

# Sachin Pundhir

## RESEARCH INTERESTS

Computational biology, 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

- 2014 - Present **Post-doctoral fellow**, BRIC, University of Copenhagen, Denmark (with Prof. Bo Porse)  
2013 **Research Associate**, RTH, University of Copenhagen, Denmark (with Prof. Jan Gorodkin)  
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: 11; first author: 8)

- 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].  
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].  
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].
- 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].
- 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. **Bioinformatics** 28(1):17-24 [PMID: 22053076] (\*joint first authors).
- 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** 6(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 Enhancer and transcription factor dynamics along the granulocytic-monocytic lineage reveals an early differentiation block in *Cebpa* mutant progenitors **Pundhir S\***, Lauridsen F\*, Jakobsen J, Schoof E, Rapin N, Waage J, Hasemann M and Porse B. (\*joint first authors).

## 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.
- Conference 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: 7<sup>th</sup> 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", Vysoka-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. Biotechnology and Bioinformatics students at Devi Ahilya University, Indore, India 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
- 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 Sever 2003

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## SOFTWARE REPOSITORY

<https://github.com/spundhir>

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## REFERENCES

Advisors Prof. Bo Porse, University of Copenhagen, Denmark | [bo.porse@finsenlab.dk](mailto:bo.porse@finsenlab.dk)  
Prof. Jan Gorodkin, University of Copenhagen, Denmark | [gorodkin@rth.dk](mailto:gorodkin@rth.dk)

Additional Dr. Gitanjali Yadav, National Institute of Plant Genome Research, India | [gy@nipgr.ac.in](mailto:gy@nipgr.ac.in)  
Prof. Anil Kumar, Devi Ahilya University, India | [ak\\_sbt@yahoo.com](mailto:ak_sbt@yahoo.com)