

Dolly Chetan Mehta

Ph.D. student (Final year)

RNA structure predictions Protein:RNA interactions Covariance analysis RNA diversity

(Hidden Markov models) (structured RNA families) (Gene regulatory mechanisms)

CONTACT

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- Dolly Mehta

TECHNICAL SKILLS

Programming PERL SHELL scripting (includes BASH, AWK and sed) R Python HTML/CSS LaTeX

Operating Systems

Linux			
Windows			

Software & Tools

-4- ----!---!-

Sequence and Structure tools

KNA	INA						
(Infernal,	Vienna	RNA	Package,	RNAz,	RNA-		
clust)							

Protein • • • • •

(Sequence homology tools, basic homology modeling, docking and MD simulations)

Data analysis	
(R-scape, bacterial synteny, bac	cterial RNA-seq,
Genome and transcriptome a	nalysis, SHAPE-

Genome and transcriptome analysis, SHAPE seq)

Visualization

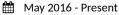
(R2R, IGV, Chimera, Pymol, Jalview, VMD) **Statistical analysis**(R and Bioconductor, GraphPad)

Adobe Illustrator
Office

Languages

EDUCATION

Ph.D. (Ongoing)



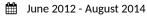
National Centre for Biological Sciences (NCBS), Bangalore, India SASTRA University, Thanjavur, India

Thesis: Discovery of structured RNA families in bacteria using computational approaches

Contributions:

- Genome-wide RNA structure predictions and systematic sequence and structure analyses of RNA families
- Re-engineered and improved the approach to identify distant homologs of structured RNAs
- Development and improvising the Hidden Markov (HMM) based RNA search models
- Genomic, transcriptomic and pathway analyses for target genes
- Proposing potential mechanisms of gene regulation mediated via structured RNAs

Masters of Science (M.Sc)
(Bioinformatics & Biotechnology)



Institute of Bioinformatics and Applied Biotechnology (IBAB), Bangalore, India Face-to-Face IGNOU program

Thesis: Structural basis of allostery of NADH induced derepression of redox sensing protein Rex from *S. agalactiae*: Targeted MD simulation studies & Principal Component Analysis

Contributions:

- Analyzed MD trajectories of protein Rex (transcription factor) using VMD and ProDY plugin
- Identified key residues that can modulate local changes in Rex structure on binding to ligands (NAD/NADH) using principal component analysis

Semester Project: Pilot scale fermentation for pectinase enzyme production from bacteria

Contributions:

- Screening and characterization of pectinase producing bacteria from different sources
- Standardizing conditions for for pectinase production and pilot scale fermentation with downstream processing was carried out to obtain purified enzymes

Bachelors of Science (B.Sc) (Biotechnology)

i June 2009 - July 2012

Chauhan Institute of Science, Mumbai,
India (Affiliated to University of Mumbai)

PUBLICATIONS

Diversity and prevalence of ANTAR RNAs across actinobacteria

Mehta D. Ramesh A.

₩ 2021

BMC Microbiology. 2021 May 29;21(1).1-5.

% Link to article

Discovery of iron-sensing bacterial riboswitches.

Bandyopadhyay S*, Chaudhury S*, **Mehta D**, Ramesh A. (*co-authors)

2021-2020

S Link to article

Nature Chemical Biology. 2020 Oct 5:1-8.
Note: This article is retracted on June 29, 2021, but the computational work remains hopeful. Clarification and my role related to this work

Discovery of ANTAR-RNAs and their Mechanism of Action in Mycobacteria

Mehta D*, Koottathazhath A*, Ramesh A. (*co-authors)

can be obtained by Referee Dr. Arati Ramesh.

₩ 2020

J Journal of Molecular Biology. 2020 Jun 26;432(14):4032-48.

& Link to article

GENERAL SKILLS

- Enthusiastic
- **Communication**
- Teamwork and collaborative
- Problem solving
- Logical reasoning
- Critical thinking
- Positive attitude

AWARDS

- ICMR Senior Research Fellow award (2019-present)
- CSIR Senior Research Fellow award (2019)
- ▼ Infosys Foundation Travel award (2018)
- DBT Junior Research Fellow award: Category-II (2017)

REFERENCES (ON REQUEST)

Referee contact details for obtaining recommendation letters will be shared on request

PUBLICATIONS (CONTINUED)

A genome-wide structure-based survey of nucleotide binding proteins in M. tuber-culosis

👺 Bhagavat R, Kim HB, Kim CY, Terwilliger TC, **Mehta D**, Srinivasan N, Chandra N. 🛗 2017

Scientific Reports. 2017 Oct 2;7(1):1-4.

% Link to article

WORK EXPERIENCE

Teaching Assistant (NCBS Ph.D. student practicals)

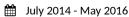
August 2017

National Centre for Biological Sciences (NCBS), Bangalore, India

Hands on training:

- 1. Protein sequence homology tools
- 2. Protein homology modeling and structure comparison

Research Assistant



Prof. Nagasuma Chandra Indian Institute of Science (IISc), Bangalore, India

Projects:

1. Understanding mechanism of action of drugs on *Mycobacterium tuberculosis* using network biology approach (Work with Dr. Abhilash Mohan)

Contributions:

- Analyses of the drug-target networks and improvising the network-based algorithm to identify paths that gets perturbed in response to antibiotics
- 2. Genome and Functional Annotation of Mycobacterium smegmatis MC2-155 (Collaborative Project)

Contributions:

- Classification of genes to functional groups based on sequence homology to M. tuberculosis
- Identification and assignment of enzyme classes using protein sequence homology tools
- Automated the pipeline for homology based structure modeling of M. smegmatis proteome
- 3. Binding Site Analysis of Mycobacterium tuberculosis proteins for NTP binding

Contributions:

- Checked the accuracy and efficiency of in-house NTP-binding protein predictions by comparison with predictions from existing tools and softwares
- NTP-binding proteins were modeled and docked with predicted NTPs to confirm the in-house predictions
- 4. Screening of potential drug targets from Mycobacterium tuberculosis H37Rv

Contributions:

- Manual curation of high-confidence potential anti-tubercular drug targets
- Aided in creating a database of potential compounds that can be tested against selected target proteins in *M. tuberculosis*.

Teaching Assistant for course: Current Trends in Drug Discovery (August 2014)

Hands on training:

- 1. Protein sequence and structure homology tools
- 2. Protein homology modeling and protein:ligand docking

Internship

June 2013

Prof. N. Yathindra
Institute of Bioinformatics and Applied
Biotechnology (IBAB),
Bangalore, India

Projects:

- 1. Conformational analysis of 5S rRNA and tRNA structures
- 2. Deciphering the configuration of amino acids at beta-chiral center

Contributions:

• For both projects, high resolution X-ray structures were analyzed using in-house PERL and R scripts to calculate different dihedrals.

MANUSCRIPTS IN PREPARATION

Metabolic enzymes as moonlighting RNA-binding proteins

👺 Sen V, **Mehta D**, Ramesh A.

WORK IN PROGRESS

• Expression of the ANTAR protein Rv1626 in its active form remodels the metabolic state of mycobacteria

嶜 Mehta D*, Koottathazhath A*, A Achuthan, Gupta R and Ramesh A. (*co-authors)

• Computational discovery of bacterial riboswitch classes likely responsive to iron

Mehta D, Ramesh A.

Note: A part of this work was retracted (mentioned in Publications) but the computational work remains hopeful.

CONFERENCES AND SYMPOSIA

NCBS Annual Talks (Presented Poster)

🛗 January 2020

NCBS, Bangalore, India

Bangalore Structural Biology Symposium (Talk)

♀ NCBS, Bangalore, India

EMBL Symposium: The Complex Life of RNA (Presented Poster)

Ctober 2018

♀ EMBL, Heidelberg, Germany

Aspects of Gene and Cellular Regulation (AOGCR) (Talk)

Hanuary 2018

♀ Institute of Mathematical Sciences (IMSc), Chennai, India

Structure Across Scales (Presented Poster, Organization Team Member)

October 2017

NCBS, Bangalore, India

Third International Symposium: Protein Folding and Dynamics (Presented Poster)

Movember 2016

NCBS, Bangalore, India

Winter School on Quantitative Systems Biology (Voluntary Attendee)

December 2015

♀ ICTS, Bangalore, India

Metabolomics (Voluntary Attendee)

🛗 January 2015

♀ IISc, Bangalore, India

Advances in non-coding genomics (Voluntary Attendee)

September 2013

♀ IBAB, Bangalore, India

PERSONAL INTERESTS

Sketching (Beginner) | Learning languages (Beginner) | Arts & Crafts | Painting | Cooking | Dancing