

# BIOGRAPHIC SKETCH

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## HIREN M. KARATHIA

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### EDUCATION

**2008 – 2012 Ph. D.** (Integrated Molecular Systems Biology) -- University of Lleida, Spain.

**Title:** “*Development and Application of Computational Methodologies for Integrated Molecular Systems Biology*”; **Supervisor:** Prof. Rui Alves.

**2002 – 2004 M. Sc** (Bioinformatics) -- Sikkim Manipal University, India.

**1999 – 2001 M. Sc** (Biomedical Technology) -- Gujarat University, India.

**1996 – 1999 B. Sc** (Biochemistry) -- Saurashtra University, Rajkot, India.

### OTHER QUALIFICATIONS

**2009 – 2010 Diploma in Advanced study in Biomedical Sciences;** University of Lleida, Spain.

**1996 – 1998 Higher Diploma in Software Engineering;** APTECH Education. Rajkot. India.

### COMPUTER, BIOLOGICAL AND BIOINFORMATICS SKILLS

<b>Programming Skills:</b>	Python, Perl, JAVA, C, C++, VB, FoxPro, R, Mathematica™.
<b>Database:</b>	MySQL, Oracle 8i, ZODB (Zope Object Database), Access.
<b>Packages:</b>	BioPerl, BioPython, BioJava, Numpy, SciPy, Matplotlib.
<b>Webserver management:</b>	Zope, Apache and Tomcat.
<b>Advance Multimedia</b>	Photoshop, Dream-Viewer MX, Flash-MX, Adobe illustrator.
<b>Molecular biology</b>	DNA & RNA isolation, cDNA library construction, Blotting techniques, Restriction Mappings.
<b>Microscopy</b>	Light and Electron microscopy
<b>Histo (Patho) logy</b>	Slide preparation and microscopic analysis of tissue samples.
<b>Cell culture</b>	Peripheral Blood Lymphocyte Culture (PBLCL).
<b>Haematology</b>	Blood collection, Total and differential WBC count.
<b>Proteomics and Genomics</b>	Pipeline development and implement for purifying, manipulating and analyzing high throughput genomic and proteomic data sets, available in public databases and scientific literatures, using in-house developed scripts. High-throughput sequence assembly and analysis using local, global and multiple sequence alignment tools.
<b>Phylogenetic profiling</b>	Algorithm development for hierarchical classification and clustering of organizations in complete proteomes/genomes at sequence levels and applied to reconstruct phylogenetic and function trees.
<b>Pathways reconstruction</b>	Metabolic network reconstructions and analyses for dynamic properties using mathematical and logical modeling.

## HONORS AND AWARDS

- 2008 – 2012** Doctoral fellowship from Agència de Gestió d'Ajuts Universitaris i de Recerca (AGAUR) Govt. of Catalunya; Spain.
- 2010** Partially funded by grants from Ministerio Ciencia y Tecnologia for presenting Posters at EMBO meeting at Barcelona; Spain.
- 2010** Full travel grant awarded by ECCB, for abstract presentation at Ghent, Belgium.

## PEER-REVIEWED PUBLICATIONS

**Karathia, H.**, Vilaprinyo, E., Sorribas, A., Alves, R. (2011). "*Saccharomyces cerevisiae* as a model organism: a comparative study." PLoS One 6(2): e16015.

Usie, A., **Karathia, H.**, Teixido, I., Valls, J., Faus, X., Alves, R., Solsona, F. (2011). "*Biblio-MetReS: a bibliometric network reconstruction application and server.*" BMC Bioinformatics 12: 387.

Salvado, B., **Karathia, H.**, Chimenos, A. U., Vilaprinyo, E., Omholt, S., Sorribas, A., Alves, R. (2011). "*Methods for and results from the study of design principles in molecular systems.*" Mathematical biosciences 231(1): 3-18.

Salvado, B., E. Vilaprinyo, **Karathia, H.**, Sorribas, A. Alves, R., (2012). "*Two component systems: physiological effect of a third component.*" PLoS One 7(2): e31095.

Mishra GR, Suresh M, Kumaran K, Kannabiran N, Suresh S, Bala P, Shivakumar K, Anuradha N, Reddy R, Raghavan TM, Menon S, Hanumanthu G, Gupta M, Upendran S, Gupta S, Mahesh M, Jacob B, Mathew P, Chatterjee P, Arun KS, Sharma S, Chandrika KN, Deshpande N, Palvankar K, Raghavnath R, Krishnakanth R, **Karathia H**, Rekha B, Nayak R, Vishnupriya G, Kumar HG, Nagini M, Kumar GS, Jose R, Deepthi P, Mohan SS, Gandhi TK, Harsha HC, Deshpande KS, Sarker M, Prasad TS, Pandey A (2006). "*Human protein reference database--2006 update*". Nucleic Acids Res. 2006 Jan 1;34 (Database issue):D411-4.

**Karathia, H.**, Teixidó, I., Usie, A., Vilaprinyo, E., Solsona, F., Sorribas, A., Alves, R. "*Homol-MetReS: An integrated framework tool to study evolutionary molecular systems biology.*" [Under Review].

**Karathia, H.**, Usie, A., Teixido, I., Vilaprinyo, E., Sorribas, A., Solsona, F., & Alves, R., "*A human centric comparison of eukaryotic proteomes: Implications for the study of human biology.*" [Under Review].

Usie, A., **Karathia, H.**, Teixido, I., Alves, R., Solsona, F. "*Biblio-MetReS*" [Submitted].

## PRESENTATIONS AND ABSTRACTS

**Karathia, H.**, Teixidó, I., Usié, A., Vilaprinyo, E., Solsona, F., Sorribas A., Alves, R. (2013) "*A human centric comparison of eukaryotic proteome: Implication for the study of human biology*", (2013), International Conference on Structural and Functional Genomics (ICSAFG-2013), Sastra University, Thanjavur, Tamilnadu, India.

**Karathia, H.**, Usié, A., Vilaprinyo, E., Solsona, F., Teixidó, I., Sorribas A., Alves, R. (2012) "*Homol-MetReS: A web application for integration between molecular systems biology and evolutionary biology*", (2012), Oral talk in Student symposium at XI Jornadas de Bioinformática, Barcelona.

**Karathia, H.**, Usié, A., Vilaprinyo, E., Sorribas A., Solsona, F., Alves, R., "*Homol-MetReS: Network Reconstruction Based on Whole Proteome Comparisons*", (2011), Poster presentation at ICMSB 2011 -XIIth International Congress on Molecular Systems Biology, Lleida, Spain.

**Karathia, H.**, Alves, R., "*A tool for comparison of complete proteomes between pairs of organisms*", (2010), Poster presentation at 9th European Conference on Computational Biology, Ghent, Belgium.

**Karathia, H.**, Alves, R., "*Saccharomyces cerevisiae as a model organism: Strengths & drawbacks*", (2010), Poster presentation at European Molecular Biology Organization (EMBO), Barcelona, Spain.

**Karathia, H.**, Aseri, G., Jain, N., Shrivastava, S., K., "*Discovery of targets for nanoparticle tagged antibodies specific to cancer biomarkers*", (2007), Poster on Application of Nanotechnology in Microbial and Herbal Product Development, at, New Delhi (Noida), India.

Usié, A., Lerida, J. L., Teixidó, I., Solsona, F., Comas, J., Torres, N., **Karathia, H.**, Alves R., and Abdelli O. "*P-Biblio-MetReS, a parallel data mining tool for the reconstruction of molecular networks*", (2013), PBio 2013, EuroMPI'13, Madrid, Spain.

Usié, A., Teixidó, I., **Karathia, H.**, Alves, R., Solsona, F., "*Biblio-MetReS: A bibliometric reconstruction application and server*", (2012), Poster at XI Jornadas de Bioinformática, Barcelona.

Abdelli, O., Usié, A., **Karathia, H.**, Vilaplana, J., Solsona F., Alves, R., "*Parallelizing Biblio-MetReS, a data mining tool*", (2011), Communication at XXII Jornadas de Paralelismo, La Laguna (Tenerife), Spain.

Usié, A., **Karathia, H.**, Solsona, F., Alves, R., "*Biblio-MetReS: A bibliometric reconstruction application and server*", (2011), Poster presentation at ICMSB 2011 -XIIth International Congress on Molecular Systems Biology, Lleida, Spain.

### **PARTICIPATION IN COMPETITIVELY FUNDED PROJECTS**

**2005 – 2006** “HPRD (Human Protein Reference Database)”, funded by National Institute of Health (NIH – Ref: RR020839), USA.

**2008 – 2010** “Development and application of computational methodologies Integrated Systems Molecular Biology”, funded by Ministry of Education and Science, Spain, (Ref: BFU2007-62772/BMC).

**2010 – 2013** “MetRES (Metabolic REconstruction and development application Server), Study on Biological Design Principles”, funded by Ministry of Education and Science, Spain, (Ref: BFU2010-17704).

## **RESEARCH EXPERIENCE**

### **2013 – 2013 Senior Research Associate; Genome Life Sciences; Chennai; India**

- Innovation and knowledge transfer for novel genomic solutions for disease related functional needs.
- Training and mentoring of junior analysts and programmers for optimisation of existing routines, enhancement and update of existing functionalities of in-house flagship products.
- Integration of Genomic resources, tools and databases.
- Implementation of NGS analysis pipelines into proprietary in-house Genomics Suite.

### **2012 – 2013 Postdoctoral research work; University of Lleida; Spain**

- Working on Homol-MetReS to make it ready for public usage.
- Comparative analyses of complete proteomes at sequence and domain fusion levels amongst human, primates and other eukaryotes at hierarchical systemic functions and pathways/networks levels in order to identify disease signature genes, proteins and pathways at evolutionary point of views using Python, Numpy and Mathematica™.

### **2008 – 2012 Doctoral candidate; University of Lleida; Spain**

- Development and implementation of Homol-MetReS, component architecture based web server tool that serves applications for automated reconstruction of molecular organizations in a complete proteome of a reference organism using PYTHON, PERL, MySQL, Mathematica™, Numpy, SciPy, Matplotlib and ZOPE.
- Identifying alternate model organisms for Human and other primates by comparing similarities and variations in complete proteomes that are involved in Catalytic, Receptors & Ligands, GO terms, Transcription factors, KEGG pathways and protein-protein interactions. The analysis was done by PYTHON, Mathematica™, Numpy, SciPy and Matplotlib.
- Knowledgebase of Proteome/Genome - Designed and implemented modeling for integration of multiple relational databases, where each database manages complete proteome/genome sequences and their relations with systemic functional annotations of an organism. The knowledgebase is implemented on MySQL.
- *Saccharomyces cerevisiae* as a model organism - in this work we propose such a method and apply it in a pilot study to test strengths and limitations of *Saccharomyces cerevisiae* as a model organism. This project was done using PERL, BioPERL and Mathematica™.
- Biblio-MetReS: is a platform that extracts genes and/or proteins contextual interactions from the literature and integrates different tools and methods for automated reconstruction of biological networks. The tool is designed on JAVA and connected to MySQL using JDBC.

- 2006 – 2008 Academic Researcher; AMITY University, Jaipur & Noida, India**
- Coordinator of a research project entitled with “*Reconstruction of HIV-Tat interfered signal transduction pathways in human to study mechanisms of AIDS and neural dementia*”.
- 2005 – 2006 Research Scientist; Institute of Bioinformatics (IOB); India**
- HPRD (Human Protein Reference Database) – Manually and automated annotation of molecular information pertaining to domain positions, post-translational modifications (PTMs), protein-protein, protein-DNA interactions and diseases for each protein in the human proteome.
  - Design and implement relational architecture of current running HPRD and mapping human proteins to the functional states in signal transduction pathways, mapping of differentially expressed cDNAs to the immune and cancer pathways and mapping Single Nucleotide Variance (SNV) information over human protein sequences using PYTHON and PIL.Image modules.
  - BioBuilder 2.0, an automated annotation tool. My contribution was to design and implement relational architecture on ORACLE 8i. The information were relationally populated PYTHON, ZOPE and PIL.Image.
  - Plasma Protein Database (PPD) – A comprehensive resource for complete plasma proteins and isoforms in human using PYTHON and ORACLE-8i.
  - Receptor induced Signal Transduction Pathways – Manual and automated mapping of receptor induced signal transduction pathways states in human.
- 2004 – 2005 Technical Consultant (Bioinformatics); Applitech Education Ltd., Ahmedabad, India**
- Design and implement a Data mining tool for identifying patterns of Alternative Splicing in reference genomes using JAVA (JSP and Servlet) and MySQL. The tool was tested by identifying ESTs (Expressed Sequence Tags) of selected protein isoforms and then mapped that to genome sequences in order to discover Intron-Exon/Exon-Intron boundaries.

### **TEACHING EXPERIENCE**

- 2006 – 2008 Lecturer (Biotechnology); AMITY University; Jaipur & Noida; India**
- Taking lectures for B.Tech, M.Sc and MBA (Biotechnology) students. The subjects - Genetic Engineering, Molecular Cloning, Cell Biology, Histology, Histo-pathology, Algorithm Development, C++, and Management in Biotechnology industries.
- 2003 – 2004 Course coordinator (Biotechnology); Applitech Education Ltd., Ahmedabad; India**
- Designing and lecturing for Advance Diploma and M.Sc Bioinformatics students. The subjects – Biostatistics, Sequence analysis, Microarray based gene expression analysis, Data mining, Database management, Bioinformatics algorithms, C++, JAVA, PERL, MySQL.

- 2004**                    **Supervisor; (Bioinformatics); Applitech Education Ltd. India.**
- Supervision of a project, entitled as “*Designing a Data mining tool for the discovery of Alternative splicing mechanism induction by SnRNPs*”, to two students of P. G. Diploma Bioinformatics. The project was done by using JAVA and MySQL technologies.
- 2001 – 2002**        **Lecturer (Med. Lab. Technology and Biotechnology); Virani Science College; Rajkot; India**
- Taking lectures of Histology, Immunology, Genetic Engineering, Cell Biology and Clinical Genetics. I was promoted as laboratory administrator of Molecular Genetics laboratory.

**ACADEMIC TRAININGS & WORK EXPERIENCES**

- Sep. to Dec. 2000**    Hospital training on Flow Cytometry, Cytochemistry, ELISA (Enzyme-Linked Immunosorbent assay) and Histopathological slide analysis from biopsy samples, Immunocytochemistry, PCR applications, Blotting techniques.
- Jan. to Jun. 2001**    Dissertation work for Masters of Science (M.Sc) - Biomedical Technology in studying toxic effect of Arsenic trioxide (As<sub>2</sub>O<sub>3</sub>) on human chromosomes for characterising structural aberrations using comparative study of Karyotyping from human Lymphocytes. The aberration effects were evaluated by investigating Sister Chromatin Exchanges (SCEs), Telomeres frequency, Chromosomal Breaks/Gaps and Cell Cycle Index parameters.
- Apr. to Jul. 2004**    Dissertation work for Master of Science (M.Sc) – Bioinformatics on Prediction of human *SnRNPs* induced splicing patterns from Rice [*Oryza sativa* (spp. Indica)] as reference model with title “*SnRNP* Proteome Correlation between *Homo sapiens* and *Oryza sativa* (spp. indica)”.
- Jun. to Aug. 1996**    Project work for Higher Diploma Software Engineering on developing Inventory Systems for Hotel Management using ‘C’ language.

**MEMBERSHIP IN PROFESSIONAL SOCIETIES**

International Society for Computational Biology (ISCB).

**REFERENCES AVAILABLE ON REQUEST**