

Priya Ranjan
Email: pranjan77@gmail.com

RESEARCH INTERESTS:

Bioinformatics, molecular evolution, microarray data analysis, alternative splicing, comparative genomics, gene annotation, statistical genetics

EDUCATION

Ph.D. in Forest Molecular Genetics and Biotechnology (Bioinformatics)

Michigan Technological University, Houghton, MI

January 2002 – January 2006

M.S. in Biotechnology

Indian Institute of Technology (IIT Bombay), Mumbai, India

June 1999 – December 2001

B.S. in Chemistry with Honors

TM Bhagalpur University, Bhagalpur, India

June 1995 – March 1999

HONORS: Recipient of annual scholarship conferred by Department of Biotechnology, Government of India

PROFESSIONAL EXPERIENCE

- Oct2006- Present **Post doctoral research associate**, University of Tennessee/ORNL
 - Jan2006-Oct 2006 **Post doctoral research scientist**, Michigan Technological university
 - 2002-2005 Research Assistant, Michigan Technological University
 - Spring 2004 **Teaching Assistant**, Michigan Technological University (Tools in Bioinformatics)
 - 1999-2001 Research Assistant, IIT Bombay, Mumbai
 - Summer 2000 Research Assistant, National Institute of Immunology, New Delhi
-

SKILLS

❖ **Bioinformatics**

1. Sequence analysis

Blast package from NCBI (blastall, formatdb, fastacmd, blastclust, blastpgp), WU-blast2 package, RECON for identification of sequence repeats in a genome, EMBOSS, GCG Wisconsin package, cap3, staden package

2. Phylogenetic analysis

Mega2, clustalw, PHYLIP, PAUP, TreeView,

3. Microarray data analysis

Genespring, Base-BioAarray Software environment

4. Gene prediction programs

Genscan, HMMgene, NetGene2

5. Other miscellaneous packages

Bioperl, NCBI C++ toolkit, Rasmol, web lab viewer, various databases

❖ **STATISTICS**

1. SAS programming for univariate and multivariate statistics

2. R-package
- ❖ **IT**
1. **Programming languages**
C, C++, java, Visual Basic
 2. **Scripting and Mark-up languages**
Perl, PHP, XML, HTML, Javascript
 3. **Database Technology**
My SQL, MS Access, Base-BioArray Software environment
 - Operating systems**
Linux, MS-DOS, Win NT/9x/2000/XP, Macintosh, Sun workstation, Experience as system administrator
 4. **Multimedia packages**
Adobe Photoshop 7, Macromedia Flash, Gif animator, GD Perl module for graphics
 5. **Other packages**
FTP, Telnet, Microsoft Office, Dreamweaver, CGI

PUBLICATIONS

- **Ranjan P**, Kao Y, Jiang H, C.P. Joshi, S.A. Harding and C.J. Tsai: Suppression Subtractive hybridization-mediated transcriptome analysis from multiple tissues of aspen (*Populus tremuloides*) trees altered in phenylpropanoid metabolism. **Planta**, 219: 694-704, 2004.
- C.P. Joshi, S. Bhandari, **P. Ranjan**, U. C. Kalluri, X. Liang, T. Fujino, and A. Samuga: Genomics of cellulose biosynthesis in poplars. **New Phytologist** 164: 53-61, 2004.

RESEARCH SUMMARY

- ❖ **Dissertation title** : Analysis of expressed sequence tags in aspen tissues and characterization of *copia* elements in *Arabidopsis* genome: A bioinformatics approach
- ❖ **PhD projects at Michigan Technological University**
 - I. Subtractive Hybridization-mediated Transcriptome Analysis from Multiple Tissues of Aspen (*Populus tremuloides*) Trees Altered in Phenylpropanoid Metabolism
 - **Automated pipeline** for processing of post sequencing data of expressed sequence tags.
 - Development of a program for identification of chimeric EST sequences
 - Establishment of a **database** for storage of the EST sequences and making this data available to the scientific community.
 - **Data mining** program to integrate the annotation of EST dataset with the metabolic pathway information available at KEGG database.
 - II. Genomics of cellulose biosynthesis in poplar
 - Development of a **graphics** program for visualizing the gene structure of cellulose synthase genes and their comparison against each other.
 - III. Diversity, distribution and features of LTR retrotransposons in selected plant genomes
 - Phylogenetic analysis of *copia*-like and gypsy like elements in *Arabidopsis* and *Populus*

- Mining the NCBI GEO datasets and analysis using **genespring** and **SAS** to study the expression profile of LTR elements in *Arabidopsis* and identification of regulatory elements.
- ❖ **MS project at IIT Bombay, India**
 - IV. Binding site analysis of enzymes in cephalosporin biosynthetic pathway
- ❖ **Summer project at National Institute of Immunology, India**
 - V. Production, characterization and purification of α -1,2 Mannosyl transferase from recombinant *E.coli*

SEMINARS

1. Plant based Edible vaccines, Michigan Technological University, 2003
2. Bioinformatics and Drug design, Michigan Technological University, 2004

POSTERS/CONFERENCES

1. Comparison of metabolic changes in control and transgenic aspen by functional evaluation of expressed sequence tag(EST), **Great Lakes Bioinformatics retreat**, Hartland, Michigan , 2002
2. Diversity, distribution and features of LTR retrotransposons in selected plant genomes, Annual ESC/BRC graduate research forum, 2005
3. A Database For Cross-Reference Of Multiple Microarray Platforms In Populus, PAG XV, San Diego, 2007

RELEVANT COURSEWORKS (MS/PhD)

1. Bioinformatics (MTU)
2. Statistical methods (MTU)
3. C++ (MTU)
4. Computational Biology I&II (IIT Bombay)
5. Computational Biology for chemical engineers (IIT Bombay)
6. **Laboratory courses**-Analytical Biochemistry, Microbiology, molecular biology, biophysics, genetic engineering (IIT Bombay)

ACTIVITIES

1. Member of GSC (Graduate Students Council) at MTU, 2002-2203
 2. Member of generations (Organized events aimed at popularizing biotechnology among Indian college students), 1999-2001
 3. Involved with literacy mission in India, 1994-2001
-