

Anton Valouev, Ph.D.

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EDUCATION / TRAINING

Stanford University School of Medicine, Dept of Pathology

Stanford, CA

Postdoctoral Fellow, advisor: Arend Sidow

2006-current

High throughput DNA sequencing (ABI SOLiD, Solexa/Illumina): statistical and computational analysis
ChIP-sequencing, methylation-sequencing, genome-wide maps of nucleosome organization

University of Southern California

Los Angeles, CA

PhD in Applied Mathematics, advisor: Michael Waterman

2002-2006

(Emphasis on Computational Biology and Statistical Methods in Genetics/Genomics)

Genome-wide analysis of restriction maps obtained by optical mapping of large DNA molecules

Thesis: "Shotgun optical mapping: a comprehensive statistical and computational analysis"

Teaching Assistant: "Statistics for Life Sciences", "Introduction to Numerical Analysis", "Probability"

Moscow State Lomonosov University

Moscow, Russia

BS in Mathematics and Applied Mechanics

1996-2001

RESEARCH INTERESTS

- Statistical methods in Genetics and Genomics, analytical methods for high throughput molecular assays and their application within a biological context
- Chromatin structure, organization, and dynamics: interaction between transcriptional and regulatory states of chromatin, its compactness, and epigenetic states such as DNA methylation and localization of specific types of histones.

PUBLICATIONS

- Johnson DS, Kim SW, Brown AL, **Valouev A**, Anton E, Chiao E, Medina C, Nguyen L, Oyulu C, Neff N, Schroth GP, Sidow A, Baker JC and Myers RM. "DNA methylation profiles change minimally during human embryonic stem cell differentiation", 2008, under review
- **Valouev** * A, Johnson * DS, Sundquist A, Medina C, Anton E, Batzoglou S, Myers RM and Sidow A. "Genome-wide analysis of transcription factor binding sites based on ChIP-Seq data." *Nature Methods*, 2008 in press
- **Valouev A**, Ichikawa J, Tonthat T, Stuart J, Ranade S, Peckham H, Zeng K, Malek JA, Costa G, McKernan K, Sidow A, Fire A, and Johnson SM. "A high-resolution, nucleosome position map of *C. elegans* reveals a lack of universal sequence-dictated positioning." *Genome Research* 2008; 18(7) 1051-63
- Li H, **Valouev A**, Schwartz DC, Waterman MS and Li L. "A quantile method for sizing optical maps." *Journal of Computational Biology* 2007 14(3):255-66
- **Valouev A**, Schwartz DC, Zhou S, and Waterman MS. "An algorithm for assembly of ordered restriction maps from single DNA molecules." *PNAS* 2006; 103: 15770-15775
- **Valouev** * A, Zhang * Y, Schwartz DC, and Waterman MS. "Refinement of optical map assemblies." *Bioinformatics* 2006; 22(10): 1217-1224
- **Valouev A**, Li L, Liu YC, Schwartz DC, Yang Y, Zhang Y, and Waterman MS. "Alignment of optical maps." *Journal of Computational Biology* 2006; 13(2): 442-462

CONFERENCE AND INVITED TALKS

- "ChIP-Seq and its applications for genome-wide TFBS analysis", Illumina, 2008, Hayward, CA
- "Mapping chromatin state in humans using ChIP-Seq", Applied Biosystems 2008, Foster City, CA
- "Nucleosome phasing and positioning in the *C. elegans* genome revealed with SOLiD sequencing technology," Biology of Genomes 2007, Cold Spring Harbor Labs
- "Alignment of Optical Maps", Research in Computational Biology 2005 (RECOMB), Boston, Massachusetts

AWARDS

- Preuss Fellowship, 2005-2006

RESEARCH STATEMENT

My research mainly addresses various aspects of chromatin function, more specifically how local organization of chromatin affects its transcriptional state and regulatory behavior. This involves dissecting interaction between nucleosome-mediated packaging of DNA, local occupancy by the transcription factors, and presence of epigenetic signatures such as DNA methylation state at individual loci and acquisition of modifications by histones locally within regions. In addressing these questions, I leverage data from high-throughput sequencing assays to build and

analyze high resolution maps of chromatin state at the genome-wide level. Understanding such data requires three essential components that I combine in my research: building statistical models and analytical tools to accurately extract useful information from the data, understanding underlying molecular biology to correctly model the data, and combine multiple data sources in the analysis to dissect biological phenomena and interpret them in the context of what is already known about chromatin and its functionality.

REFERENCES

- Andrew Fire, Departments of Pathology and Genetics, Stanford University School of Medicine (afire@stanford.edu)
- David Schwartz, Departments of Genetics and Chemistry, University of Wisconsin (dcschwartz@wisc.edu)
- Arend Sidow, Departments of Pathology and Genetics, Stanford University School of Medicine (arend@stanford.edu)
- Michael Waterman, Department of Computational and Molecular Biology, University of Southern California (msw@usc.edu)