Sachin Pundhir

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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

2014 - Present   **Post-doctoral fellow**, BRIC, University of Copenhagen, 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: 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].

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].

Structured RNAs and synteny 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.
Bioinformation 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: 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, trimmnomatic, 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

SOFTWARE REPOSITORY

https://github.com/spundhir

PERSONAL PARTICULARS

Name	Sachin Pundhir
Contact	pundhir.cph@gmail.com | +45-9186 8345
Nationality	Indian
Date of birth	August 11, 1982

REFERENCES

Advisors	Prof. Bo Porse, University of Copenhagen, Denmark | bo.porse@finsenlab.dk
	Prof. Jan Gorodkin, University of Copenhagen, Denmark | gorodkin@rth.dk
Additional	Dr. Gitanjali Yadav, National Institute of Plant Genome Research, India | gy@nipgr.ac.in
	Prof. Anil Kumar, Devi Ahilya University, India | ak_sbt@yahoo.com