

Sachin Pundhir

RESEARCH INTERESTS

Computational biology, big data analysis, non-coding RNA and transcriptional regulation

- RNA-seq and ChIP-seq data analysis using robust quantification and normalization methods to understand transcriptional regulation.
- RNA splicing and expression analysis.
- Statistical analysis using R packages.
- Reproducibility analysis and quality control.
- Machine learning approaches (HMM, SVM, random forest, regression analysis).
- Design and implement novel algorithms using Bash, Perl, R and C.

EDUCATION

- 2010 - 2013 Ph.D. Bioinformatics, University of Copenhagen, Denmark
2002 - 2004 M.Sc. Bioinformatics, C.C.S. University, India

EMPLOYMENT

- 2018 – Present **Senior Scientist**, BRIC and Rigshospitalet, Denmark
2014 - 2018 **Post-doctoral fellow**, Biotech Research and Innovation Centre, Denmark (with Prof. Bo Porse)
2010 – 2013 **Ph.D.**, RTH, University of Copenhagen, Denmark (with Prof. Jan Gorodkin)
2008 – 2010 **Researcher**, BIC, National Institute of Plant Genome Research, India
2005 – 2008 **Researcher**, BIC, Devi Ahilya University, India
2004 – 2005 **Instructor** (Bioinformatics and IT), Graphic Era Institute of Technology, India

RESEARCH PUBLICATIONS (total: 13; first author: 9)

- 2018 Differences in Cell Cycle Status Underlie Transcriptional Heterogeneity in the HSC Compartment. Lauridsen FKB, Jensen TL, Rapin N, Aslan D, Wilhelmson AS, **Pundhir S**, Rehn M, Paul F, Giladi A, Hasemann MS, Serup P, Amit I, Porse BT.
Cell Reports 24(3):766-780 [PMID: 30021172]
- 2018 Enhancer and transcription factor dynamics during myeloid differentiation reveal an early differentiation block in *Cebpa* null progenitors.
Pundhir S*, Lauridsen FB*, Schuster MB, Jakobsen J, Ge Y, Schoof E, Rapin N, Waage J, Hasemann M and Porse BT. (*joint first authors).
Cell Reports 23(9):2744-2757 [PMID: 29847803]
- 2016 Peak-valley-peak pattern of histone modifications delineate active regulatory elements and their directionality.
Pundhir S, Bagger FO, Lauridsen FB, Rapin N and Porse BT.
Nucleic Acids Research 44:4037-4051 [PMID: 27095194]
- 2016 BloodSpot: A database of gene expression profiles and transcriptional programs for healthy and malignant haematopoiesis.
Bagger F, Sasivarevic D, Sohi S, Laursen L, **Pundhir S**, Sønderby C, Winther O, Rapin, N and Porse, B.
Nucleic Acids Research 44:D917-24 [PMID: 26507857]

- 2015 Differential and coherent processing patterns from small RNAs.
Pundhir S and Gorodkin J.
Scientific Reports (Nature) 5:12062 [PMID: 26166713]
- 2015 Emerging applications of read profiles towards the functional annotation of the genome.
Pundhir S, Poirazi Y and Gorodkin J.
Frontiers in Genetics 6:118 [PMID: 26042150]
- 2014 EssOilDB: A database of essential oils reflecting terpene composition and variability in the plant kingdom.
Kumari S, **Pundhir S**, Priya P, Jeena G, Punetha A, Chawla K, Jafaree Z, Mondal S and Yadav G.
Database (Oxford) 2014:bau120 [PMID: 25534749]
- 2014 Spatially conserved long non-coding RNA and cis-regulatory elements identified within Cd247 gene in human and mouse using high-throughput sequencing data from ENCODE project.
Pundhir S, Hannibal T, Bang-Berthelsen C, Wegener A, Pociot F, Holmberg D and Gorodkin J.
Gene 545(1):80-87 [PMID: 24797614]
- 2014 Structured RNAs and syntenic regions in the pig genome.
Anthon C, Tafer H, Havgaard J, Thomsen B, Hedegaard J, Seemann S, **Pundhir S**, Kehr S, Bartschat S, Nielsen M, Nielsen R, Fredholm M, Stadler P, Gorodkin J.
BMC Genomics 15:459 [PMID: 24917120]
- 2013 MicroRNA discovery by similarity search to a database of RNA-seq profiles.
Pundhir S and Gorodkin J.
Frontiers in Genetics 4:133 [PMID: 23874353]
- 2012 deepBlockAlign: a tool for aligning RNA-seq profiles of read block patterns.
Langenberger D*, **Pundhir S***, Ekstrøm C, Stadler P, Hoffmann S and Gorodkin J. (*joint first authors)
Bioinformatics 28(1):17-24 [PMID: 22053076]
- 2011 SSPred: a prediction server based on SVM for the identification and classification of protein involved in bacterial secretion systems.
Pundhir S and Kumar A.
Bioinformatics 25(10):380-382 [PMID: 21904425]
- 2008 PredictBias: a server for the identification of genomic and pathogenicity islands in prokaryotes.
Pundhir S, Vijaywargiya H and Kumar A.
In Silico Biology 8(3-4):223-234 [PMID: 19032158]
- Submitted/ In preparation Antagonistic activity of Chd4 and Brg1 depends upon the context dependent binding of EP400 and Polycomb complexes at promoters
Pundhir S and Porse BT.

ORAL PRESENTATIONS

- Invited 2016: National Workshop on NGS Data: Assembly and Exploration, "Next-generation sequencing data analysis", NIPGR, New Delhi, India.
- 2016: Symposium, "Patterns from next-generation sequencing data delineate non-coding RNA processing and active regulatory elements", JNU, New Delhi, India.
- 2016: Symposium, "Novel approaches to predict non-coding RNAs using RNA-seq data", IIIT, Delhi, India.
- 2014: Symposium, "A novel computational approach for the efficient prediction of small non-coding RNAs and to understand their post-transcriptional processing mechanism", NIPGR, New Delhi, India.
- Contributed 2016: Next Generation Sequencing conference (NGS 2016), "Genome-wide prediction of active regulatory elements and their directionality using peak-valley-peak histone modification patterns", Barcelona, Spain.
- 2015: Symposium, "Genome-wide prediction of active regulatory elements and their directionality using peak-valley-peak histone modification patterns", Copenhagen, Denmark.

2013: 7th International SHARE symposium, "Differential and coherent processing of small RNAs in the human transcriptome", Copenhagen, Denmark.

2013: TBI Winterseminar, "Application of read profiles in genome annotation", Bled, Slovenia.

2012: TBI Winterseminar, "Comparative analysis of read processing patterns across 11 total RNA-seq datasets", Bled, Slovenia.

2011: Herbstseminar Bioinformatik, "Processing Patterns: Significance and Analysis", Vyoska-lipa, Czech Republic.

2011: TBI Winterseminar, "Identification and Classification of ncRNAs using Deep Sequencing data", Bled, Slovenia.

2010: Herbstseminar Bioinformatik, "In-silico identification and classification of non-coding RNA using high-throughput sequences", Vyoska-lipa, Czech Republic.

2008: International Conference on Bioinformatics (InCoB), "PredictBias: a server for the identification of genomic and pathogenicity islands in prokaryotes", Taipei, Taiwan.

2006: National Conference on Biotechnology, Science & Environment, "In Silico Classification of bacterial virulence factors", Indore, India (Best paper award).

AWARDS AND ACTIVITIES

Reviewer	PLoS One, RNA biology
Fellowships	Ph.D. fellowship from University of Copenhagen, Denmark Ph.D. fellowship from DBT, India (cleared BINC examination; Rank 30/2374)
Travel awards	From NCBS, Bangalore to attend YIM 2016, India From Department of Biotechnology, India to attend conference at Taiwan

TEACHING EXPERIENCE

Teaching	2005-2008: Bioinformatics and Biostatistics to M.Sc. students at Devi Ahilya University, Indore, India; Responsibilities included preparing and delivering lectures (PowerPoint) and practical exercises. 2005: Bioinformatics to B.Tech. Students at Graphic Era Institute of Technology, Dehradun, India
Mentorship	2014: Ricard Argelaguet (University of Copenhagen, Denmark) 2012: Kortine Kleinheinz (University of Copenhagen, Denmark) 2007: Namrata Tomar (Banasthali University, India) 2007: Shalu Jhanwar (Banasthali University, India)

COURSE WORK DURING Ph.D.

2013	Project leadership, University of Copenhagen, Denmark (ECTS: 3.5)
2012	Algorithms in Bioinformatics, Denmark Technical University, Denmark (ECTS: 10) Advanced signal processing, Denmark Technical University, Denmark (ECTS: 2.5) Computational statistics for genome biology, University of Padua, Italy (ECTS: 4)
2011	Scientific and academic writing, University of Copenhagen, Denmark (ECTS: 2) Biostatistics, University of Copenhagen, Denmark (ECTS: 7.5)

TECHNICAL SKILLS

Bioinformatics:

- Mapping and quality control of NGS data: bowtie, FastX, trimmomatic, FastQC, SAMtools, bedtools, tophat
- ChIP-seq: Macs2, IDR, HOMER, Gviz, KaryoploteR
- Expression enrichment analysis: DESeq, EdgeR
- Machine learning: HMMER, SVMlight (Support Vector Machine)
- EST data analysis: LUCY, CAP3, Seq_clean, ESTScan, Phrap, TGICL, BLAST2GO, AmiGO
- Phylogenetic analysis: Phylip
- Clustering: Blastclust, CD-HIT, hclust, k-means, pvclust
- Functional annotation: Ensembl, UCSC, GenBank, Prosite, Pfam, PRINTS, InterPro, KEGG
- Statistical: R

Language and Tools:

- CGI/Perl, Shell scripting, C, Bioperl, R, JavaScript, HTML, ASP.Net

Application Servers:

- Apache Web Server and IIS Web Server

Databases:

- MySQL, SQL Server 2000

Systems:

- Linux, Mac OS X, Windows Server 2003

SOFTWARE REPOSITORY

<https://github.com/spundhir>

PERSONAL PARTICULARS

Name	Sachin Pundhir
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Nationality	Indian
Date of birth	August 11, 1982

REFERENCES

Available upon request