

## Cole Trapnell, Ph.D.

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Department of Genome Sciences  
University of Washington  
Seattle, WA, 98105, USA

APPOINTMENT **University of Washington**  
Assistant Professor of Genome Sciences, July 2014 - present

TRAINING **Harvard University**  
Postdoctoral Scholar, July 2010 - June 2014  
**Mentor:** John L. Rinn

**The Broad Institute of MIT and Harvard**  
Visiting Postdoctoral Fellow, July 2010 - June 2014

**University of Maryland, College Park**  
Ph.D. Computer Science, August 2006 - May 2010  
Advisors: Steven Salzberg, Lior Pachter

**University of California, Berkeley**  
Visiting student researcher, July 2008 - May 2010  
Department of Mathematics

**University of Maryland, College Park**  
B.S. Computer Science, May 2005  
B.S. Mathematics, May 2005

HONORS AND DAMON RUNYON DALE F. FREY AWARD FOR BREAKTHROUGH SCIENTISTS, 2014  
AWARDS DAMON RUNYON POSTDOCTORAL FELLOWSHIP, 2011-2014  
Finalist, Burroughs-Wellcome Career Award at the Scientific Interface, 2013  
Genome Biology Award, *BioMed Central*, 2010. (Bowtie, with Langmead, *et al*)  
Next-Generation Sequencing Paper of the Year, 2009. *Bioinformatics* (TopHat)  
Teaching Excellence Award, 2007, University of Maryland Computer Science Department

## SOFTWARE

**Cufflinks:** Transcriptome assembly and differential expression with RNA-Seq.

Total downloads since release<sup>‡</sup>: 23,000+

Citations for related article<sup>†</sup> Trapnell *et al*, 2010: 1,049

Highlighted as a notable breakthrough in Computational Biology, 2010.

See: H. Craig Mak, *Nature Biotechnology* Vol. 29, 45 (2011)

**TopHat:** Spliced short read alignment for RNA-Seq.

Total downloads since release<sup>‡</sup>: 29,000+

Citations for related article<sup>†</sup> Trapnell *et al*, 2009: 1,220

**Bowtie:** Ultrafast short read mapping (with Ben Langmead)

Total downloads since release<sup>§</sup>: 198,000+

Citations for related article<sup>†</sup> Langmead *et al*, 2009: 2,780

**Spats:** RNA structure with SHAPE-Seq (with Sharon Aviran)

**MUMmerGPU:** Fast sequence alignment on the GPU (with Michael Schatz)

## PUBLICATIONS

Journal Articles:

1. **Cole Trapnell\***, Davide Cacchiarelli\*, Jonna Grimsby, Prapti Pokharel, Shuqiang Li, Michael Morse, Niall J. Lennon, Kenneth J. Livak, Tarjei S. Mikkelsen, John L. Rinn, The dynamics and regulators of cell fate decisions are revealed by pseudotemporal ordering of single cells.  
*Nature Biotechnology*, 32: 381-386. (2014)
2. Ezgi Hacisuleyman, Loyal A. Goff, **Cole Trapnell**, Adam Williams, Jorge Henao-Mejia, Lei Sun, Patrick McClanahan, David G. Hendrickson, Martin Sauvageau, David R. Kelley, Michael Morse, Jesse Engreitz, Eric S. Lander, Mitch Guttman, Harvey F. Lodish, Richard Flavell, Arjun Raj, John L. Rinn. Topological organization of multichromosomal regions by the long intergenic noncoding RNA Firre  
*Nature Structural & Molecular Biology*, 21: 198-206. (2014)
3. Ian M. Silverman, Fan Li, Anissa Alexander, Loyal Goff, **Cole Trapnell**, John L. Rinn, Brian D. Gregory, RNase-mediated protein footprint sequencing reveals protein-binding sites throughout the human transcriptome.  
*Genome Biology* 15:R3 (2014)
4. Stephen Altschul, Barry Demchak, Richard Durbin, Robert Gentleman, Martin Krzywinski, Heng Li, Anton Nekrutenko, James Robinson, Wayne Rasband, James Taylor, **Cole Trapnell**, The anatomy of successful computational biology software.  
*Nature Biotechnology*, 31, 894-897. (2013)
5. Casey A Gifford\*, Michael J Ziller\*, Hongcang Gu, **Cole Trapnell**, Julie Donaghey, Alexander Tsankov, Alex K Shalek, David R Kelley, Alexander A Shishkin, Robby Issner, Xiaolan Zhang, Michael Coyne, Jennifer L Fostel, Laurie Holmes, Jim Meldrim, Mitchell Guttman, Charles Epstein, Hongkun Park, Oliver Kohlbacher, John Rinn,

<sup>†</sup>Google Scholar, as of 8/16/2013

<sup>‡</sup>Google Analytics, as of 8/16/2013

<sup>§</sup>SourceForge.net, as of 8/16/2013

- Andreas Gnirke, Eric S Lander, Bradley E Bernstein, Alexander Meissner, Transcriptional and epigenetic dynamics during specification of human embryonic stem cells. *Cell*, 153, 5, 1149-1163. (2013)
6. Daehwan Kim, Geo Pertea, **Cole Trapnell**, Harold Pimentel, Ryan Kelley, Steven L Salzberg, TopHat2: Accurate alignment of transcriptomes in the presence of insertions, deletions and gene fusions. *Genome Biology*, 14:R36. (2013)
  7. Stefanie A Mortimer, **Cole Trapnell\***, Sharon Aviran\*, Lior Pachter, Julius B Lucks, SHAPE-Seq: High-Throughput RNA Structure Analysis. *Current Protocols in Chemical Biology* DOI: 10.1002/9780470559277.ch120019. (2013)
  8. Lei Sun\*, Loyal A Goff\*, **Cole Trapnell\***, Ryan Alexander, Kinyui Alice Lo, Ezgi Hacisuleyman, Martin Sauvageau, Barbara Tazon-Vega, David R Kelley, David G Hendrickson, Bingbing Yuan, Manolis Kellis, Harvey F Lodish, John L Rinn, Long noncoding RNAs regulate adipogenesis. *Proc. of the National Academy of Sciences* 110, 9, 3387-3392. (2013)
  9. **Cole Trapnell\***, David Hendrickson\*, Martin Sauvageau, Loyal Goff, John Rinn, Lior Pachter, Differential analysis of gene regulation at transcript resolution with RNA-seq. *Nature Biotechnology*, 31, 4653. (2013)
  10. **Cole Trapnell**, Adam Roberts, Loyal Goff, Geo Pertea, Daehwan Kim, David R. Kelley, Harold Pimentel, Steven L. Salzberg, John L. Rinn, Lior Pachter, Differential gene and transcript expression analysis of RNA-Seq experiments with TopHat and Cufflinks. *Nature Protocols*, 7, 562578. (2012)
  11. Tim R. Mercer, Daniel J. Gerhardt, Marcel E. Dinger, Joanna Crawford, **Cole Trapnell**, Jeffrey A. Jeddloh, John S. Mattick, and John L. Rinn, Targeted RNA sequencing reveals the deep complexity of the human transcriptome. *Nature Biotechnology*, AOP doi:10.1038/nbt.2024. (2011)
  12. Moran N. Cabili, **Cole Trapnell**, Loyal Goff, Magdalena Koziol, Barbara Tazon-Vega, Aviv Regev and John L. Rinn, Integrative annotation of human large intergenic noncoding RNAs reveals global properties and specific subclasses. *Genes and Development*, 2011.25. (2011)
  13. Adam Roberts, Harold Pimentel, **Cole Trapnell\***, and Lior Pachter\*, Identification of novel transcripts in annotated genomes using RNA-Seq. *Bioinformatics*, 27 (17): 2325-2329. (2011)
  14. Julius B. Lucks, Stefanie A. Mortimer, **Cole Trapnell**, Shujun Luo, Sharon Aviron, Lior Pachter, Jennifer A. Doudna, and Adam P. Arkin, SHAPE-Seq: Multiplexed RNA Secondary and Tertiary Structure Determination. *Proc. of the National Academy of Sciences* 108, 27. (2011)
  15. Sharon Aviran, **Cole Trapnell**, Julius B. Lucks, Stefanie A. Mortimer, Jennifer A. Doudna, Adam P. Arkin, and Lior Pachter, Modeling and automation of SHAPE-Seq analysis. *Proc. of the National Academy of Sciences*, 108, 27. (2011)

16. Manuel Garber, Manfred Grabherr, Mitchell Guttman, and **Cole Trapnell**, Computational Methods for Transcriptome Annotation and Quantification. *Nature Methods*, 8, 469-477. (2011)
17. Adam Roberts, **Cole Trapnell**, Julie Donaghey, John L. Rinn, and Lior Pachter, Improving RNA-Seq expression estimates by correcting for fragment bias. *Genome Biology* 12:R22. (2011)
18. **Cole Trapnell**, Brian Williams, Geo Pertea, Ali Mortazavi, Gordon Kwan, Marijke J. van Baren, Steven L. Salzberg, Barbara Wold, and Lior Pachter, Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation. *Nature Biotechnology*, 28, 511-515. (2010)
19. Robert K. Bradley\*, Xiao-Yong Li\*, **Cole Trapnell**, Stuart Davidson, Lior Pachter, Hou Cheng Chu, Mark D. Biggin, and Michael B. Eisen, Binding site turnover produces pervasive quantitative changes in transcription factor binding between closely related *Drosophila* species. *PLoS Biology*, 8(3): e1000343. (2010)
20. **Cole Trapnell** and Steven L. Salzberg, How to map billions of short reads onto genomes. *Nature Biotechnology*, 27, 455-457. (2009)
21. **Cole Trapnell\***, Michael C. Schatz\*, Optimizing Data Intensive GPGPU Computations for DNA Sequence Alignment. *Parallel Computing*, 35:8-9. (2009)
22. **Cole Trapnell**, Lior Pachter, and Steven L. Salzberg, TopHat: discovering splice junctions with RNA-Seq. *Bioinformatics* 25(9):1105-1111. (2009)
23. Ben Langmead, **Cole Trapnell**, Mihai Pop, and Steven L. Salzberg, Ultrafast and memory-efficient alignment of short DNA sequences to the human genome. *Genome Biology*, 10:R25. (2009)
24. Steven L. Salzberg *et al*, Genome sequence and rapid evolution of the rice pathogen *Xanthomonas oryzae* pv. *oryzae* PXO99. *BMC Genomics* 9:204. (2008)
25. Michael C. Schatz\*, **Cole Trapnell\***, Arthur L. Delcher, and Amitabh Varshney, High-throughput sequence alignment using Graphics Processing Units. *BMC Bioinformatics*, 8:474. (2007)

Conference Papers:

- Bruce C. Trapnell, Jr**, A Peer-to-Peer Blacklisting Strategy Inspired by Leukocyte-Endothelial Interaction. *Proceedings of the Fourth International Conference on Artificial Immune Systems* (2005)

Book Chapters:

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\*Equal contribution

Mark Neal and **Bruce C. Trapnell, Jr**, Go Dutch: Exploit Interactions and Environments with Artificial Immune Systems.  
*In Silico Immunology*, Springer (2007)

## INVITED TALKS

*Investigating the role of long, noncoding RNAs in cellular differentiation*

Boston University Bioinformatics Student-Organized Symposium. (2013)

Broad Institute retreat. (2012)

*Isoform-resolution differential expression analysis with RNA-Seq*

VIZBI: Visualizing Biological Data (2013)

Special seminar, Cincinnati Children's Hospital Research Center. (2012)

UC Berkeley \*-Seq I. (2012)

Biomatters Geneious User Group meeting. (2011)

*Assembly, quantification, and cloning of human long, noncoding RNAs*

Keynote, Roche RNA-Seq BARN. (2011)

*Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation*

UNC Charlotte Bioinformatics Dept. seminar series. (2011)

Johns Hopkins Biostatistics Dept. special seminar. (2010)

*RNA-seq analysis with TopHat and Cufflinks*

Illumina live global webcast. (2010)

Life Technologies platform user webinar. (2010)

*The Tuxedo Tools: ultrafast short read mapping*

UC San Diego Next-Generation Sequencing Meeting. (2008)

Illumina. (2008)

UC Berkeley Mathematical Biology Seminar. (2008)

*Bowtie: ultrafast and memory-efficient alignment of short DNA sequences to the human genome*

Applied Biosystems. (2008)

*Transcriptome discovery and quantitation with the Tuxedo tools*

Short-SIG: Next Generation Sequencing and Algorithms for Short Read Analysis, ISMB. (2009)

MGED 12, Phoenix, Arizona. (2009)

Broad Institute Computational Biology and Bioinformatics program seminar series. (2009)

## TALKS

*Long noncoding RNAs regulate adipogenesis*

Keystone Symposium on the Genetic and Molecular Basis of Obesity and Body Weight Regulation. (2012)

*Investigating the role of long, noncoding RNAs in pluripotency and self renewal*

Harvard Stem Cell and Regenerative Biology departmental seminar series. (2012)

Quantitative Biology departmental seminar series, Cold Spring Harbor Laboratory. (2012)

*“The Clone Wars:” Mechanistic characterization of long, noncoding RNAs*

Broad Epigenomics seminar (2011)

## POSTERS

1. Mapping the myogenic regulatory network with single cell RNA-Seq.  
*Gordon Research Conference on Myogenesis.* (2013)
2. Differential gene and transcript expression analysis with TopHat and Cufflinks.  
*Abcam Chromatin.* (2011)
3. Transcript assembly and quantification by RNA-Seq reveals unannotated transcripts and isoform switching during cell differentiation.  
*Cold Spring Harbor Meeting on the Biology of Genomes.* (2010)
4. High-speed transcript isoform discovery and quantitation in RNA-seq data using TopHat.  
*Cold Spring Harbor Meeting on the Biology of Genomes.* (2009)
5. High-throughput sequence alignment using Graphics Processing Units.  
*15th Annual Microbial Genomes Conference.* (2007)

## TEACHING

**Guest lecturer** for MIT 6.047/6.878: Computational Biology: Genomes, Networks, Evolution. This is a graduate course that covers the fundamentals of computational biology.

**Guest lecturer** for Harvard STAT 115: Introduction to computational biology and bioinformatics. This is a course for undergraduates and graduate students that provides a statistical introduction to computational biology.

**Recitation teaching assistant** for University of Maryland CMSC 212: Intro to Hardware-level Programming, Fall 2006 and Spring 2007.

## PROFESSIONAL SERVICE

**Principal developer and maintainer** of several open-source tools that are widely-used by computational biologists.

**Developed** and routinely offer a hands-on **workshop** to train biologists in the analysis of RNA-Seq experiments, *Gene and transcript expression analysis with RNA-Seq*:

Tufts Computational Biology Initiative Transcriptomics Symposium 2012

Broad-E workshop series, Summer 2012 and 2013

Functional Genomics Data Society (FGED) meeting, 2009.

**Regular reviewer** for:

*Nature Biotechnology*

*Genome Research*

*Genome Biology*

*Bioinformatics*

*BMC Bioinformatics*

*PLoS Computational Biology*

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*Human Molecular Genetics*  
*Genomics*

INDUSTRY EXPERIENCE	<b>Actuate Corporation</b> <i>Software Engineer</i>	<b>August 2005 - August 2006</b>
	<b>TopGun Software</b> <i>Co-founder and Software Engineer</i>	<b>June 2002 - July 2005</b>
	<b>U.S. Army Research Laboratory</b> <i>Student engineer</i>	<b>June 1999 - June 2002</b>