species
-------	------------------

**Returns**

snames: array of characters containing species names, each name is LENGTHOFSPECNAME characters

References LENGTHOFSPECNAME, TC\_Nspec\_, and TC\_sNames\_.

**7.10.2.3 int TC\_getSpos ( const char \* sname, const int slen )**

Returns position a species in the list of species.

**Parameters**

sname	: string containing the name of the species
slen	: length of species "sname" name

**Returns**

position of species sname in the list of species, 0...(Nspec -1)

References LENGTHOFSPECNAME, TC\_Nspec\_, and TC\_sNames\_.

## 7.11 TC\_src.c File Reference

Source term and Jacobian functions.

### Functions

- int [TCDND\\_getSrc](#) (double \*scal, int Nvars, double \*omega)

*Returns dimensional/non-dimensional source term for*

$$\frac{\partial T}{\partial t} = \omega_0, \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on temperature T and species mass fractions Y's.*

- int [TC\\_getSrc](#) (double \*scal, int Nvars, double \*omega)

*Returns source term for*

$$\frac{\partial T}{\partial t} = \omega_0, \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on temperature T and species mass fractions Y's.*

- int [TCDND\\_getSrcCons](#) (double \*scal, int Nvars, double \*omega)

*Returns source term (dimensional/non-dimensional) for*

$$\frac{\partial \rho}{\partial t} = \omega_0, \rho \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on  $\rho$  and Y's.*

- int [TC\\_getSrcCons](#) (double \*scal, int Nvars, double \*omega)

*Returns source term for*

$$\frac{\partial \rho}{\partial t} = \omega_0, \rho \frac{\partial Y_i}{\partial t} = \omega_i,$$

*based on  $\rho$  and Y's.*

- int [TCDND\\_getJacTYNm1anl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on temperature T and species mass fractions Y's.*

- int [TC\\_getJacTYNm1anl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on T and Y's.*

- int [TCDND\\_getJacTYNanl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.*

- int [TC\\_getJacTYNanl](#) (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.*

- int [TCDND\\_getJacTYNm1](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical or numerical) Jacobian (dimensional/non-dimensional) for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on temperature T and species mass fractions Y's.*

- int [TC\\_getJacTYNm1](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical or numerical) Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_{N-1})$  based on T and Y's.*

- int [TCDND\\_getJacTYN](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical or numerical) Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on T and Y's.*

- int [TC\\_getJacTYN](#) (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical or numerical) Jacobian for the system  $(T, Y_1, Y_2, \dots, Y_N)$  based on  $T$  and  $Y$ 's.*

- int **TC\_getJacRPTYN** (double \*scal, int Nspec, double \*jac, unsigned int useJacAnl)

*Computes (analytical) Jacobian for the system  $(\rho, P, T, Y_1, Y_2, \dots, Y_N)$  based on  $T$  and  $Y$ 's.*

- int **TC\_getJacRPTYNanl** (double \*scal, int Nspec, double \*jac)

*Computes analytical Jacobian for the system  $(\rho, P, T, Y_1, Y_2, \dots, Y_N)$  based on  $T$  and  $Y$ 's.*

- int **TC\_getJacRPTYNnum** (double \*scal, int Nspec, double \*jac)

*Computes numerical Jacobian for the system  $(\rho, P, T, Y_1, Y_2, \dots, Y_N)$  based on  $T$  and  $Y$ 's.*

### 7.11.1 Detailed Description

Source term and Jacobian functions.

## 7.12 TC\_thermo.c File Reference

Equation of state and thermodynamic functions.

### Functions

- int **TCDND\_getRhoMixMs** (double \*scal, int Nvars, double \*rhomix)

*Computes density based on temperature and species mass fractions using the equation of state. Input temperature is normalized, output density also normalized before exit.*

- int **TC\_getRhoMixMs** (double \*scal, int Nvars, double \*rhomix)

*Computes density based on temperature and species mass fractions using the equation of state.*

- int **TCDND\_getRhoMixMI** (double \*scal, int Nvars, double \*rhomix)

*Computes density based on temperature and species mole fractions using the equation of state. Input temperature is normalized, output density also normalized before exit.*

- int **TC\_getRhoMixMI** (double \*scal, int Nvars, double \*rhomix)

*Computes density based on temperature and species mole fractions using the equation of state.*

- int **TCDND\_getTmixMs** (double \*scal, int Nvars, double \*Tmix)

*Computes temperature based on density and species mass fractions using the equation of state. Input density is normalized, output temperature also normalized before exit.*

- int [TC\\_getTmixMs](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mass fractions using the equation of state.*
- int [TCDND\\_getTmixMI](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mole fractions using the equation of state. Input density is normalized, output temperature also normalized before exit.*
- int [TC\\_getTmixMI](#) (double \*scal, int Nvars, double \*Tmix)  
*Computes temperature based on density and species mole fractions using the equation of state.*
- int [TCDND\\_getMs2CpMixMs](#) (double \*scal, int Nvars, double \*cpmix)  
*Computes mixture specific heat at constant pressure based on temperature and species mass fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
- int [TC\\_getMs2CpMixMs](#) (double \*scal, int Nvars, double \*cpmix)  
*Computes mixture specific heat at constant pressure based on temperature and species mass fractions.*
- int [TCDND\\_getMs2CvMixMs](#) (double \*scal, int Nvars, double \*cvmix)  
*Computes mixture specific heat at constant volume based on temperature and species mass fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
- int [TC\\_getMs2CvMixMs](#) (double \*scal, int Nvars, double \*cvmix)  
*Computes mixture specific heat at constant volume based on temperature and species mass fractions.*
- int [TCDND\\_getMI2CpMixMI](#) (double \*scal, int Nvars, double \*cpmix)  
*Computes mixture heat capacity at constant pressure based on temperature and species mole fractions. Input temperature is normalized, output specific heat is also normalized before exit.*
- int [TC\\_getMI2CpMixMI](#) (double \*scal, int Nvars, double \*cpmix)  
*Computes mixture specific heat at constant pressure based on temperature and species mole fractions.*
- int [TCDND\\_getCpSpecMs](#) (double t, int Nspec, double \*cpi)  
*Computes species specific heat at constant pressure based on temperature. Input temperature is normalized, output specific heats are also normalized before exit.*
- int [TC\\_getCpSpecMs](#) (double t, int Nspec, double \*cpi)  
*Computes species specific heat at constant pressure based on temperature.*
- int [TCDND\\_getCpSpecMI](#) (double t, int Nspec, double \*cpi)  
*Computes species heat capacities at constant pressure based on temperature. Input temperature is normalized, output heat capacities are also normalized before exit.*
- int [TC\\_getCpSpecMI](#) (double t, int Nspec, double \*cpi)  
*Computes species heat capacities at constant pressure based on temperature.*
- int [TCDND\\_getMs2HmixMs](#) (double \*scal, int Nvars, double \*hmix)

*Computes mixture specific enthalpy based on temperature and species mass fractions.  
Input temperature is normalized, output enthalpy is normalized before exit.*

- int **TC\_getMs2HmixMs** (double \*scal, int Nvars, double \*hmix)  
*Computes mixture specific enthalpy based on temperature and species mass fractions.*
- int **TCDND\_getMI2HmixMI** (double \*scal, int Nvars, double \*hmix)  
*Computes mixture molar enthalpy based on temperature and species mole fractions.  
Input temperature is normalized, output enthalpy is normalized before exit.*
- int **TC\_getMI2HmixMI** (double \*scal, int Nvars, double \*hmix)  
*Computes mixture molar enthalpy based on temperature and species mole fractions.*
- int **TCDND\_getHspecMs** (double t, int Nspec, double \*hi)  
*Computes species specific enthalpies based on temperature. Input temperature is normalized, output enthalpies are also normalized before exit.*
- int **TC\_getHspecMs** (double t, int Nspec, double \*hi)  
*Computes species specific enthalpies based on temperature.*
- int **TCDND\_getHspecMI** (double t, int Nspec, double \*hi)  
*Computes species molar enthalpies based on temperature. Input temperature is normalized, output enthalpies are also normalized before exit.*
- int **TC\_getHspecMI** (double t, int Nspec, double \*hi)  
*Computes species molar enthalpies based on temperature.*
- int **TC\_getCpSpecMsFcn** (double t, double \*cpi)
- int **TC\_getCpSpecMs1Fcn** (double t, int i, double \*cpi)
- int **TC\_getCpSpecMIFcn** (double t, double \*cpi)
- int **TC\_getCpSpecMI1Fcn** (double t, int i, double \*cpi)
- int **TC\_getCpSpecMsTab** (double t1, double \*cpi)
- int **TC\_getCpSpecMITab** (double t1, double \*cpi)
- int **TC\_getCpMixMsP** (double \*scal, int Nvars, double \*cpmix)
- int **TC\_getCpSpecMsP** (double t, int Nspec, double \*cpi)
- int **TC\_getCpSpecMsPFcn** (double t, double \*cpi)
- int **TC\_getCpSpecMs1PFcn** (double t, int i, double \*cpi)
- int **TC\_getCpSpecMsPtab** (double t1, double \*cpi)
- int **TC\_getHspecMsFcn** (double t, double \*hi)
- int **TC\_getHspecMIFcn** (double t, double \*hi)
- int **TC\_getHspecMsTab** (double t1, double \*hi)
- int **TC\_getHspecMITab** (double t1, double \*hi)

### 7.12.1 Detailed Description

Equation of state and thermodynamic functions.

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## 7.13 TC\_utils.c File Reference

Various utilities used by other functions.

### Functions

- static double **fastIntPow** (double val, int exponent)

*Much faster version of pow for small integers (considering that reactions are generally no more than 3rd order). The C version of pow requires a double exponent; pow is the slowest part of the code when used instead of fastIntPow.*

### 7.13.1 Detailed Description

Various utilities used by other functions.

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