

Mathematical modelling of skin sensitization: Practicalities of the modelling process

Dr Cameron MacKay

**Safety & Environmental
Assurance Centre**



Skin Sensitization



- Allergic Contact Dermatitis:
 - occurs due to the presence of allergen-specific T cells in the circulation (sensitisation)
 - allergen re-exposure induces recruitment of allergen-specific T cells into the skin where they mediate an inflammatory response (elicitation)
- To assure consumer safety, animal data (e.g. mouse local lymph node assay) is currently used in risk assessment of skin sensitisation

EU Cosmetics Directive

7th Amendment – March 2003

If the cosmetic product is to be marketed in the EU:

- alternative, non-animal tests must be used once validated
- animal testing and marketing bans on finished products
- animal testing and marketing bans on ingredients:
 - from March 2009: tests for acute (local) effects
 - from March 2013: more complex tests (including LLNA)
- threat to innovation and a major business risk
- challenge: market safe products without animal testing
- opportunity: apply new technologies in risk assessment

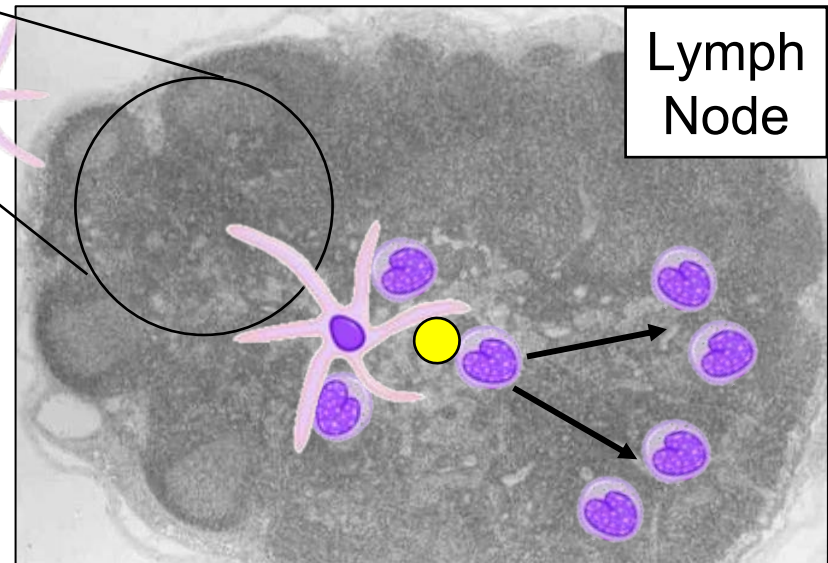
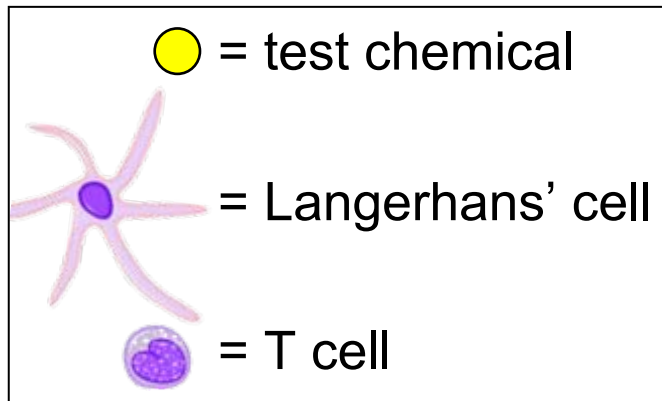
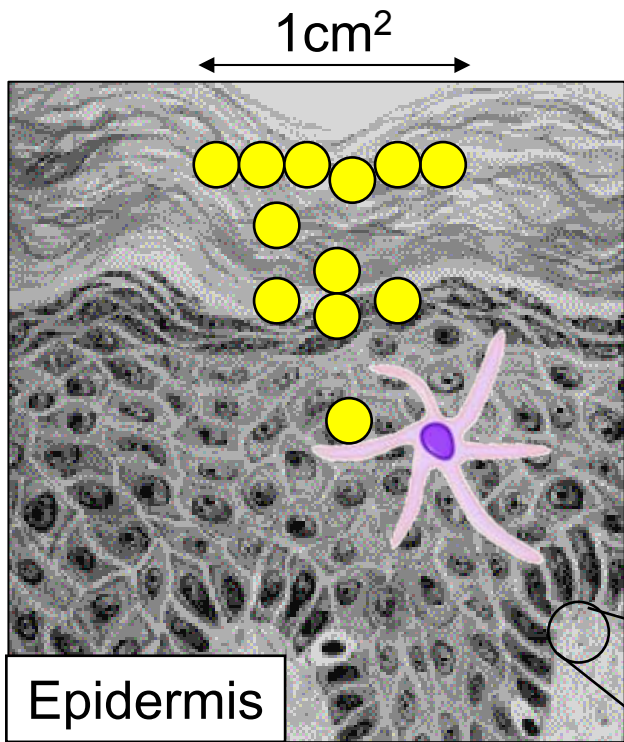
Project Objectives

- Use data in the published literature to construct a computer-based mathematical model of the induction of skin sensitization
- Use this model to interrogate the biology and determine the biological pathways having the greatest influence on the endpoint (T-cell proliferation)
- Use this information to build a strategy for obtaining *in vitro* assays that are predictive of the induction of skin sensitization



Biological scope of *in silico* model

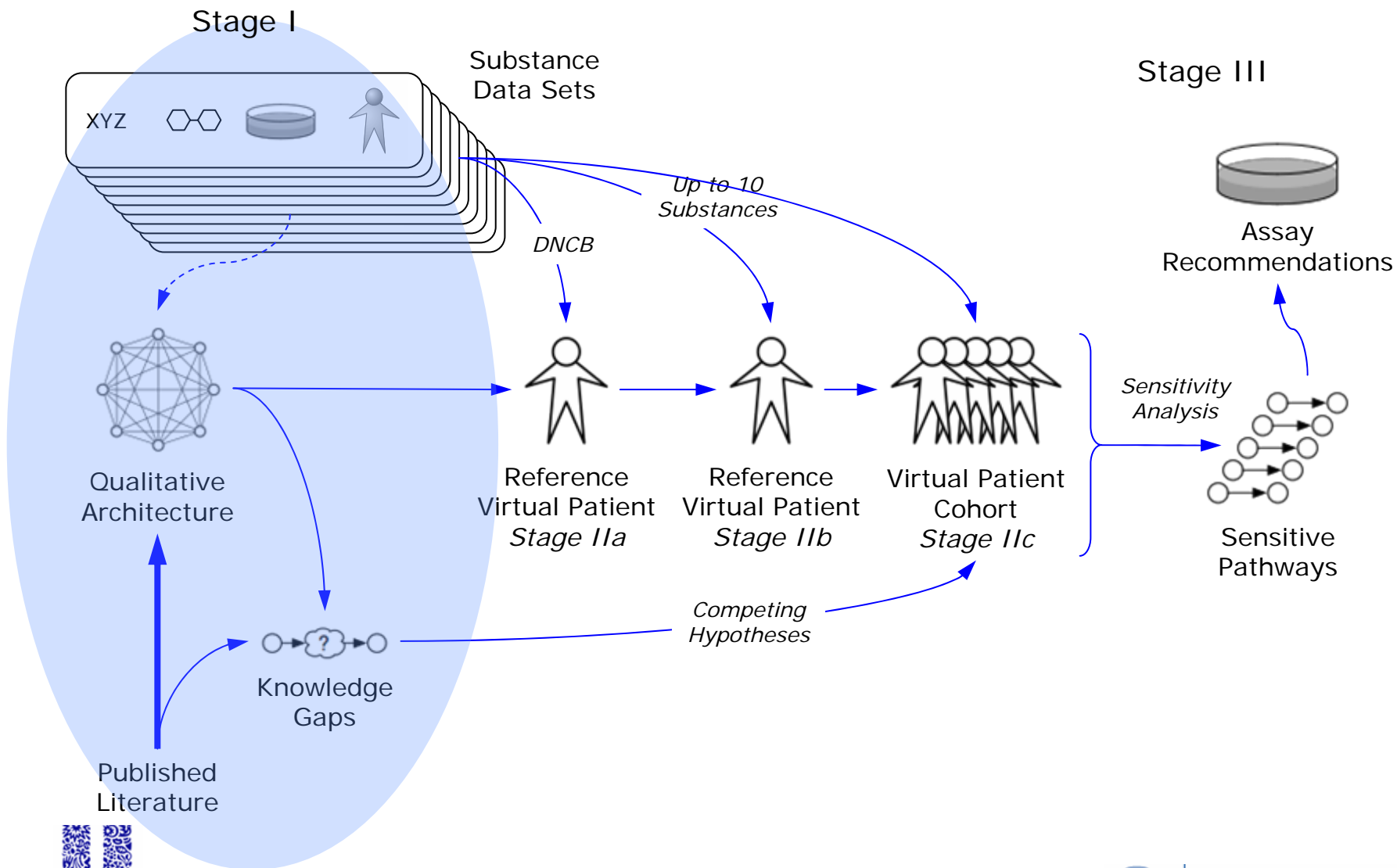
- Model covers biological pathways required for sensitization induction
- Two main biological compartments



Approach Overview

- Stage I: Qualitative platform design
 - Documentation of pathways
 - Knowledge gaps
- Stage II: Quantitative platform development
 - Calibration experiments
 - Virtual patients
- Stage III: Platform validation & exploration
 - Validation experiments
 - Sensitivity analysis
 - Assay recommendations
 - Areas for additional platform development identified

Skin Sensitization Induction PhysioLab Platform (SSIPP)



Model development – stage I

- Qualitative Modelling
 - 496 papers used in mapping biological processes
- Types of information required
 - Released cell mediators
 - Regulated surface markers
 - Regulators of T-cell proliferation
- Identify knowledge gaps

Create Object: State Node

Properties | Notes | Arguments | Specified Data | Transform

Name: Active

Description:

Short Name:

Calculation

Baseline Status

Computed: $dS/dt = \text{arrow terms}$

So (initial val.)

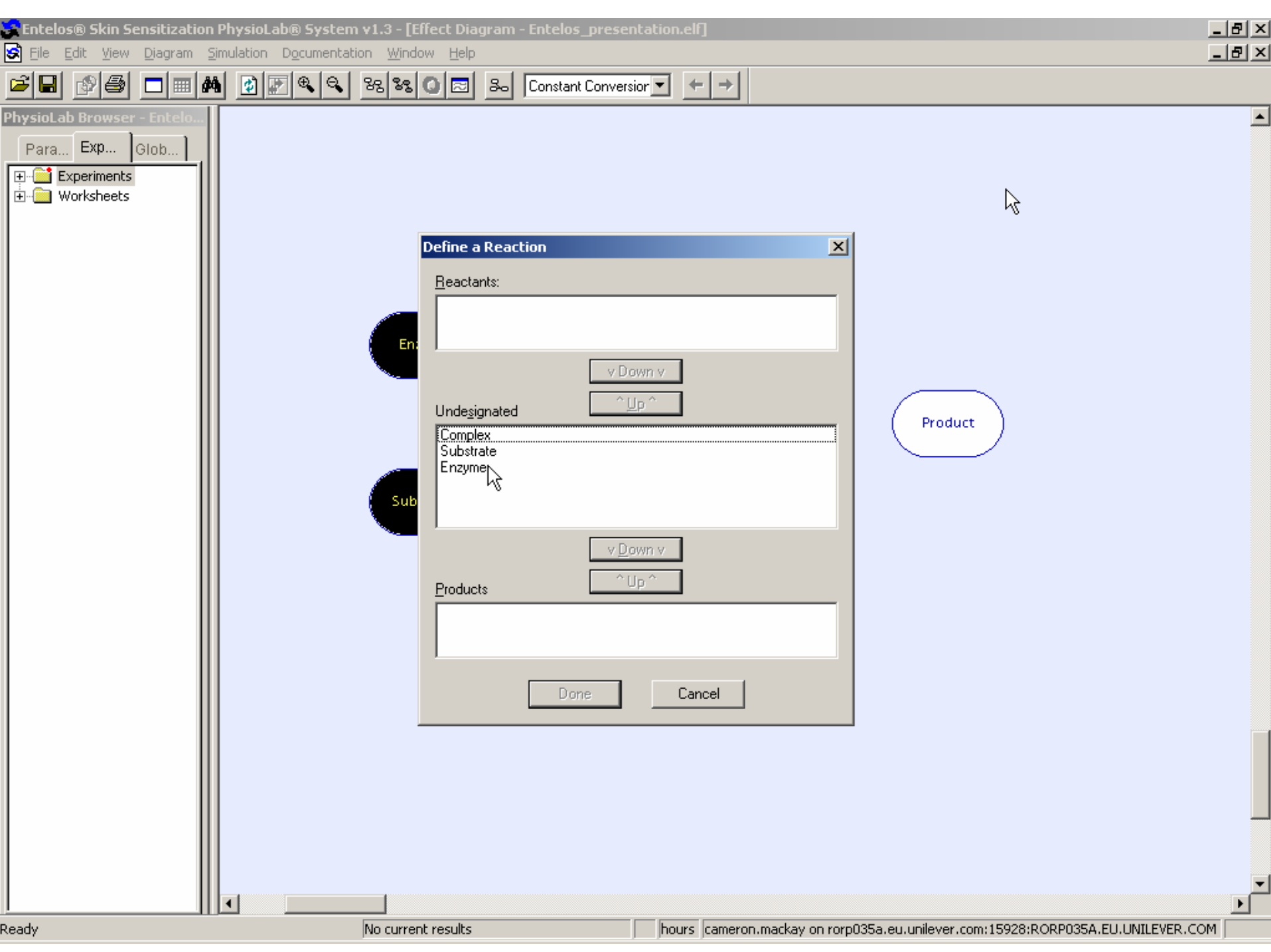
h (half life)

Specified - Locked at So

Specified Data

Constraints:

OK Cancel



Define a Reaction

Reactants:

Undesignated

- Complex
- Substrate
- Enzyme

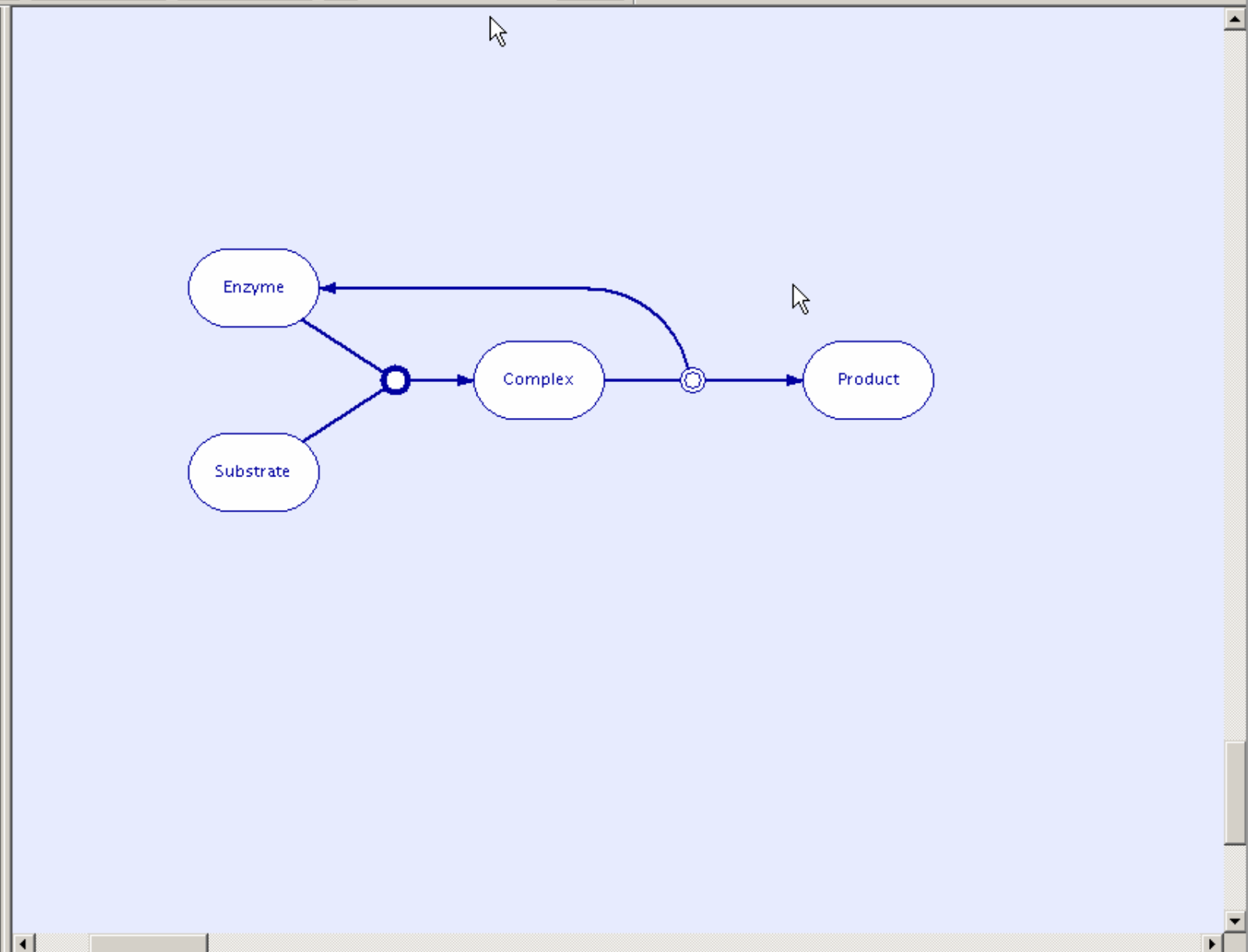
Products

Done Cancel

Product

Para... Exp... Glob...

- Experiments
- Worksheets

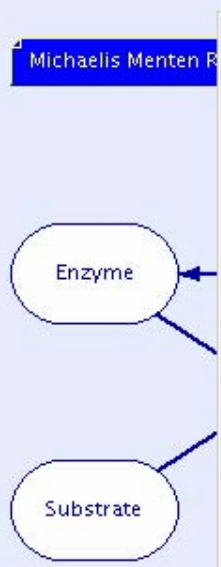




PhysiLab Browser - Entelo...

Para... Exp... Glob...

Experiments
Worksheets



Create Object: Diagram Note

Properties Notes

Note entries:

Module Observation Options

Module Observation Edit

Comment:
This module contains a representation of the Michaelis-Menten Reaction

Enzyme + Substrate <--> Complex --> Product + Enzyme

Owner: cameron.mackay	Created: 17/11/2006	Owner Type: User	Last Modified by: cameron.mackay	Modified: 17/11/2006
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[-Top-](#)

OK Cancel

Competing Hypothesis: programmed vs. progressive T-cell expansion

- Two competing theories of T-cell expansion
- Programmed hypothesis
 - Single APC encounter triggers T-cell division ([Foulds 2002](#))
 - Quality of encounter determines the time spent in cell division
- Progressive hypothesis
 - Repeated stimulation required to maintain cell division (*Gett 2003, Lanzavecchia 2002*)
 - Number of available APCs and the quality of the stimulation determines the time spent in cell division
- Approach
 - Implement and evaluate both mechanisms

CD4+ T cells

AP Competition and Costimulation Integration

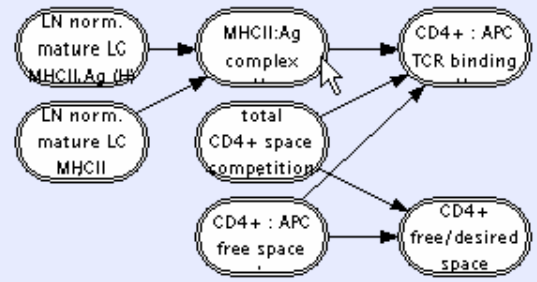
- + Stimulates
- Inhibits
- = Regulates
- A Allows
- D Decreases
- H Half-Life
- I Increases
- L Leads
- M Moves
- P Produces
- S Changes State

CD4+ T cells AP Competition and Costimulation Integration Overview

Programmed vs. Progressive Hypothesis

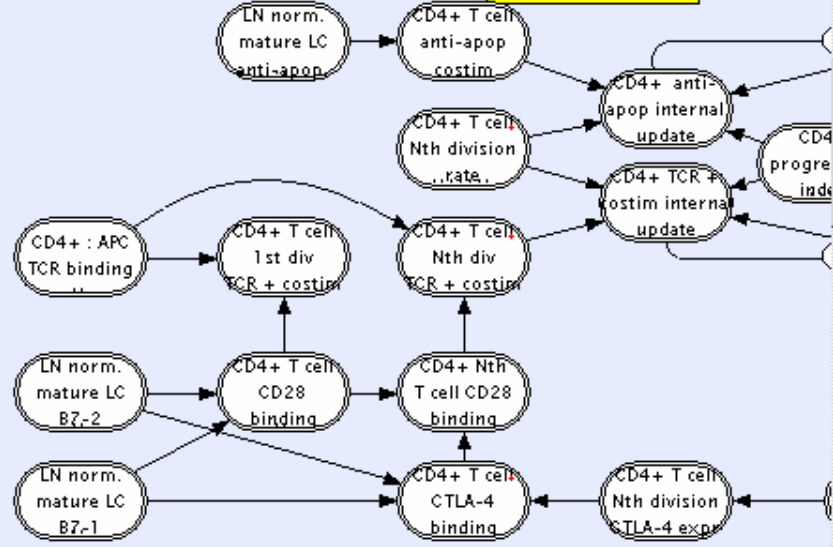
CD4+ TCR binding

TCR Binding



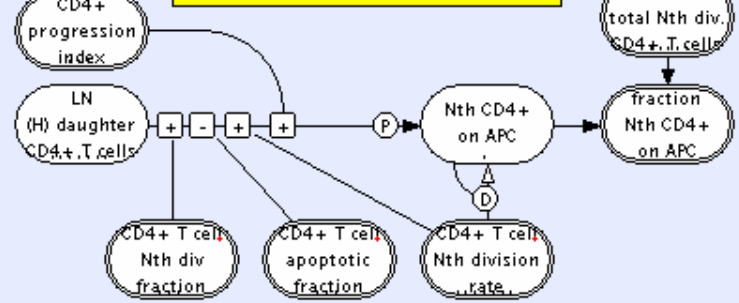
CD4+ costimulation

Costimulation Effects



Nth CD4+ APC occupation

Nth Division Cell APC Binding and Release



CD4+ vs CD8+ competition and space

CD4+ T cells

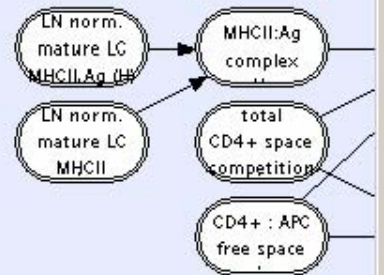
AP Competition

- + Stimulates
- Inhibits
- = Regulates
- A Allows
- D Decreases
- H Half-Life
- I Increases
- L Leads
- M Moves
- P Produces
- S Changes State

CD4+ T cells AP Competition and Costim
 Programmed vs. Progressive Hypothesis

CD4+ TCR binding

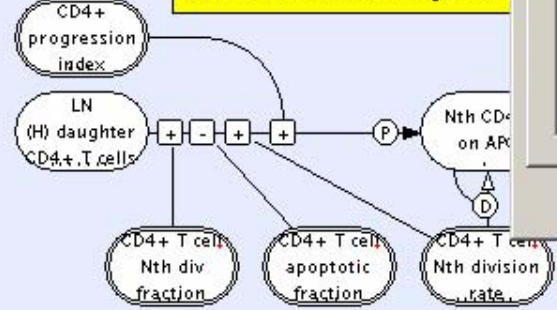
TCR Binding



- CD8+ AP & Costim.
- CD4+ T cell Life Cycle
- LC Life Cycle & Memory

Nth CD4+ APC occur

Nth Division Cell APC Binding and Rel



Object: Diagram Note

Properties Notes

Note entries:

- Programmed and Progress
- Progressive Differentiation
- Bevan 2001a
- Gett 2003a
- Gudmundsdottir 1999a

Options

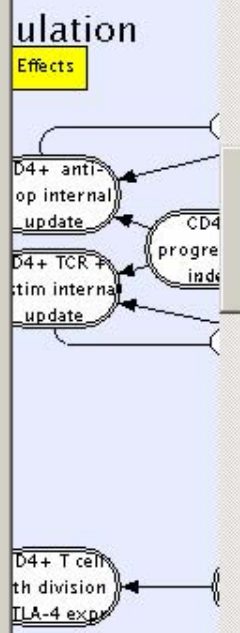
Programmed and Progressive Hypotheses

Comment:
 Two competing theories of T cell requirements for proliferation and differentiation are known as the programmed and progressive model.

According to the progressive model, T cell proliferation is dependent on repeated encounters with antigen (Ag), and it is essential that each daughter cell be stimulated with Ag. T cell divisions would stop if the Ag was withdrawn.

According to the programmed model, the initial encounter with Ag triggers a developmental program in T cells that allows them to go

OK Cancel Apply



CD4+ vs CD8+ competition and space

J Immunol. 2002 Feb 15;168(4):1528-32.

Cutting edge: CD4 and CD8 T cells are intrinsically different in their proliferative responses.

Foulds KE, Zenewicz LA, Shedlock DJ, Jiang J, Troy AE, Shen H

Department of Microbiology, School of Medicine, University of Pennsylvania, Philadelphia, PA 19104, USA.

In this study, we compared the proliferation and differentiation of Ag-specific CD4 and CD8 T cells following *Listeria* infection. Our results show that CD4 T cells responding to infection divide a limited number of times, with progeny exhibiting proliferative arrest in early divisions. Even with increased infectious doses, CD4 T cells display this restricted proliferative pattern and are not driven to undergo extensive clonal expansion. This is in striking contrast to CD8 T cells, which undergo extensive proliferation in response to infection. These differences are also evident when CD4 and CD8 T cells receive uniform anti-CD3 stimulation *in vitro*. Together, these results suggest that CD4 and CD8 T cells are programmed to undergo limited and extensive proliferation, respectively, to suit their function as regulator and effector cells.

MeSH

- Adoptive Transfer
- Animals
- CD4-Positive T-Lymphocytes/*immunology
- CD8-Positive T-Lymphocytes/*immunology
- Cells, Cultured
- Comparative Study
- Flow Cytometry
- Kinetics
- *Listeria* Infections/*immunology
- *Lymphocyte Activation
- Mice
- Mice, Inbred BALB C
- Mice, Inbred C57BL
- Mice, Transgenic
- Ovalbumin/genetics/immunology
- Recombinant Proteins/immunology

The Journal of Immunology

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Foulds et al. 168 (4): 1528. (2002)

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Cutting Edge: CD4 and CD8 T Cells Are Intrinsically Different in Their Proliferative Responses¹

Kathryn E. Foulds, Lauren A. Zenewicz, Devon J. Shedlock, Jiu Jiang, Amy E. Troy, and Hao Shen²

In this study, we compared the proliferation and differentiation of Ag-specific CD4 and CD8 T cells following *Listeria* infection. Our results show that CD4 T cells responding to infection divide a limited number of times, with progeny exhibiting proliferative arrest in early divisions. Even with increased infectious doses, CD4 T cells display this restricted proliferative pattern and are not driven to undergo extensive clonal expansion. This is in striking contrast to CD8 T cells, which undergo extensive proliferation in response to infection. These differences are also evident when CD4 and CD8 T cells receive uniform anti-CD3 stimulation *in vitro*. Together, these results suggest that CD4 and CD8 T cells are programmed to undergo limited and extensive proliferation, respectively, to suit their function as regulator and effector cells. *The Journal of Immunology*, 2002, 168: 1528–1532.

Murine listeriosis has been a useful model for investigating T cell responses to infection (reviewed in Ref. 1). The infectious agent, *Listeria monocytogenes* (LM)² is a Gram-positive bacterium that invades host cells, escapes from the endosome, and replicates within the host cell cytosol (2). LM proteins are presented by both MHC class I and class II pathways and stimulate strong CD8 and CD4 T cell responses (1, 3). The *in vivo* dynamics of the CD8 T cell response to infection has been studied extensively through the analysis of specific responses to native LM epitopes as well as foreign epitopes expressed by recombinant LM (3–5). Two recent studies have shown that the extent of CD8 T cell proliferation is not determined by the amount or duration of Ag presentation (6, 7), leading to the hypothesis that CD8 T cells undergo autonomous clonal expansion in

an Ag-independent fashion following *in vivo* priming. Further studies both *in vitro* and *in vivo* have demonstrated that stimulation of CD8 T cells triggers a developmental program that instructs daughter cells to continue to divide and differentiate into effector and memory T cells (7–10).

Much less is known about the *in vivo* dynamics of CD4 T cell responses to infection. While several MHC class II-restricted LM epitopes have been defined through the *in vitro* analysis of T cell clones (1, 11), the frequencies of CD4 T cells responding to these known epitopes are too low to allow the direct measurement of Ag-specific CD4 T cell responses. This limitation has thus far hindered our ability to assess the *in vivo* dynamics of CD4 T cell responses in most infections. In this study, we developed a system to quantitate Ag-specific CD4 T cell responses *in vivo*, using an adoptive transfer model (12) that couples the use of a recombinant LM expressing OVA with OVA-specific transgenic cells. Our results show that the extent of CD4 T cell proliferation and differentiation is strikingly different from that of CD8 T cells.

Materials and Methods

Mice, Ags, and bacterial strains

BALB/c-Tg(DO11.10)01.01.01, C57BL/6-P14, OT-I, and OT-II mice were previously described (13–16). OT-I and OT-II mice were bred onto the B6.PL-Thy1.1 background. B6.PL-Thy1.1 mice were obtained from The Jackson Laboratory (Bar Harbor, ME) and BALB/c-Thy1.1 mice were obtained from C. Sack at The Scripps Institute (La Jolla, CA). All mice were from BD HarlanMilton (San Diego, CA), except the KJ1-26 from Caltech Laboratories (Berkeley, CA). Construction and Western blot analysis of rLM-OVA and rLM-gp33 strains was performed as described (17). Both strains were derived from the wild-type strain 1040ts and described previously (18, 19). The LD₅₀ of rLM-OVA in BALB/c mice is ~5 × 10⁵ CFU and the LD₅₀ of rLM-OVA and rLM-gp33 in C57BL/6 mice is ~5 × 10⁶ CFU.

Analysis of T cell proliferation following LM infection *in vivo*

Splenocytes from DO11.10, P14, OT-I, or OT-II transgenic mice were labeled with CFSE as described (20). A total of 2 × 10⁶ CFSE-labeled splenocytes (2 × 10⁵ specific cells) were transferred into Thy1.1 or Thy1.2 congenic mice (21), which were then infected with the indicated doses of rLM-OVA or rLM-gp33. For the OT-IOT-II combined transfer, T cells were enriched by depleting splenocytes with B220 and MHC II MHC-II^{hi} by MACS (Miltenyi Biotec, Auburn, CA) and CFSE labeled, and 2 × 10⁶ of each cell type were transferred per mouse. Proliferation of transferred cells was visualized by FACS analysis of their CFSE profile. Transferred DO11.10 cells were identified by staining with mAb to Thy1.2, CD4, and the KJ1-26 chromotypic mAb. P14 cells were identified by staining with mAb to Thy1.2, CD8, and the DP-gp33 intracell (22, 23), and OT-I and OT-II cells were identified by staining with mAb to Thy1.1, Vα2, and CD8 or CD4, respectively. Intracellular IFN-γ staining was performed as described following 5 h of *in vitro* stimulation with 3 μM OVA₃₂₃₋₃₃₉ or 1 μM gp33–41 peptides (25).

Department of Microbiology, School of Medicine, University of Pennsylvania, Philadelphia, PA 19104
Received for publication September 18, 2001. Accepted for publication December 21, 2001.

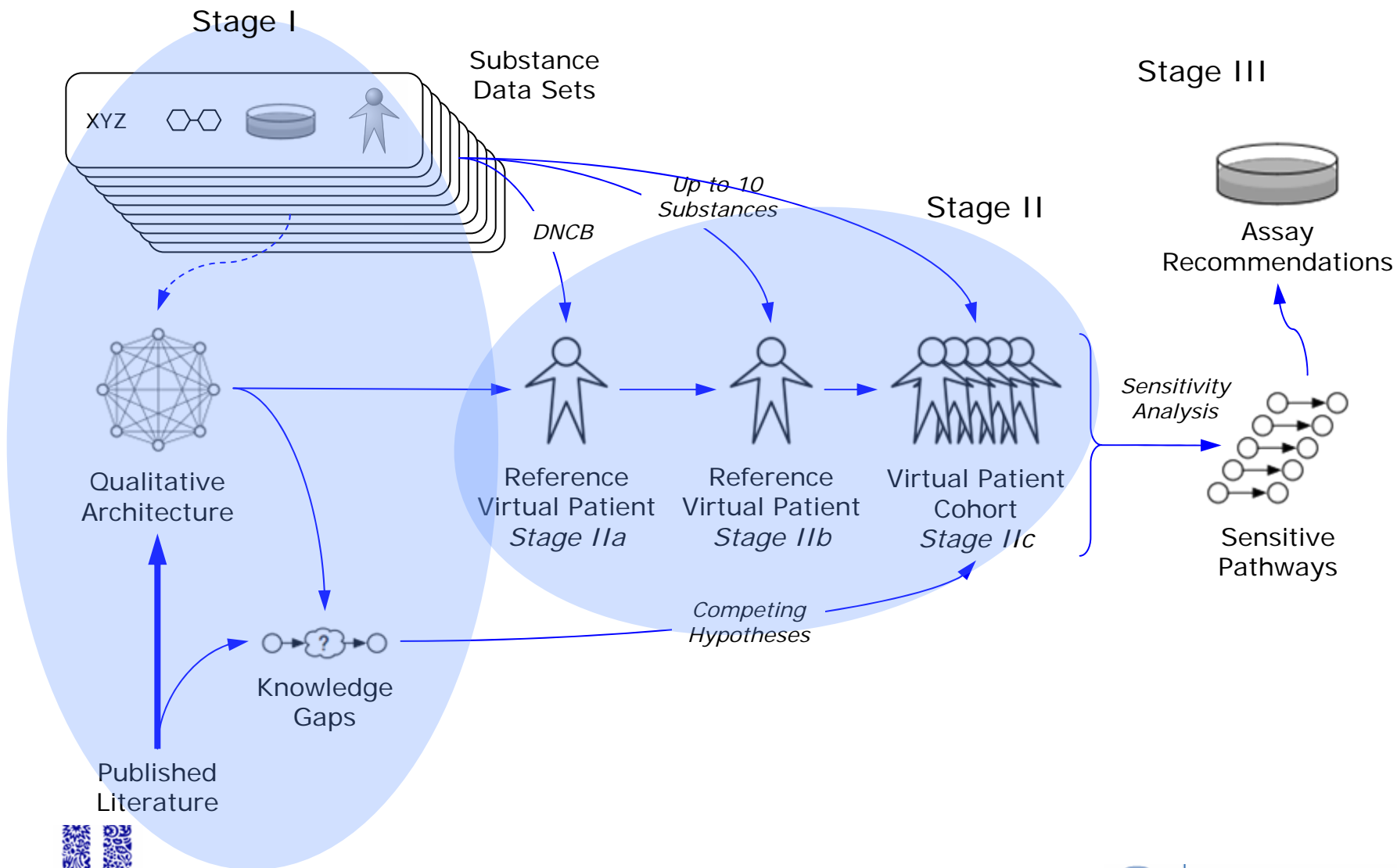
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¹This work was supported by National Institutes of Health Grants AI-6025 and AI-6048 (to H.S.).

²Address correspondence and reprint requests to Dr. Hao Shen, Department of Microbiology, School of Medicine, University of Pennsylvania, 3610 Hamilton Walk, Philadelphia, PA 19104. E-mail address: shen@gsml.med.upenn.edu

³Abbreviations used in this paper: LM, *Listeria monocytogenes*; LCMV, lymphocytic choriomeningitis virus.

Skin Sensitization Induction PhysioLab Platform (SSIPP)



Model development – stage II

- Quantitative Modelling
 - The dynamic interactions of the biological system were represented using mathematical equations (ordinary differential equations)
- Model Calibration: published results from 35 key experiments were replicated by the model including:
 - Epidermal cytokine production
 - Langerhans cell and T cell surface marker expression
 - Langerhans cell migration
 - Lymph node cytokine production

Parameter Sets

- Static function nodes
- Epidermal and lymph node physiology
- Culture conditions (epidermal-based)
- Culture conditions (LN-based)
- Dose regime
- Normalizations
- Chemical specific
- Epidermis
- Lymph node
- Sensitivity analysis
 - Untitled
- Active Sets
- Diagram Parameters

Parameter Set Format

Name: Michaelis-Menten Parameters

Description:

Short Name:

Parameters

Value Sets

Remove

Add

Duplicate

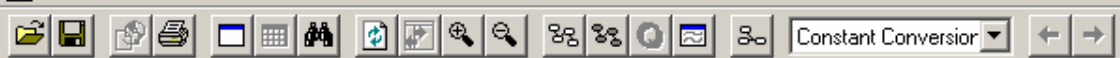
Edit

Remove

OK

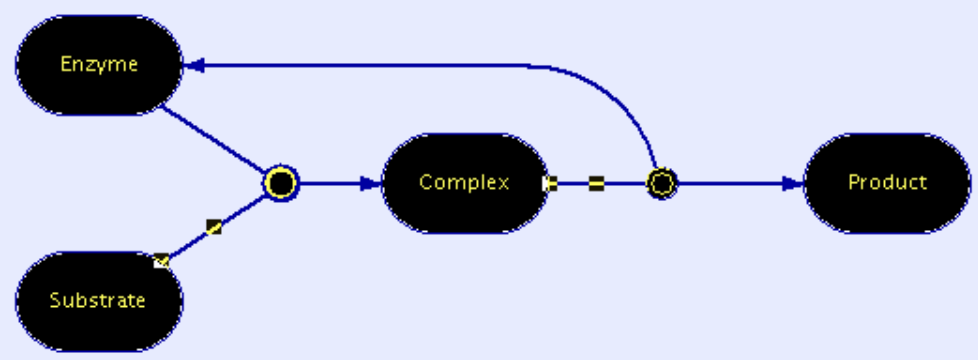
Cancel





- Parameter Sets
 - Static function nodes
 - Epidermal and lymph node physiology
 - Culture conditions (epidermal-based)
 - Culture conditions (LN-based)
 - Dose regime
 - Normalizations
 - Chemical specific
 - Epidermis
 - Lymph node
 - Sensitivity analysis
 - Michaelis-Menten Parameters
- Active Sets
- Diagram Parameters

Michaelis Menten Reaction



Parameter ... Experiments Global Res...

- Parameter Sets
 - Static function nodes
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 - Culture conditions (LN-based)
 - Dose regime
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 - Epidermis
 - Lymph node
 - Sensitivity analysis
 - Michaelis-Menten Parameters
- Active Sets
- Diagram Parameters

Parameter Set

Name: Michaelis-Menten Parameters

Description:

Value Set

Name: Reference Patient

Description:

Notes... Format...

Type	Location	Parameter	Baseline Value Set	Alternate Value Set
				Reference Patient
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<input checked="" type="checkbox"/>	'Substrate' and 'Enzyme' -> 'Complex'	Kr	1.0	
<input checked="" type="checkbox"/>	'Substrate' and 'Enzyme' -> 'Complex'	sto_Substrate	1.0	
<input checked="" type="checkbox"/>	'Substrate' and 'Enzyme' -> 'Complex'	sto_Enzyme	1.0	
<input checked="" type="checkbox"/>	'Substrate' and 'Enzyme' -> 'Complex'	sto_Complex	1.0	
<input checked="" type="checkbox"/>	'Complex' -> 'Enzyme' and 'Product'	Kf	1.0	
<input checked="" type="checkbox"/>	'Complex' -> 'Enzyme' and 'Product'	sto_Complex	1.0	
<input checked="" type="checkbox"/>	'Complex' -> 'Enzyme' and 'Product'	sto_Enzyme	1.0	
<input checked="" type="checkbox"/>	'Complex' -> 'Enzyme' and 'Product'	sto_Product	1.0	
<input type="checkbox"/>	Product	Status	Computed	
<input type="checkbox"/>	Product	So	0.0	
<input type="checkbox"/>	Product	h	0	
<input type="checkbox"/>	Complex	Status	Computed	
<input type="checkbox"/>	Complex	So	0.0	
<input type="checkbox"/>	Complex	h	0	
<input type="checkbox"/>	Substrate	Status	Computed	
<input type="checkbox"/>	Substrate	So	0.0	1
<input type="checkbox"/>	Substrate	h	0	
<input type="checkbox"/>	Enzyme	Status	Computed	
<input type="checkbox"/>	Enzyme	So	0.0	1
<input type="checkbox"/>	Enzyme	h	0	

Parameter ... Experiments Global Res...

- Parameter Sets
 - Static function nodes
 - Epidermal and lymph node physiology
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 - Culture conditions (LN-based)
 - Dose regime
 - Normalizations
 - Chemical specific
 - Epidermis
 - Lymph node
 - Sensitivity analysis
 - Michaelis-Menten Parameters
- Active Sets
- Diagram Parameters

Parameter Set

Name: Michaelis-Menten Parameters

Description:

Value Set

Name: Virtual Patient 1

Description:

Notes... Format...

Type	Location	Parameter	Baseline Value Set	Alternate Value Set
				Virtual Patient 1
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<input checked="" type="checkbox"/>	'Complex' -> 'Enzyme' and 'Product'	Kf	1.0	
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<input type="checkbox"/>	Substrate	Status	Computed	
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<input type="checkbox"/>	Enzyme	h	0	



PhysiLab Browser - Entelos_presentation.elf

Parameter ... Experiments Global Res...

- Parameter Sets
 - Static function nodes
 - Epidermal and lymph node physiology
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 - Dose regime
 - Normalizations
 - Chemical specific
 - Epidermis
 - Lymph node
 - Sensitivity analysis
 - Michaelis-Menten Parameters
- Active Sets
- Diagram Parameters

- Michaelis Menten (RP)
 - Notes
 - Charts
 - Plots
 - Monitors
 - Measurement Sets

Name: Michaelis Menten (RP)
Short Name:
Description:

Simulation Method: <Use Parent> : Adaptive
Active Set: <Use Parent> : MM

Experiment Protocol

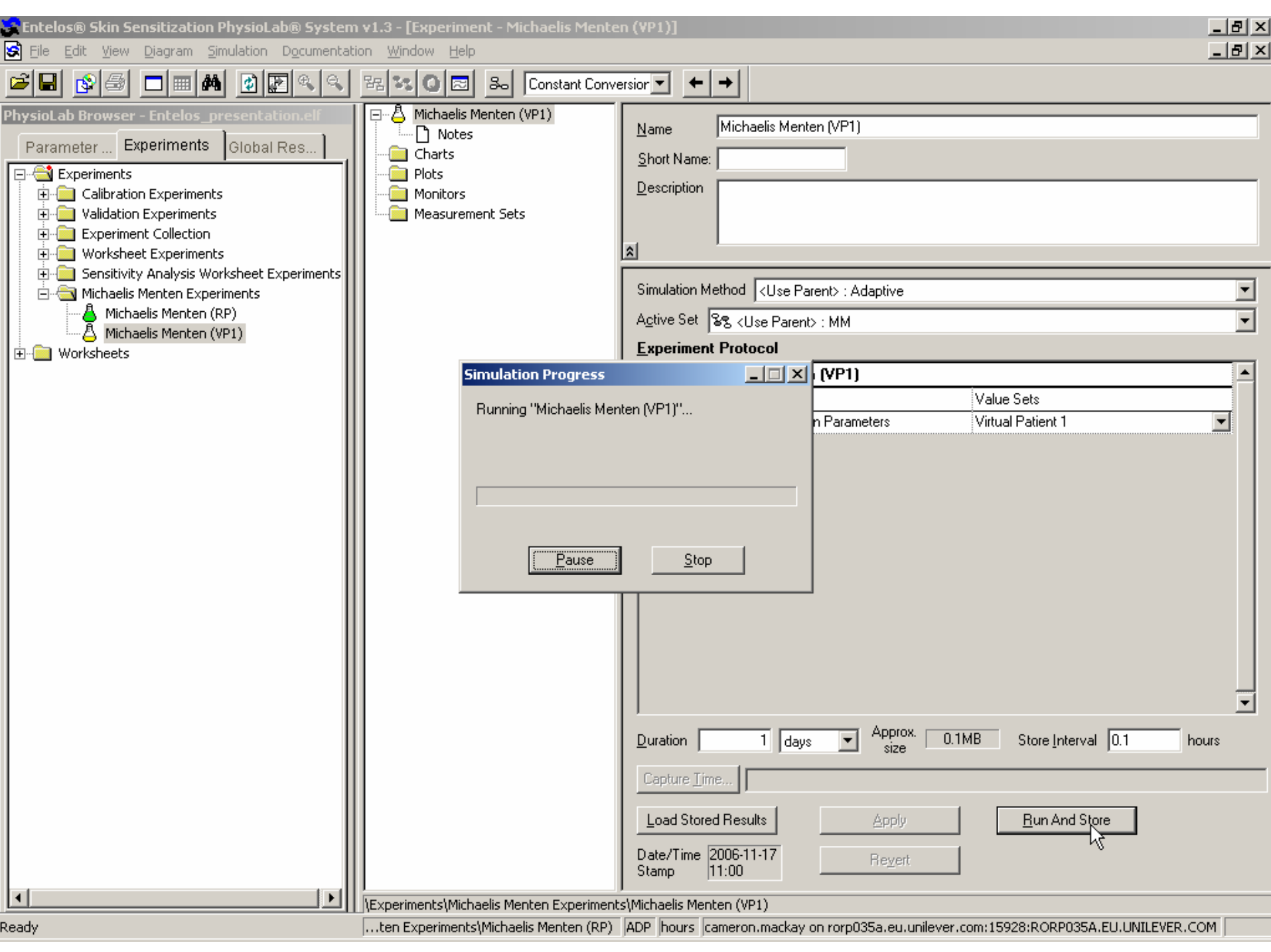
Parameter Sets	Value Sets
Michaelis-Menten Parameters	Reference Patient

Duration: 1 days Approx. size: 63 MB Store Interval: 0.1 hours

Capture Time:

Load Stored Results Apply Run And Store

Date/Time: 2006-11-17 11:00 Revert



- Experiments
 - Calibration Experiments
 - Validation Experiments
 - Experiment Collection
 - Worksheet Experiments
 - Sensitivity Analysis Worksheet Experiments
 - Michaelis Menten Experiments
 - Michaelis Menten (RP)
 - Michaelis Menten (VP1)
 - Worksheets

- Michaelis Menten (VP1)
 - Notes
 - Charts
 - Plots
 - Monitors
 - Measurement Sets

Name: Michaelis Menten (VP1)
Short Name:
Description:

Simulation Method: <Use Parent> : Adaptive
Active Set: <Use Parent> : MM

Experiment Protocol

Simulation Progress

Running "Michaelis Menten (VP1)"...

Michaelis Menten (VP1)

Parameters	Value Sets
Virtual Patient 1	Virtual Patient 1

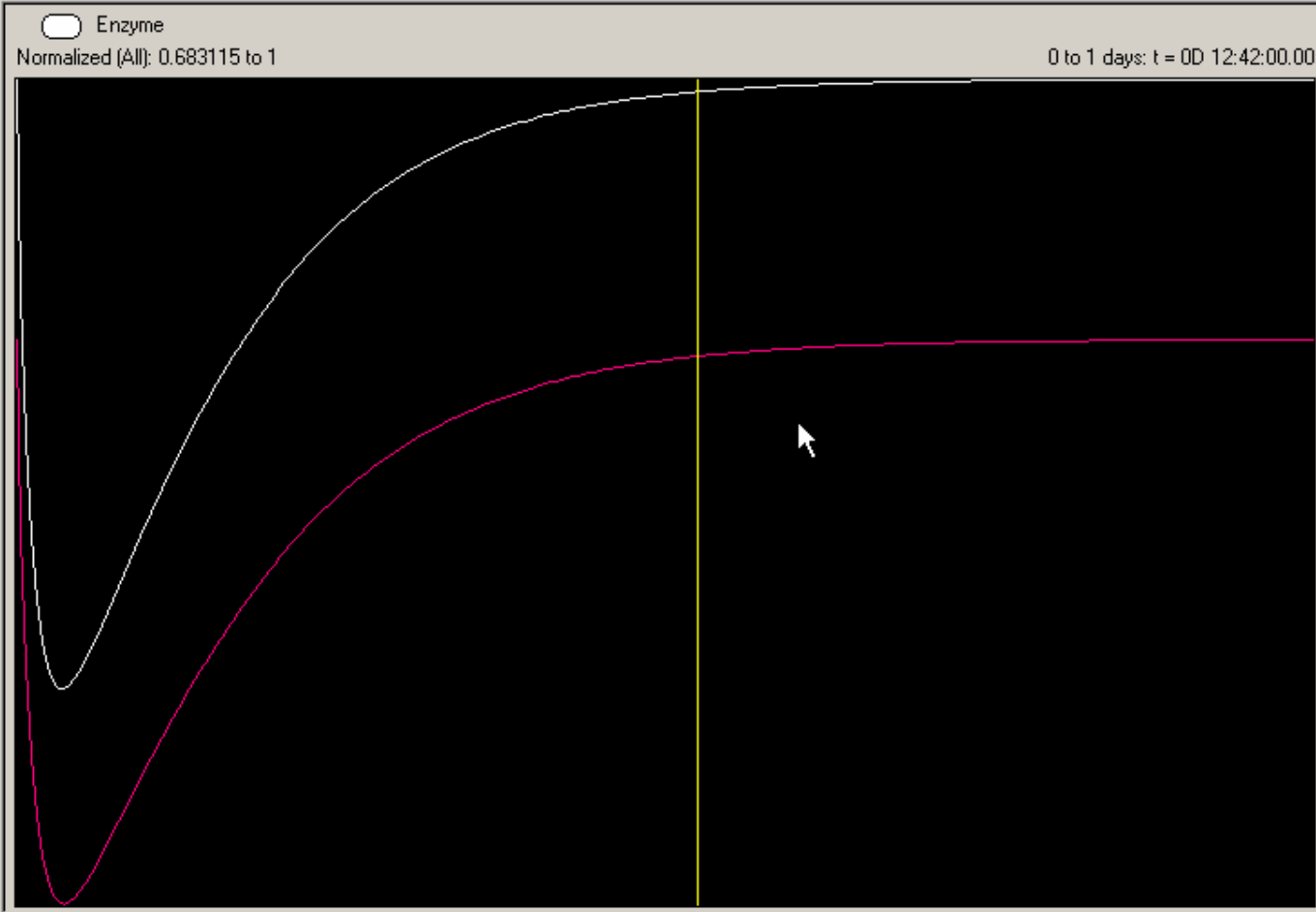
Duration: days Approx. size: Store Interval: hours

Capture Time:

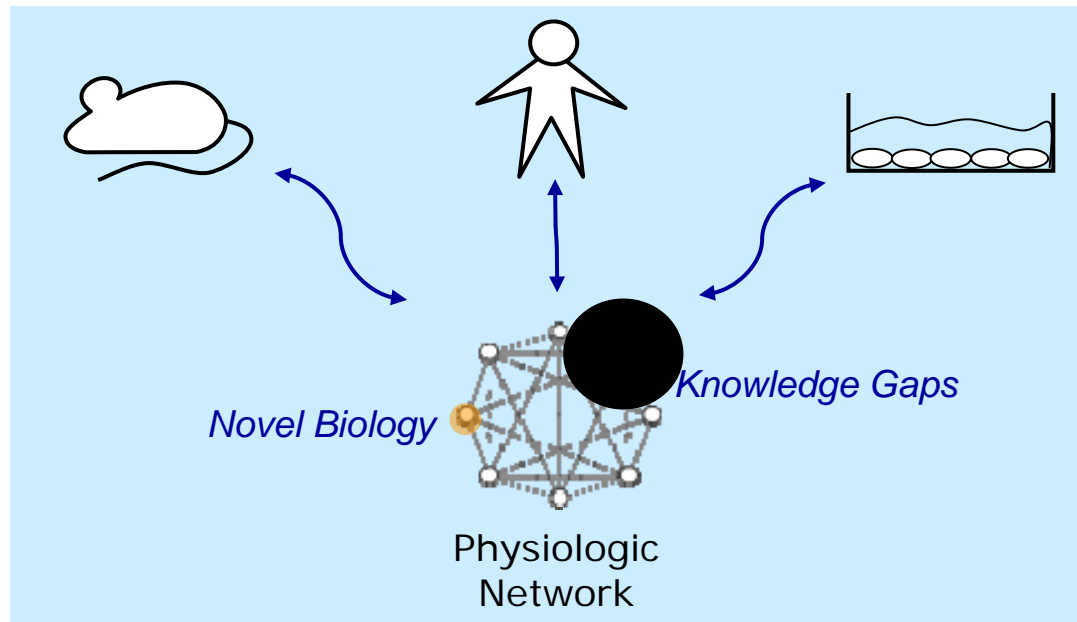
Date/Time: 2006-11-17 11:00

- Experiments
 - Calibration Experiments
 - Validation Experiments
 - Experiment Collection
 - Worksheet Experiments
 - Sensitivity Analysis Worksheet Experiments
 - Michaelis Menten Experiments
 - Michaelis Menten (RP)
 - Michaelis Menten (VP1)
 - Worksheets

Experiment Name	Value	Units
\Experiments\Michaelis Menten Experiments\Michaelis Menten (RP)	0.995154	
\Experiments\Michaelis Menten Experiments\Michaelis Menten (VP1)	0.893545	



Calibration process ensures proper subsystem behavior



- Implemented > 35 *in vitro*, *in vivo*, *ex vivo* experiments from 31 references

Model development – stage II

- Reference Patient (RP)
 - The calibration of the model thought to be most like the underlying biology

- Identification of knowledge gaps in Stage I leads to the formulation of alternative hypotheses

- Virtual Patients (VPs)
 - Alternative biological hypotheses to the RP represented by a number of distinct Virtual Patients (VPs)
 - The model can be interrogated for each VP
 - Conclusions robust to the knowledge gaps are obtained



PhysiLab Browser - Entelos

Para... Exper... Globa...

- Experiments
 - Calibration Experiment
 - Induction of Epide
 - LC Maturation
 - LC Migration
 - Physiological s
 - Calibrator
 - Calibrator
 - Calibrator
 - Xenobiotic stir
 - DC Stimulation
 - T Cell Naive Resp
 - Other LN Cells
 - LLNA and Other Bi
 - Validation Experiments
 - Experiment Collection
 - Worksheet Experiment
 - Sensitivity Analysis Wk
 - Michaelis Menten Expe
 - Worksheets

- Calibration: Accumulation of LC in
 - Notes
 - Charts
 - Plots
 - Monitors
 - Measurement Sets
 - Epidermal LC
 - Mature LN LC
 - LC numbers

Name: Calibration: Accumulation of LC in LN following IL-1 alpha or IL-1 beta treatment (Cumberbatch 2002a)

Short Name:

Description: Reproduction of IL-1 injection-induced migration of epidermal LC. System: in-vivo murine

Simulation Method: <Use Parent>: Adaptive

Active Set: <All nodes>

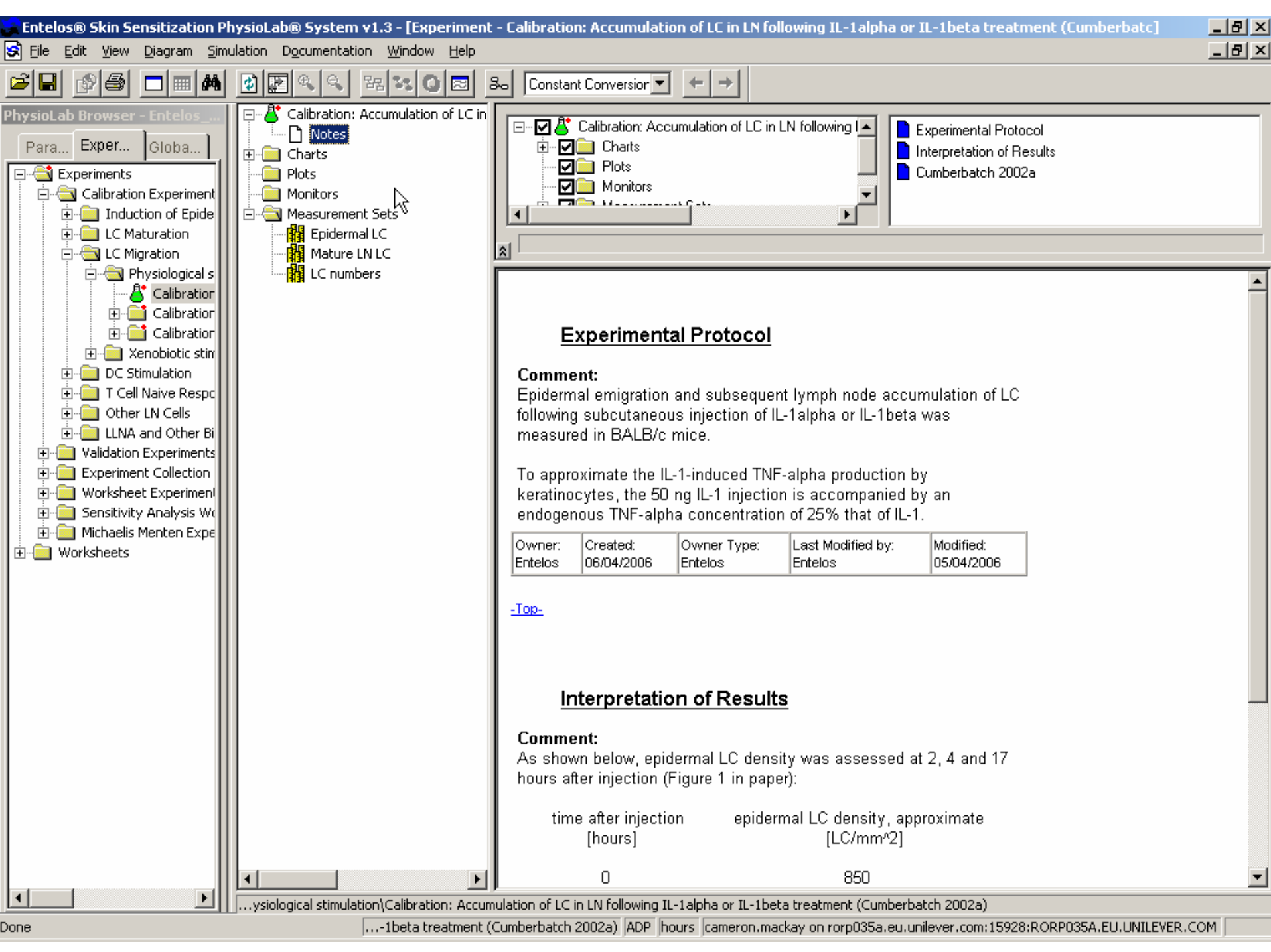
Experiment Protocol

+	Reference patient 1.3 (murine)	
-	Calibration: Accumulation of LC in LN following IL-1 alpha or IL-1 beta treatment (Cumberbatch	
	Parameter Sets	Value Sets
	Epidermal and lymph node physiology	mouse
	Epidermal cytokines	50 ng IL-1a injection (+ 25% endogenous TNF-a) into
	Dose regime	surface area = 1 cm ²
	Static function nodes	relink

Duration: 24 hours Approx. size: 0.9MB Store Interval: 0.1 hours

Capture Time: End of initialization experiment: 1 days

Date/Time Stamp: 2006-11-17 11:32



- Experiments
 - Calibration Experiment
 - Induction of Epide
 - LC Maturation
 - LC Migration
 - Physiological s
 - Calibration
 - Calibrator
 - Calibrator
 - Xenobiotic stir
 - DC Stimulation
 - T Cell Naive Respc
 - Other LN Cells
 - LLNA and Other Bi
 - Validation Experiments
 - Experiment Collection
 - Worksheet Experiment
 - Sensitivity Analysis Wc
 - Michaelis Menten Expe
 - Worksheets

- Calibration: Accumulation of LC in
 - Notes
 - Charts
 - Plots
 - Monitors
 - Measurement Sets
 - Epidermal LC
 - Mature LN LC
 - LC numbers

- Calibration: Accumulation of LC in LN following
 - Charts
 - Plots
 - Monitors
 - Measurement Sets

- Experimental Protocol
- Interpretation of Results
- Cumberbatch 2002a

Experimental Protocol

Comment:
 Epidermal emigration and subsequent lymph node accumulation of LC following subcutaneous injection of IL-1alpha or IL-1beta was measured in BALB/c mice.

To approximate the IL-1-induced TNF-alpha production by keratinocytes, the 50 ng IL-1 injection is accompanied by an endogenous TNF-alpha concentration of 25% that of IL-1.

Owner:	Created:	Owner Type:	Last Modified by:	Modified:
Entelos	06/04/2006	Entelos	Entelos	05/04/2006

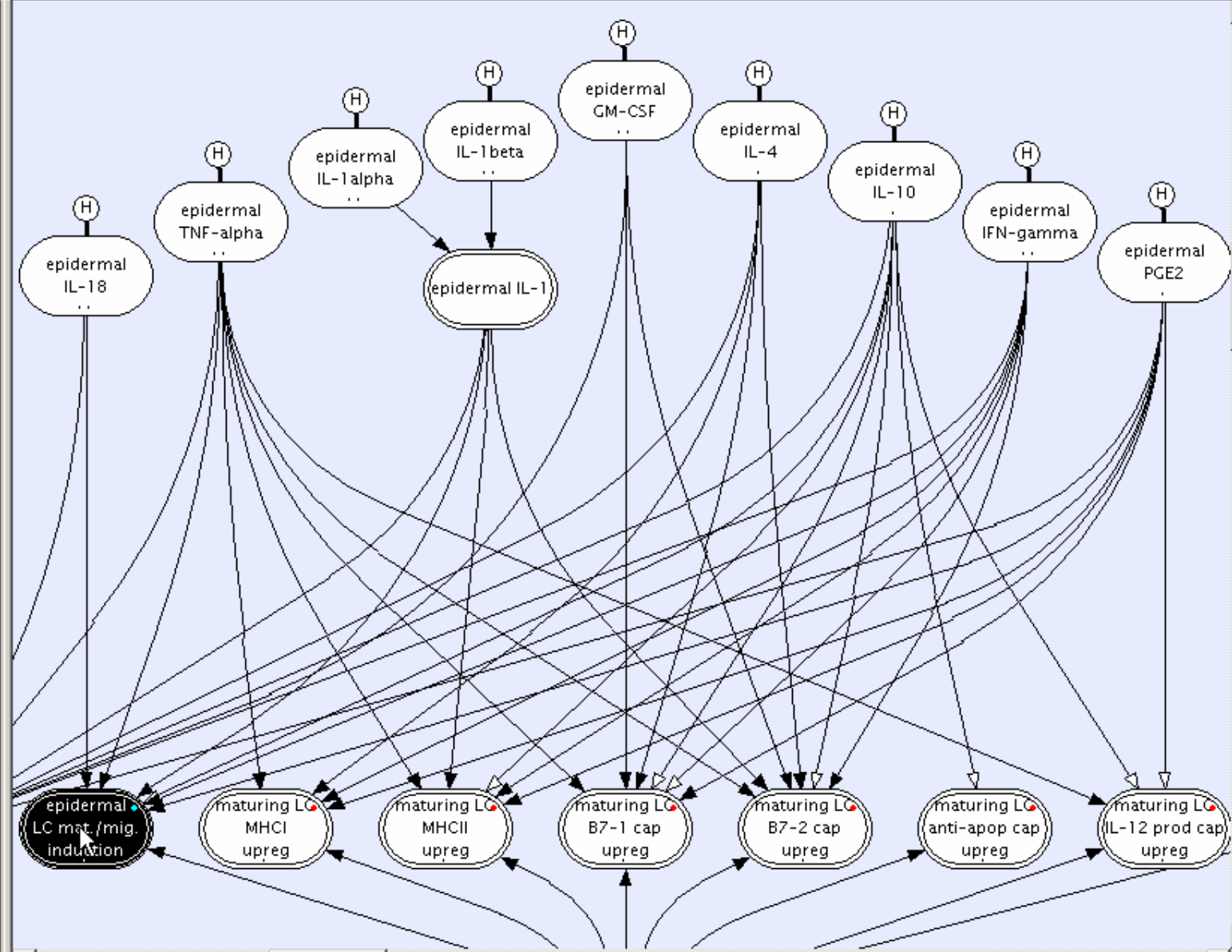
[-Top-](#)

Interpretation of Results

Comment:
 As shown below, epidermal LC density was assessed at 2, 4 and 17 hours after injection (Figure 1 in paper):

time after injection [hours]	epidermal LC density, approximate [LC/mm ²]
0	850

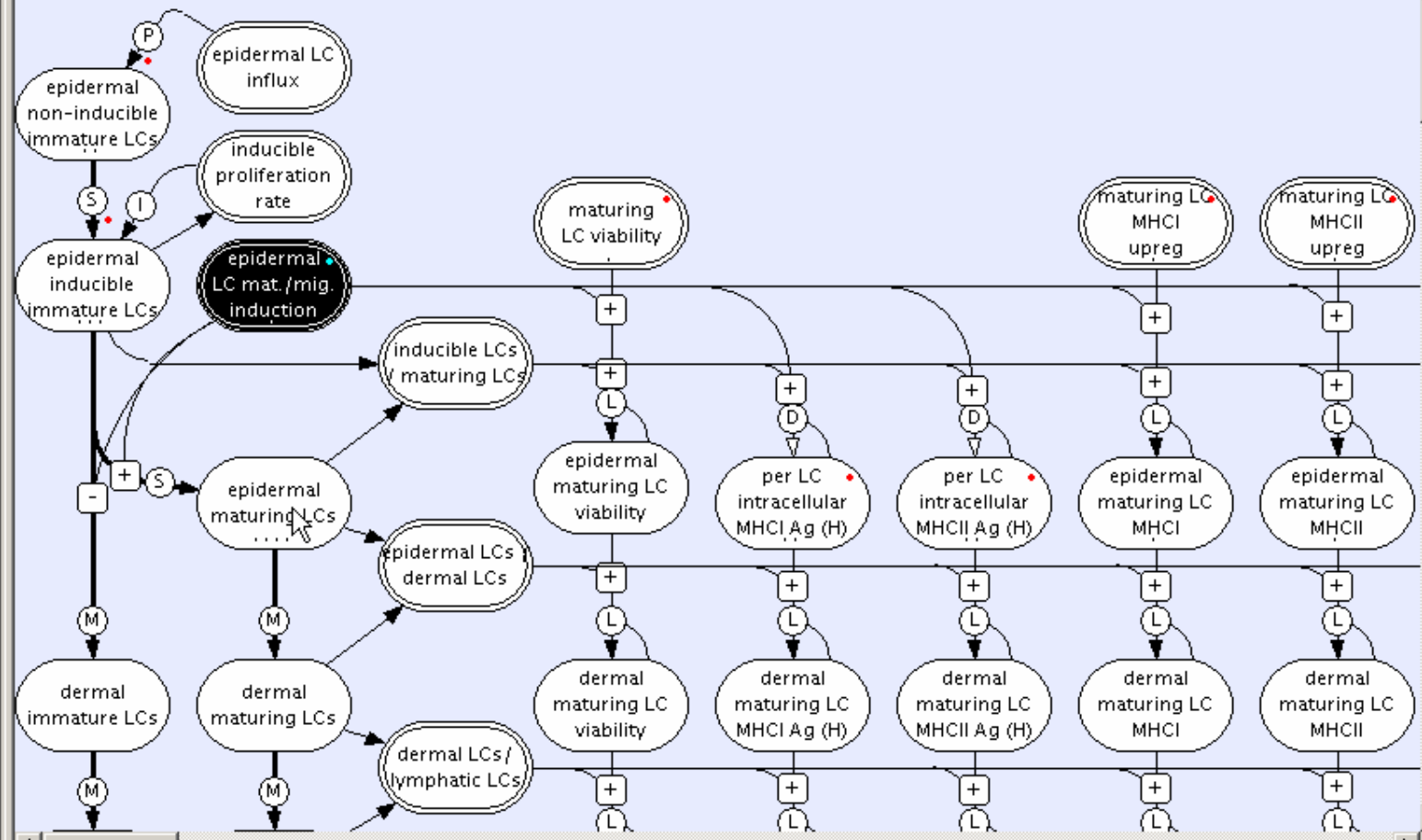
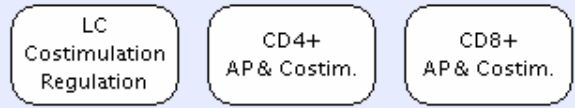
- Para... Exper... Globa...
- Experiments
 - Calibration Experiment
 - Induction of Epide
 - LC Maturation
 - LC Migration
 - Physiological s
 - Calibrator
 - Calibrator
 - Calibrator
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 - Validation Experiments
 - Experiment Collection
 - Worksheet Experiment
 - Sensitivity Analysis Wk
 - Michaelis Menten Expe
 - Worksheets

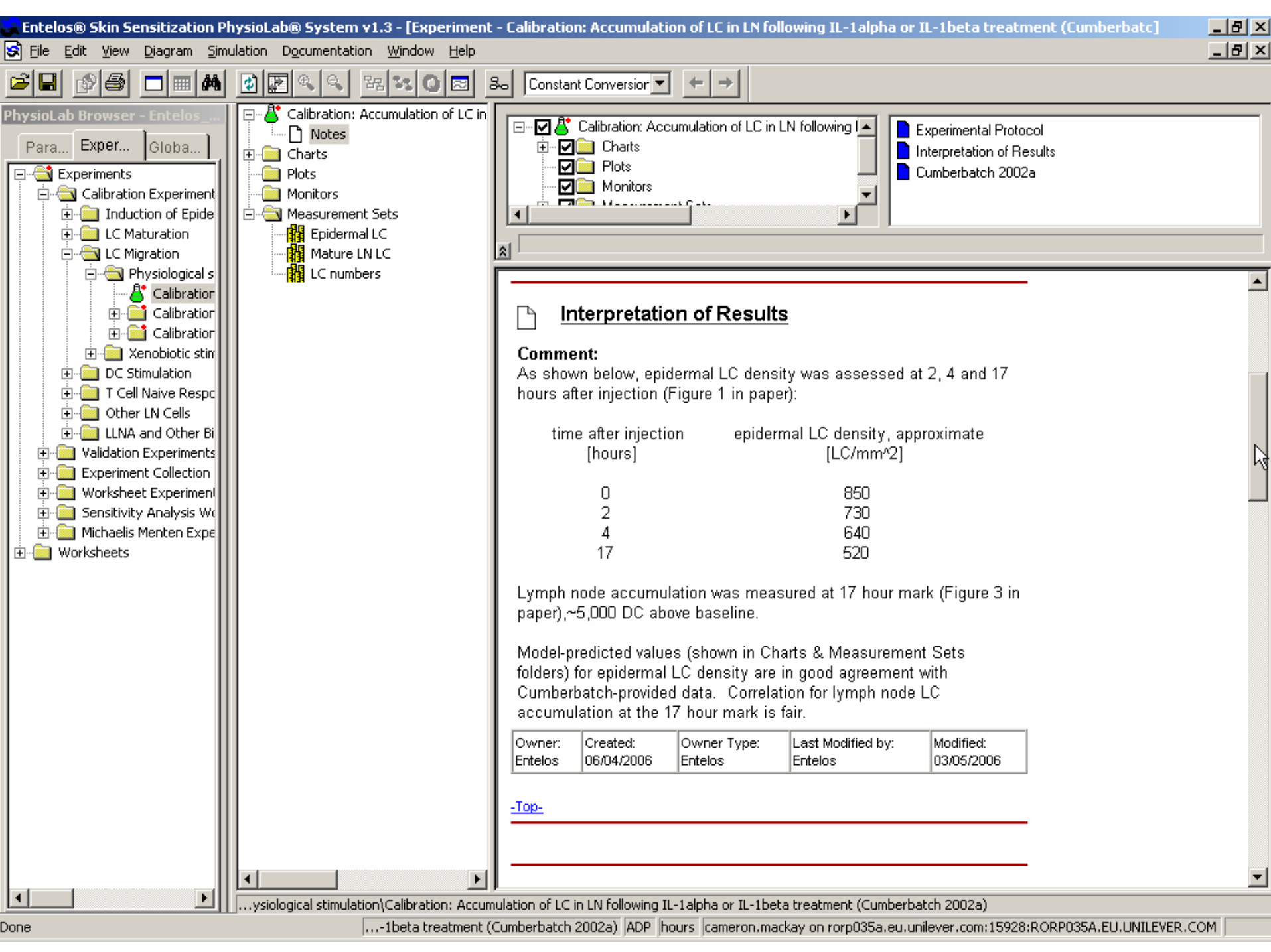


- Para... Exper... Globa...
- Experiments
 - Calibration Experiment
 - Induction of Epide
 - LC Maturation
 - LC Migration
 - Physiological s
 - Calibration
 - Calibrator
 - Calibration
 - Xenobiotic stir
 - DC Stimulation
 - T Cell Naive Respc
 - Other LN Cells
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 - Validation Experiments
 - Experiment Collection
 - Worksheet Experiment
 - Sensitivity Analysis Wc
 - Michaelis Menten Expe
 - Worksheets

- A Allows
- D Decreases
- H Half-Life
- I Increases
- L Leads
- M Moves
- P Produces
- S Changes State

Effects of Epidermal Cytokines on LC Mobilization and Migration





Para... Exper... Globa...

- Experiments
 - Calibration Experiment
 - Induction of Epide
 - LC Maturation
 - LC Migration
 - Physiological s
 - Calibration
 - Calibrator
 - Calibrator
 - Xenobiotic stir
 - DC Stimulation
 - T Cell Naive Respc
 - Other LN Cells
 - LLNA and Other Bi
 - Validation Experiments
 - Experiment Collection
 - Worksheet Experiment
 - Sensitivity Analysis Wc
 - Michaelis Menten Expe
- Worksheets

Calibration: Accumulation of LC in LN follo

- Notes
- Charts
- Plots
- Monitors
- Measurement Sets
 - Epidermal LC
 - Mature LN LC
 - LC numbers**

Name: LC numbers

Short Name:

Description:

	i	Name	Object	Definition	Value	Units
<input type="checkbox"/>			epidermal LC area density	Value at 0 hours	850.076	cells/mm ²
<input type="checkbox"/>			epidermal LC area density	Value at 2 hours	745.622	cells/mm ²
<input type="checkbox"/>			epidermal LC area density	Value at 4 hours	666.218	cells/mm ²
<input type="checkbox"/>			epidermal LC area density	Value at 17 hours	478.528	cells/mm ²

PhysiLab Browser - Entelos_presentation.elf

Parameter Sets Experiments Global Results

- Experiments
 - Calibration Experiments
 - Validation Experiments
 - Experiment Collection
 - Worksheet Experiments
 - Virtual Patients
 - Reference patients
 - [RP1.3] Reference patient 1.3 (murine)
 - Reference patient history
 - Alternate virtual patients
 - VP2 - fewer clones, more proliferation
 - VP3 - more clones, less proliferation
 - VP4 - vary influx to lymph node
 - VP5 - CD4+ progressive, CD8+ progr
 - Virtual Chemicals
 - Generic Application Protocols
 - Chemical-Specific Application Protocols
 - Sensitivity Analysis Worksheet Experiments
 - Michaelis Menten Experiments
 - Worksheets

Name: Reference patient 1.3 (murine)

Short Name: RP1.3

Description: This experiment initializes the first generation murine reference patient.

Simulation Method <Use Parent> : Adaptive

Active Set <All nodes>

Experiment Protocol

Reference patient 1.3 (murine)	
Parameter Sets	Value Sets
CD4+ T cells initial populations	300 clones
CD8+ T cells initial populations	300 clones
APC competition	CD4+ index = 0.5; CD8+ index = 0.5
Thymidine specific activity	standard LLNA
Non-Ag-specific background proliferation	0.0014
Epidermal and lymph node physiology	mouse

Duration: 1 days Approx. size: 0.26MB Store Interval: 1 hours

Capture Time...

Load Stored Results Apply Run And Store

Date/Time: 2006-11-17 11:32 Revert

PhysiLab Browser - Entelos_presentation.elf

Parameter Sets Experiments Global Results

Experiments

- Calibration Experiments
- Validation Experiments
- Experiment Collection
- Worksheet Experiments
 - Virtual Patients
 - Reference patients
 - [RP1.3] Reference patient 1.3 (murine)
 - Reference patient history
 - Alternate virtual patients
 - VP2 - fewer clones, more proliferation
 - VP3 - more clones, less proliferation
 - VP4 - vary influx to lymph node
 - VP5 - CD4+ progressive, CD8+ programmed
 - [VP5.0] VP5.0 - CD4+ progressive
 - [VP5.1] VP5.1 - CD4+ progressive
 - Virtual Chemicals
 - Generic Application Protocols
 - Chemical-Specific Application Protocols
 - Sensitivity Analysis Worksheet Experiments
 - Michaelis Menten Experiments
 - Worksheets

Name: VP5.1 - CD4+ progressive, CD8+ programmed, compensatory changes

Short Name: VP5.1

Description: This virtual patient is a variation on the reference patient, with a more progressive behavior for CD4+ T cells, and a more programmed behavior for CD8+ T cells, along with compensatory changes to meet data constraints. Being more programmed gives CD8+ T cells a proliferative advantage, since they have less of a need to revisit the I.C. to keep proliferation. In order to meet the data constraint that the CD4:CD8 ratio remain relatively constant...

Simulation Method: <Use Parent> : Adaptive

Active Set: <All nodes>

Experiment Protocol

+	Reference patient 1.3 (murine)
-	VP5.1 - CD4+ progressive, CD8+ programmed, compensatory changes
-	Parameter Sets
	Value Sets
	APC competition
	CD4+ progressive index = 0.8
	APC competition
	CD8+ progressive index = 0.2
	CD8+ T cell life cycle regulation
	greater CD28 activation requirement
	CD8+ T cell life cycle regulation
	greater TCR + costim requirement (apoptosis)
	CD8+ T cell life cycle regulation
	greater TCR + costim requirement (Nth div.)
	CD8+ T cell life cycle regulation
	greater avg cell div effect on Nth div fraction
	CD4+ T cell life cycle regulation
	greater TCR + costim effect (Nth div fraction)
	CD4+ T cell life cycle regulation
	greater TCR + costim effect (apoptosis)
	CD4+ T cell life cycle regulation
	less CTLA-4 effect (max = 0.6) on Nth div fraction

Duration: 10 hours

Approx. size: 0.48MB

Store Interval: 0.1 hours

Capture Time: End of initialization experiment: 1 days

Buttons: Load Stored Results, Apply, Run And Store, Revert

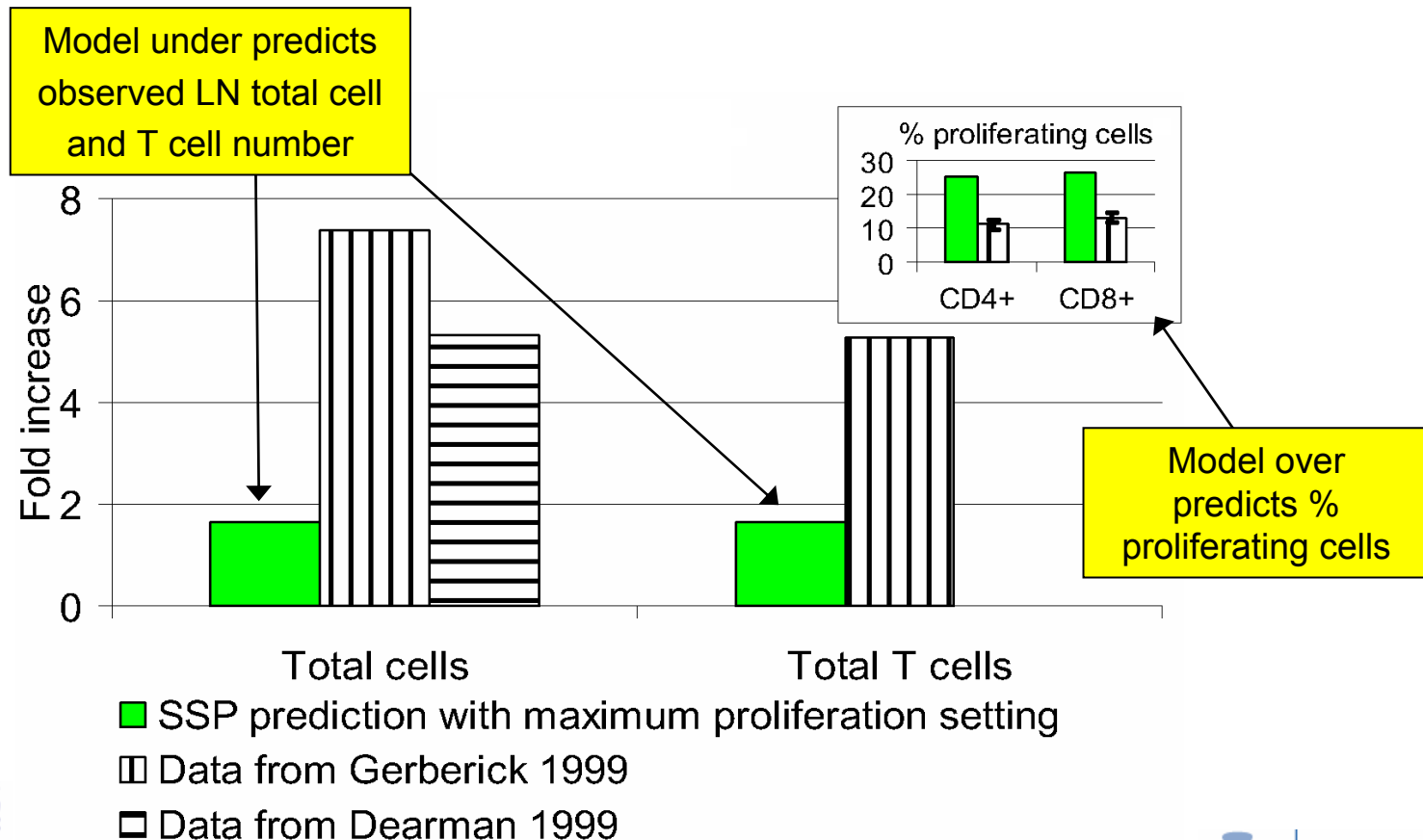
Date/Time: 2006-11-17 11:51

Stamp: 11:51

...te virtual patients\VP5 - CD4+ progressive, CD8+ programmed\VP5.1 - CD4+ progressive, CD8+ programmed, compensatory changes

Model Insights

- During calibration phase, model was unable to reproduce published lymph node cell number data (example: 0.25% DNCB exposure in LLNA shown)



Modelling reveals new biological insights

- **Hypothesis 1:** T cells must undergo > 7 proliferations in sensitizer-induced responses.
- Model required > 20 proliferations to match data
 - Still over predicted % of proliferating cells
 - No experimental evidence to support this hypothesis and runs against infection data (approx. 5-6 proliferations)
- **Hypothesis 2:** Increased recruitment of lymphocytes to the lymph node supplements the total cell population
- Does experimental evidence support this hypothesis?

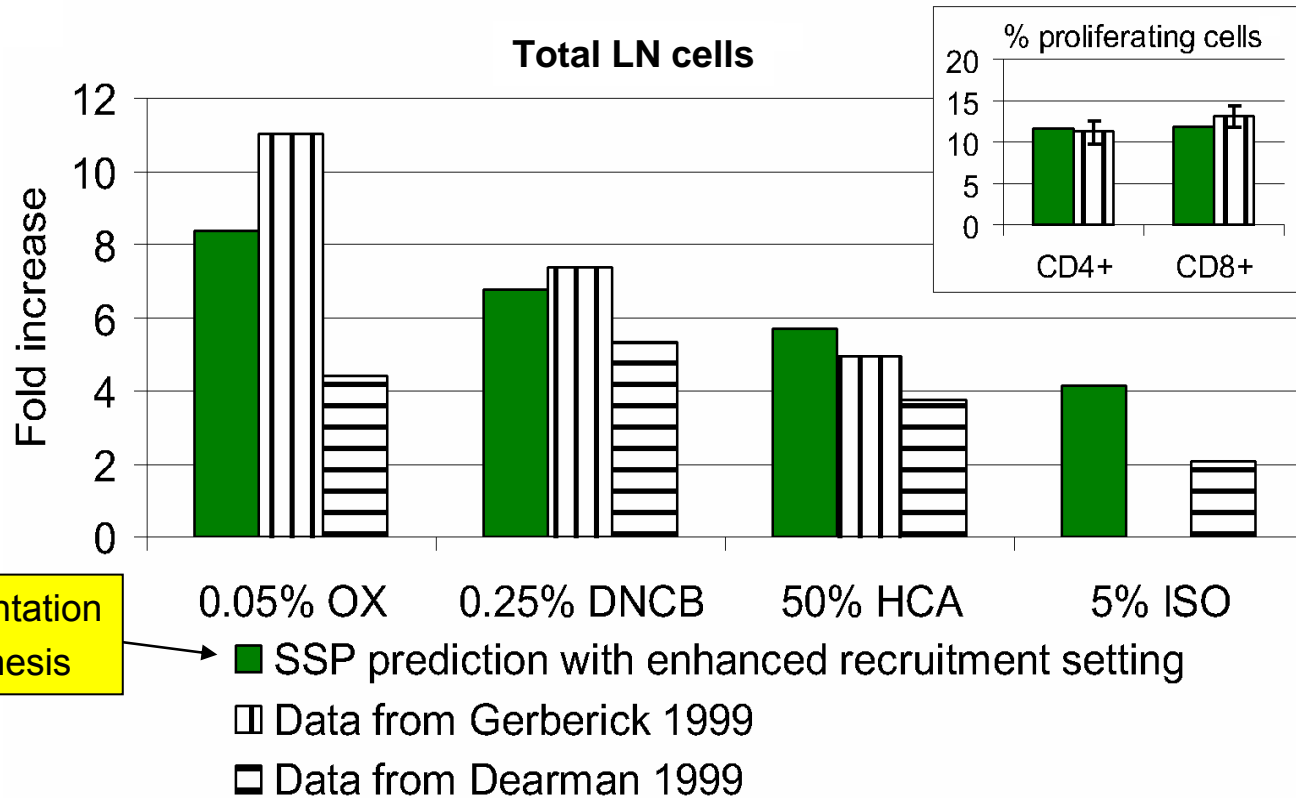
Modelling reveals new biological insights

- Tedla *et al.* 1998. *J. Immunol.* **161**. 5663-5672
 - DNFB (sensitizer) exposure on skin induces mouse LN chemokine production (MIP-1 α/β)
 - Peripheral leukocyte numbers depleted by 50% at 30mins after exposure

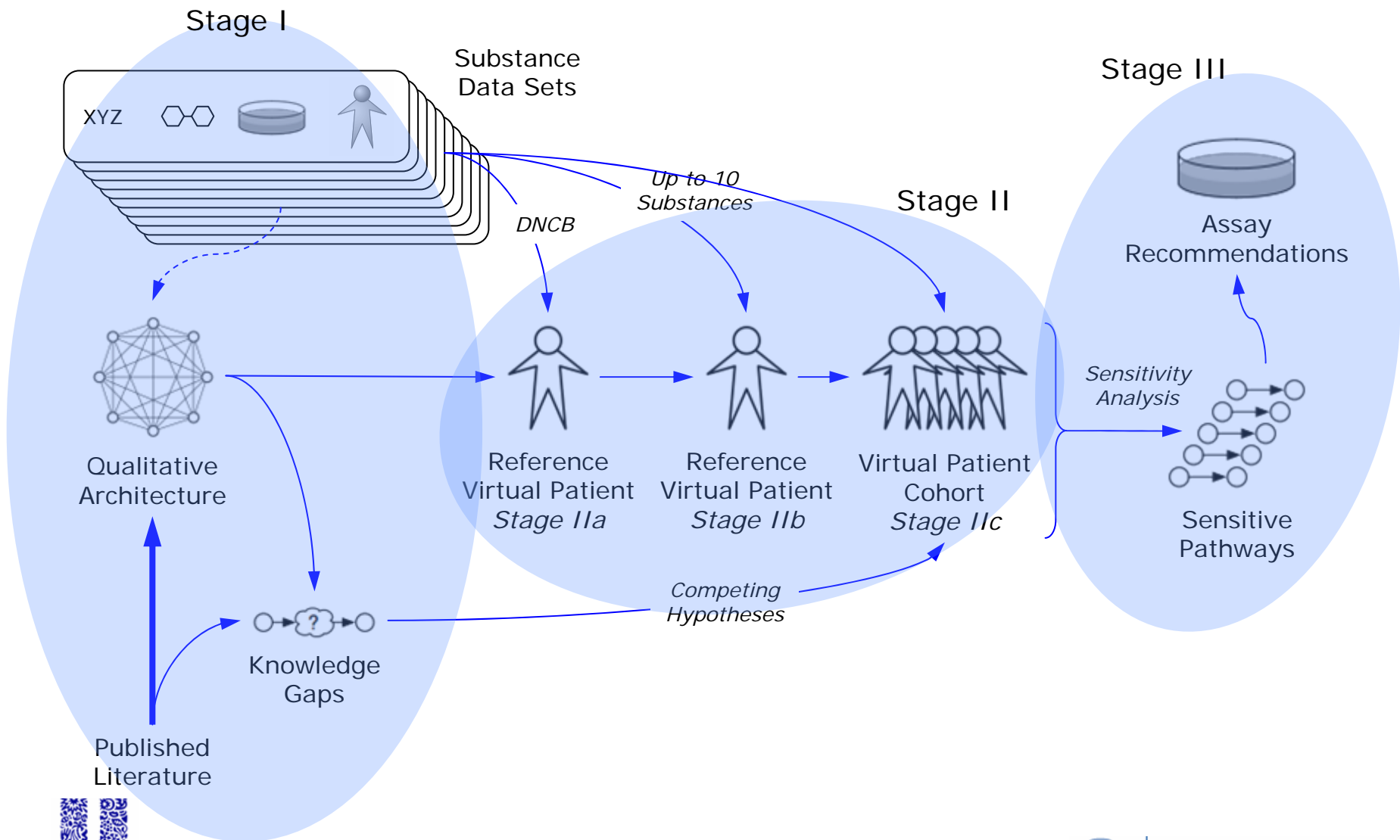
- Soderberg *et al.* 2005. *PNAS.* **45**. 16315-16320
 - TLR agonist intradermal exposure and Herpes Simplex virus infection caused massive recruitment of naïve lymphocytes to LN.
 - Most LN cells are non-proliferating (95%)
 - Proposed mechanism is via vessel re-modelling: greatly increases LN cell turnover.

New Insight: Cell recruitment to the lymph node

Hypothesis 2 implemented



Skin Sensitization Induction PhysioLab Platform (SSIPP)



Model development – stage III: validation process

- **Goal:** Ensure that the calibrated mechanisms together reproduce the system-level physiologic behaviors associated with chemical sensitization
 - Demonstrate accurate prediction of T cell count and proliferation rate
 - Demonstrate the ability to capture chemical properties and behaviors
- **Approach:** Implementation of 30 validation experiments from 15 papers
- **Considerations:**
 - Protocol: standard & modified LLNA
 - Outputs: SI, relative LN composition, absolute cell numbers
 - Other literature: supporting or inconsistent data
 - Relevance: quantitative or qualitative match expected
- **Outcome:**
 - Complete agreement with 28/30 experiments
 - Partial agreement with 2/30 experiments

- Virtual Patients reduced
 - Notes
 - Comparison Charts
 - Measurement Sets
 - Comparison Measurement Tables

Name: Virtual Patients reduced

Short Name:

Description: This worksheet tests the DNCB responses in the various virtual patients.

	RP 1.3	VP 2.1	VP 3.1	VP 4.1	VP 5.1
0.025% DNCB/AOO					
0.1% DNCB/AOO: 3					
0.25% DNCB/AOO:					
1% DNCB/AOO: 3 a					

Reference patient 1.3 (murine)--0.025% DNCB/AOO: 3 apps



Name: Reference patient 1.3 (murine)--0.025% DNCB/AOO: 3 apps

Short Name: RP1.3--0.025% DNC

Description: This experiment initializes the first generation murine reference patient.

Simulation Method: <Use Parent> : Adaptive

Active Set: <All nodes>

Experiment Protocol

Reference patient 1.3 (murine)		
Duration	1	days
Parameter Sets	Value Sets	
CD4+ T cells initial populations	300 clones	
CD8+ T cells initial populations	300 clones	
APC competition	CD4+ index = 0.5; CD8+ index = 0.5	
Thymidine specific activity	standard LLNA	
Non-Ag-specific background proliferation	0.0014	
Epidermal and lymph node physiology	mouse	
Reference patient 1.3 (murine)--0.025% DNCB/AOO: 3 apps		
Parameter Sets	Value Sets	
Chemical specific exposure	murine baseline DNCB/AOO	
Chemical specific effects	murine baseline DNCB	
Dose regime	0.025%	
Dose regime	3 dose (LLNA timings)	

Duration: 10 days Approx. size: 7.3MB Store Interval: 0.1 hours

Capture Time...: End of initialization experiment: 1 days

Load Stored Results Apply Run And Store

Date/Time Stamp: 2006-11-17 12:24 Revert

Constant Converter

Name VP5.1 - CD4+ progressive, CD8+ programmed, compensatory changes--1% DNCB/AOO: 3 apps

Short Name: VP5.1--1% DNCB/A

Description This virtual patient is a variation on the reference patient, with a more progressive behavior for CD4+ T cells, and a more programmed behavior for CD8+ T cells, along with compensatory changes to meet data constraints. Being more programmed gives CD8+ T cells a proliferative advantage, since they have less of a need to revisit the LC to keep proliferating. In order to meet the data constraint that the CD4:CD8 ratio remain relatively constant across doses (Suda 2002a), it was necessary to make adjustments to proliferation parameters that would give CD4+ T cells an advantage. With this implementation, CD8+ proliferation is marginally low but within a reasonable range considering

Simulation Method <Use Parent> : Adaptive

Active Set <Use Parent> : <All nodes>

Experiment Protocol

+ Reference patient 1.3 (murine)	
+ VP5.1 - CD4+ progressive, CD8+ programmed, compensatory changes	
Duration	10 hours
Capture Time	1 days
- Parameter Sets	Value Sets
APC competition	CD4+ progressive index = 0.8
APC competition	CD8+ progressive index = 0.2
CD8+ T cell life cycle regulation	greater CD28 activation requirement
CD8+ T cell life cycle regulation	greater TCR + costim requirement (apoptosis)
CD8+ T cell life cycle regulation	greater TCR + costim requirement (Nth div.)
CD8+ T cell life cycle regulation	greater avg cell div effect on Nth div fraction
CD4+ T cell life cycle regulation	greater TCR + costim effect (Nth div fraction)
CD4+ T cell life cycle regulation	greater TCR + costim effect (apoptosis)
CD4+ T cell life cycle regulation	less CTLA-4 effect (max = 0.6) on Nth div fraction
- VP5.1 - CD4+ progressive, CD8+ programmed, compensatory changes--1% DNCB/AOO: 3 apps	

Duration 10 days Approx. size 7.3MB Store Interval 0.1 hours

Capture Time... End of initialization experiment: 10 hours

Load Stored Results Apply Run And Store

Date/Time 2006-11-17 Revert Stamp 12:29

- Virtual Patients reduced
 - Notes
 - Comparison Charts
 - Compare VPs
 - Dose response
 - Total cells with varying division time:
 - Total cells with varying division time:
 - Total proliferation rate - 1% DNCB
 - Total proliferation rate - 0.25% DNCB
 - Measurement Sets
 - Comparison Measurement Tables

Name: Virtual Patients reduced

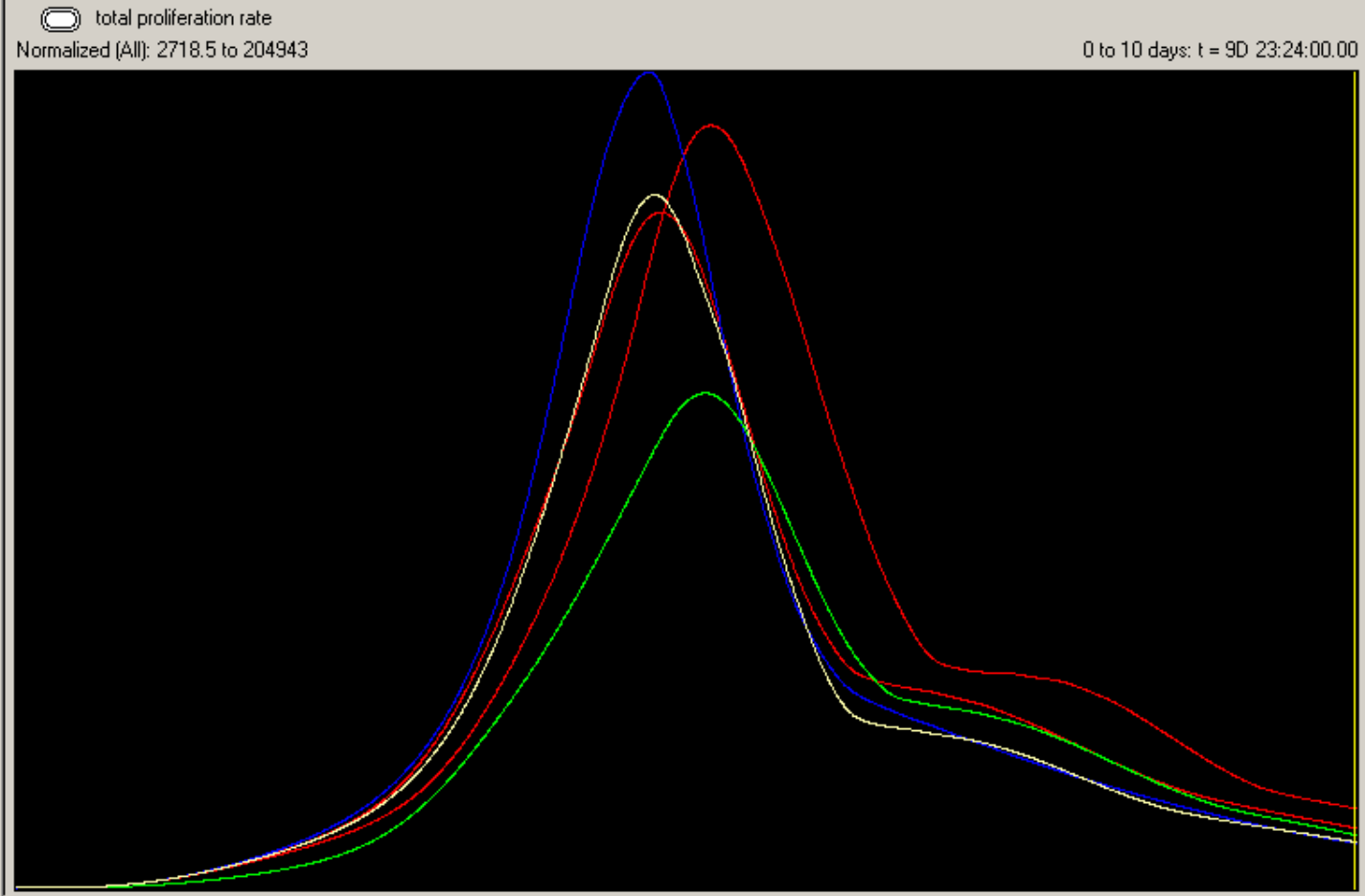
Short Name:

Description: This worksheet tests the DNCB responses in the various virtual patients.

	RP1.3	VP2.1	VP3.1	VP4.1	VP5.1
0.025% DNCB/AOO					
0.1% DNCB/AOO: 3					
0.25% DNCB/AOO:					
1% DNCB/AOO: 3 a					

- Virtual Patients reduced
 - Notes
 - Comparison Charts
 - Measurement Sets
 - Comparison Measurement Tables
 - 0.25% DNCB response type compar
 - 0.25% DNCB - % activated and pro
 - 1% DNCB response type comparison

Experiment Name	Value	Units
Reference patient 1.3 (murine)--1% DNCB/AOO: 3 apps	17623.6	cell...
VP2.1 - fewer clones, more proliferation, compensatory changes--1% ...: 3 apps	22480.7	cell...
VP3.1 - more clones, less proliferation, compensatory changes--1% D...: 3 apps	13927.1	cell...
VP4.1 - reduced influx modulation--1% DNCB/AOO: 3 apps	15953.6	cell...
VP5.1 - CD4+ progressive, CD8+ programmed, compensatory change...: 3 apps	14203	cell...



Name	Object	RP1.3--1% D...	VP2.1--1% D...	VP3.1--1% D...	VP4.1--1% D...	VP5.1--1% D...	Units
LN total cells (Value at 0 days)		1.950000e+006	1.950000e+006	1.950000e+006	1.950000e+006	1.950000e+006	cells
LN total cells (Value at 5.2083 days)		1.565468e+007	1.579994e+007	1.627434e+007	8.218700e+006	1.568219e+007	cells
LN total cells (Value at 5.2083 days - delta%)		702.804	710.253	734.581	321.472	704.215	%
LN total cells (Time at max)		4.91426	5.27235	4.85272	5.1923	4.90061	
LN total T cells (Value at 0 days)		1.521000e+006	1.521000e+006	1.521000e+006	1.521000e+006	1.521000e+006	cells
LN total T cells (Value at 5.2083 days)		1.003534e+007	1.049808e+007	1.012458e+007	5.809979e+006	1.003230e+007	cells
LN total T cells (Value at 5.2083 days - delta%)		559.786	590.209	565.653	281.984	559.586	%
LN total T cells (Time at max)		4.65636	5.0071	4.62372	5.04461	4.66082	
LN total CD4+ T cells (Value at 5.2083 days)		6.555542e+006	6.611684e+006	6.404027e+006	3.691862e+006	6.629299e+006	cells
LN total CD8+ T cells (Value at 5.2083 days)		3.479799e+006	3.886397e+006	3.720550e+006	2.118117e+006	3.403002e+006	cells
LN (H) proliferating CD4+ T cells (Value at 5.2083 days)		705562	920695	609260	617832	772923	cells
LN (H) proliferating CD8+ T cells (Value at 5.2083 days)		301108	587441	341710	372041	234303	cells
LN (H) proliferating CD4+ T cells (Time at max)		4.89765	5.47684	4.88169	5.15308	4.98204	
LN (H) proliferating CD8+ T cells (Time at max)		4.4835	4.84626	4.48651	4.85518	4.47072	
LN CD4+ T cell % prolif. (Value at 5.2083 days)		10.7628	13.9253	9.51369	16.735	11.6592	%
LN CD8+ T cell prolif. % (Value at 5.2083 days)		8.65304	15.1153	9.18438	17.5647	6.8852	%
LN B cell fraction (Value at 0 days)		0.11	0.11	0.11	0.11	0.11	fraction
LN B cell fraction (Value at 5.2083 days)		0.285234	0.262516	0.306965	0.220636	0.28668	fraction
LN T cell fraction (Value at 0 days)		0.78	0.78	0.78	0.78	0.78	fraction
LN T cell fraction (Value at 5.2083 days)		0.641044	0.664438	0.622119	0.706922	0.639726	fraction

Model Sensitivity Analysis

■ Aim:

- To evaluate relative contribution of individual pathways to overall biological response (e.g. Max Ag-specific T cell proliferation)

■ Method:

- Controls – assigned control dose for prototypic weak/moderate/strong sensitizers
- Experiments – vary model parameters to up/down-regulate biological pathways

■ Results:

- Record model predicted outcomes under control and perturbed conditions – approx. 30,000 simulations performed
- Calculate fold change in outcome relative to control
- High fold change = high influence of pathway on response

- Experiments
- Worksheets
 - Sensitivity Analysis
 - Virtual Patients
 - Virtual Chemicals
 - Virtual Patients reduced

- Sensitivity Analysis
 - Notes
 - Comparison Charts
 - Measurement Sets
 - Comparison Measurement Tables

Name: Sensitivity Analysis

Short Name:

Description: This worksheet includes the various experiments associated with the platform sensitivity analysis, for the primary virtual patients.

	RP1.3	VP2.1	VP3.1	VP4.1	VP5.1
A1: Sensitivity analysis baselines (6)					
Binding efficiency (11)					
Haptenated protein half-life (6)					
LN mature LCs (6)					
Epidermal LC mat and mig induction (6)					
Epidermal cytokine production (6)					
Epidermal IL-1a production (6)					
Epidermal IL-1b production (6)					
Epidermal TNF-a production (6)					
Epidermal IL-8 production (6)					
Epidermal IL-10 production (6)					
Epidermal GM-CSF production (6)					
Influx modulation (6)					
Space per LC (4)					
LN norm mature LC MHC I (6)					
LN norm mature LC MHC II (6)					

- Experiments
- Worksheets
 - Sensitivity Analysis
 - Virtual Patients
 - Virtual Chemicals
 - Virtual Patients reduced

[RP1.3--Epidermal TNF-a prod

- Views
- Measurement Sets

Name: Reference patient 1.3 (murine)--Epidermal TNF-a production (6)

Short Name: RP1.3-Epidermal T

Description: This experiment initializes the first generation murine reference patient.

Simulation Method: Adaptive

Active Set: <All nodes>

Experiment Protocol

Parameter Analysis Group		Runs	15
		Scale	Logarithmic
Dose regime		Initial Value Set	0.00001%
		Ending Value Set	100%
Parameter Analysis Group		Runs	11
		Scale	Logarithmic
Epidermal activation and irritation		Initial Value Set	low TNF-a production
		Ending Value Set	high TNF-a production
Parameter Analysis Group		Runs	3
		Scale	Logarithmic

Duration: 10 days

Store Interval: 1 hours

Capture Time: End of initialization experiment: 1 days

Buttons: Load Stored Results, Apply, Run And Store, Revert

Date/Time: 2006-07-15 11:14

- Experiments
- Worksheets
 - Sensitivity Analysis
 - Virtual Patients
 - Virtual Chemicals
 - Virtual Patients reduced

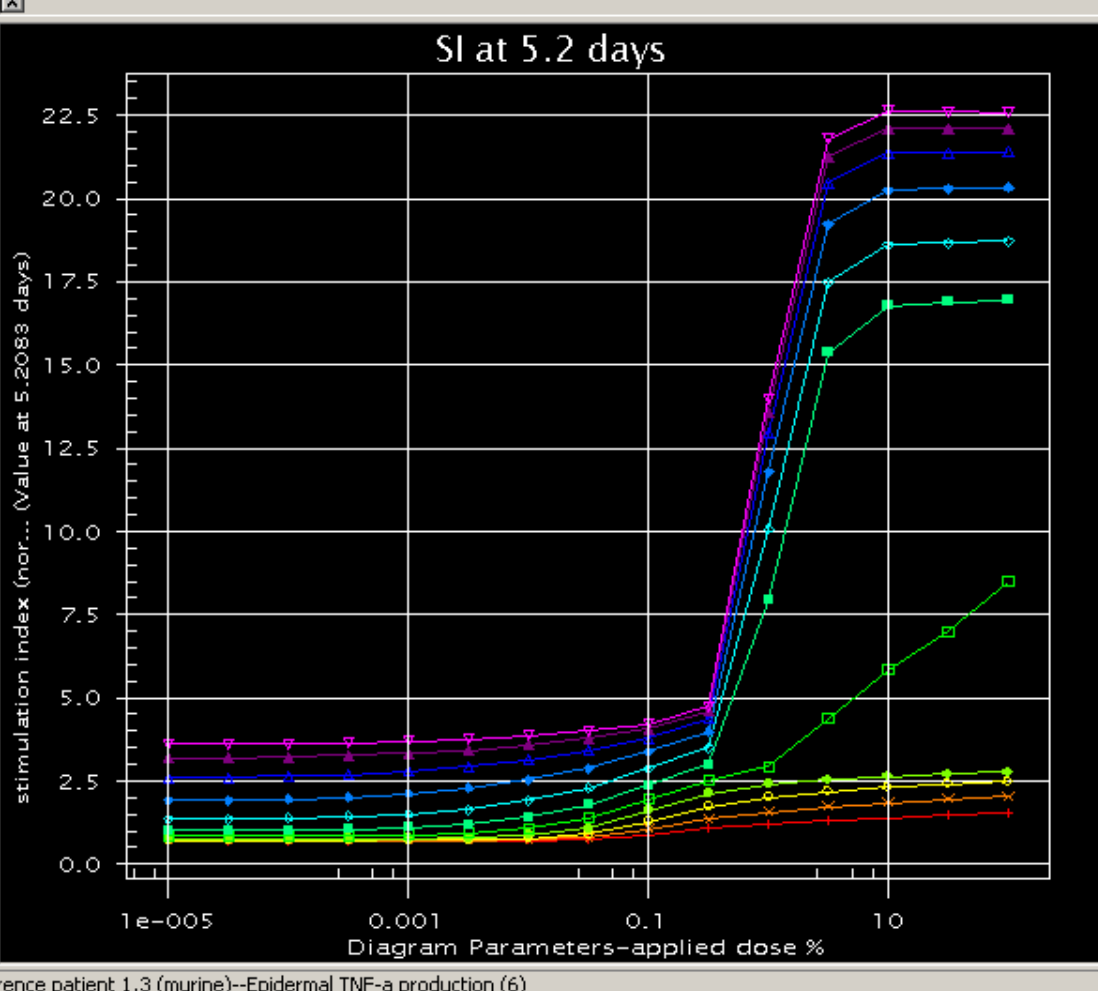
[RP1.3--Epidermal TNF-a prod

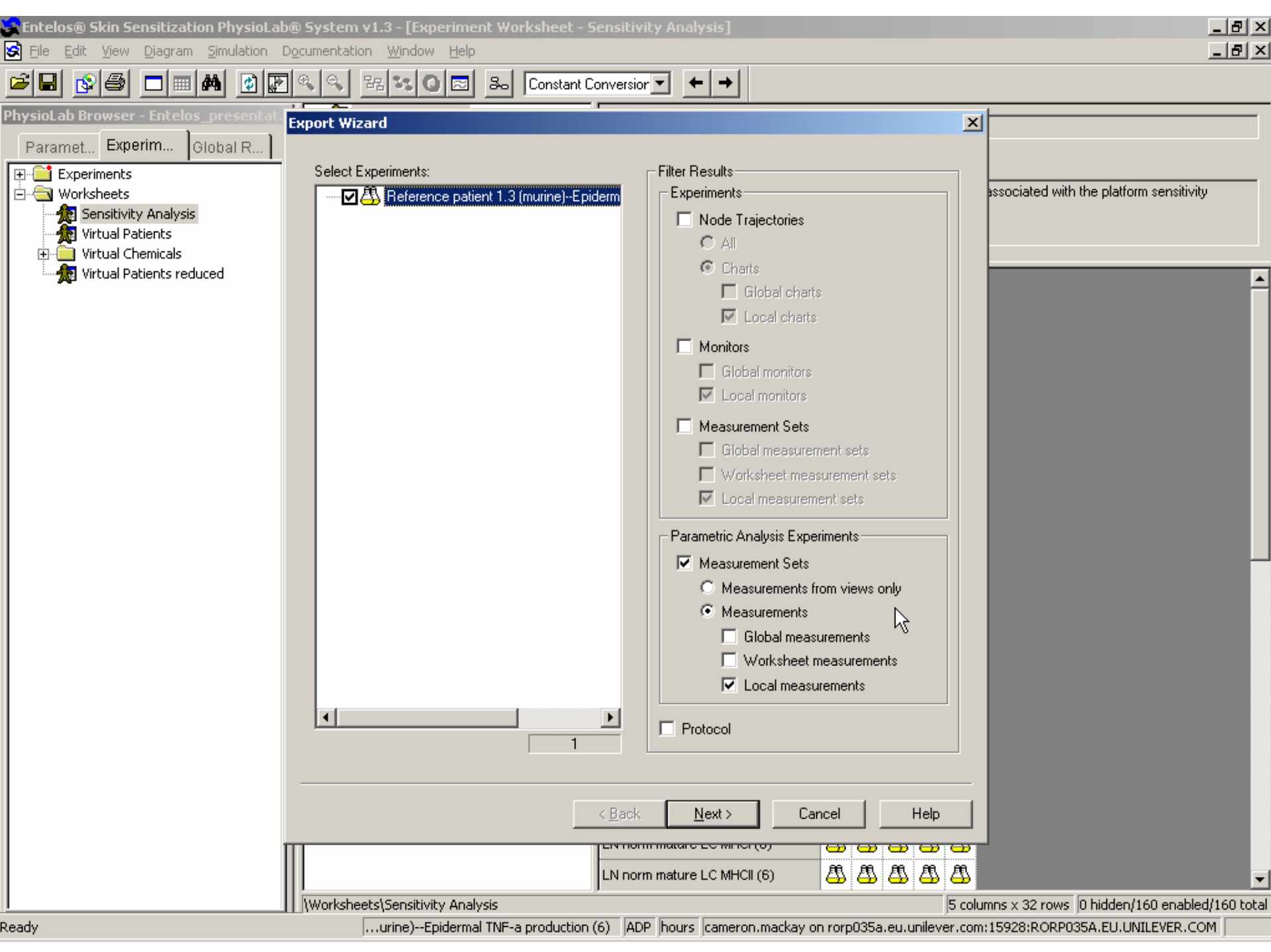
- Views
 - SI at 5.2 days
 - Radioactivity at 5.2 days
- Measurement Sets

Name: SI at 5.2 days

Short Name:

Description:





- Experiments
- Worksheets
 - Sensitivity Analysis
 - Virtual Patients
- Virtual Chemicals
- Virtual Patients reduced

Export Wizard

Select Experiments:

- Reference patient 1.3 (murine)--Epiderm

Filter Results

- Experiments
- Node Trajectories
 - All
 - Charts
 - Global charts
 - Local charts
 - Monitors
 - Global monitors
 - Local monitors
 - Measurement Sets
 - Global measurement sets
 - Worksheet measurement sets
 - Local measurement sets

Parametric Analysis Experiments

- Measurement Sets
 - Measurements from views only
 - Measurements
 - Global measurements
 - Worksheet measurements
 - Local measurements

Protocol

< Back Next > Cancel Help

LN norm mature LC MHCII (6)					
LN norm mature LC MHCII (6)					

	K	L	M	N	O	
1	User name on DB					
2	cameron.mackay					
3						
4						
5						
6						
7						
8						
9						
10						
11						
12	SA: Primary outputs	SA: Key outputs	SA: Key outputs	SA: Key outputs	SA: Key outputs	SA: Key outputs
13						
14						
15	total Ag specific prolif. rate	LN CD4+ T cell % prolif.	LN CD8+ T cell prolif. %	CD4+ T cell TCR + costim internal state	CD8+ T cell TCR + costim internal state	LN no
16	Time at max	Value at 5.2 days	Value at 5.2 days	Value at 5.2 days	Value at 5.2 days	Value
17	17.19595047	4.82E-14	8.11E-14	1.56E-11	4.46E-11	
18	17.15483495	4.93E-14	8.16E-14	1.61E-11	4.51E-11	
19	17.14196564	1.70E-13	2.56E-13	4.80E-11	1.19E-10	
20	73.19260172	1.90E-12	2.75E-12	5.60E-10	1.30E-09	
21	77.49140239	2.97E-11	4.64E-11	7.53E-09	1.61E-08	
22	85.07462546	8.42E-10	1.47E-09	1.27E-07	2.42E-07	
23	102.7949666	2.78E-08	4.68E-08	2.75E-06	4.51E-06	
24	117.4150049	7.32E-07	6.24E-07	6.41E-05	8.75E-05	
25	119.6859492	1.14E-05	8.41E-06	0.001137851	0.001340279	
26	114.6299825	0.000173063	0.000123746	0.014026579	0.015494343	
27	104.6320234	0.003034383	0.002033218	0.139458569	0.143765668	
28	145.3592711	0.177602645	0.22863282	0.635312663	0.589084166	
29	195.7560905	1.434695045	1.693532041	0.848223081	0.775397154	
30	184.0506442	1.861931787	2.526689322	0.876246879	0.813223898	
31	183.1347231	1.878842556	2.564813968	0.877464828	0.814849304	
32	68.31804773	3.01E-13	4.73E-13	2.12E-11	5.53E-11	

Virtual patient exploration revealed the sensitivity analysis to be robust

- The same 14 pathways came up as most sensitive across all virtual patients (ranking did change slightly)
- Biological knowledge gaps/variability explored in the virtual patients does not materially affect the importance of the sensitive pathways

Areas for model development

Computational/Analysis

- Enhanced sensitivity analysis (global)

Data generation

- Epidermal cytokine profiles
- Exposure parameters
- Activated LC phenotypes
- Number of naïve reactive clones

Expansion of scope

- Increased KC/LC cross-regulation in epidermis
- Expanded LC phenotype
- Mechanisms of LN lymphocyte recruitment regulation
- Memory T cell generation

Acknowledgements

■ Unilever

- Catherine Clapp
- Ian Jowsey
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- Katherine Kudrycki
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