

Aaron R. Quinlan, Ph.D.

CONTACT INFORMATION	Assistant Professor Department of Public Health Sciences Center for Public Health Genomics University of Virginia	(O): 434.243.1669 (F): 434.924.1312 arq5x@virginia.edu cphg.virginia.edu/quinlan
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RESEARCH INTERESTS	Chromosome stability and somatic genome evolution; Genomics software development; Cancer genomics; Population genomics; Genetics of complex disease
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EDUCATION	Boston College , Chestnut Hill, MA, USA Ph.D., Biology, 2008 College of William and Mary , Williamsburg, VA, USA B.S., Computer Science, 1997
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ACADEMIC EXPERIENCE	University of Virginia , Charlottesville, VA, USA <i>Assistant Professor of Public Health Sciences</i> Center for Public Health Genomics 2011- University of Virginia , Charlottesville, VA, USA <i>NRSA Postdoctoral Fellow (NHGRI)</i> 2008-2011
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HONORS AND AWARDS	Co-chair, NHLBI Exome Sequence Project Structural Variation Group. 2011- Instructor for CSHL Advanced Sequencing Technologies Course. 2009- Fund for Excellence in Science and Technology Awardee, UVa. (1 of 5). 2011 Ruth L. Kirschstein (NRSA / F32) Postdoctoral Fellowship, NHGRI. 2009-2010 Presidential Fellowship, Boston College. 2004-2007
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EDITING AND REVIEW	<i>Ad hoc</i> reviewer for <i>Genome Research</i> , <i>Genome Biology</i> , <i>Bioinformatics</i> , <i>BMC Bioinformatics</i> , <i>Bioessays</i> , and <i>Genes</i>
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NIH: Special Emphasis Panel for Computational Analysis of ENCODE (U01) (16-May-2012)

PUBLICATIONS	† <i>denotes corresponding author</i> ★ <i>denotes joint first authors</i>
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16. Krumm N, Sudmant PH, Ko A, O’Roak BJ, NHLBI Exome Sequencing Project, **Quinlan AR**, Nickerson DA, Eichler EE. Copy number variation detection and genotyping from exome sequence data. Under review.
15. Layer R†, **Quinlan AR**†, Robins G, Skadron K. Binary Interval Search (BITS): A Massively Parallel Interval Intersection Algorithm. Under review.
14. **Quinlan AR** and Hall IM. Structural variation in mammalian genomes. Invited book chapter for *Methods in Molecular Biology*. In press.
13. **Quinlan AR**, Boland MJ, Leibowitz ML, Shumilina S, Pehrson SM, Baldwin KK, Hall IM. Paired-end DNA sequencing of induced pluripotent stem cell genomes reveals rare structural mutations and retroelement stability. *Cell Stem Cell*, 9:366-373, 2011.

12. Keene KL, **Quinlan AR**, Hou X, Hall IM, Mychaleckyj, Onengut-Gumuscu S, Concannon P. Evidence for two independent associations with type 1 diabetes at the 12q13 locus. *Genes and Immunity*, 13:66-70, 2011.
11. **Quinlan AR**, Hall IM. The landscape of complex chromosomal rearrangements in the germline and somatic lineages. *Trends in Genetics*, 18:43-53, 2011.
10. Dale R, Pedersen B, **Quinlan AR**†. Pybedtools: a flexible Python library for manipulating genomic datasets and annotations. *Bioinformatics*, 24:3423-3424, 2011.
packages.python.org/pybedtools/
9. Barnett D, Garrison E, **Quinlan AR**, Stromberg M, Marth G. BamTools: a C++ API and toolkit for analyzing and managing BAM files. *Bioinformatics*, 12:1691-1692, 2011.
code.google.com/p/bamtools
8. 1000 Genomes Project Consortium.. A map of human genome variation from population-scale sequencing. *Nature* 7319:1061-73, 2010.
7. **Quinlan AR** and Hall IM. BEDTools: A flexible framework for comparing genomic features. *Bioinformatics*, 6:841-842, 2010.
code.google.com/p/bedtools
6. **Quinlan AR**, Clark RA, Sokolova, S, Leibowitz ML, Zhang Y, Hurles ME, Mell JC, Hall IM. Genome-wide mapping and assembly of structural variant breakpoints in the mouse genome. *Genome Research*, 20:623-635, 2010.
code.google.com/p/hydra-sv
5. Sackton, TB, Kulathinal RJ, Bergman CM, Quinlan AR, Dopman E, Marth GT, Hartl DL, Clark AG. Population Genomic Inferences from Sparse High-Throughput Sequencing of Two Populations of *Drosophila melanogaster*. *Genome Biol Evol*, 1:439-455, 2009.
4. Smith D, **Quinlan AR***, Peckham HR, *et al.* Rapid whole-genome mutational profiling using next-generation sequencing technologies. *Genome Research*, 18:1638-1642, 2008.
3. Hillier LW, Marth GT, **Quinlan AR**, *et al.* Whole Genome Sequencing and SNP Discovery for *C. elegans* using massively parallel sequencing-by-synthesis. *Nature Methods*, 5:183-188, 2008.
2. **Quinlan AR**, Stewart D, Stromberg M, Marth GT. PyroBayes: Accurate quality scores for 454 Life Science pyrosequences. *Nature Methods*, 5:179-181, 2008.
1. **Quinlan AR**, Marth GT. Primer-site SNPs mask mutations. *Nature Methods*, 4:192, 2007.

RESEARCH SUPPORT Project Title: *New algorithms and tools for large-scale genomic analysis.*

PI: Aaron Quinlan

Source: NIH/NHGRI (R01 HG006693-01)

Amount: \$437,112; Period funded: 19-Apr-2012 - 31-Mar-2016

Project Title: *Identification of radiation sensitivity alleles by whole exome sequencing.*

PI: Pat Concannon

Co-investigator: Aaron Quinlan

Source: NIH/NIEHS (R21 ES020521-01)

Amount: \$153,376; Period funded: 19-Aug-2011 - 31-Jul-2013

Project Title: *New oncogenes and regions of genome instability in ovarian cancer.*

PI: Aaron Quinlan

Source: University of Virginia Fund for Excellence in Science and Technology (FEST)

Amount: \$50,000; Period funded: 01-May-2011 - 30-Apr-2012

Project Title: *Defining the genomic architecture of glioblastoma for improved therapy.*

PI: Aaron Quinlan

Source: University of Virginia Cancer Center Pilot Fund
Amount: \$53,125; Period funded: 01-Apr-2011 - 31-Mar-2012

Project Title: *Rates and patterns of recurrent structural variation in the mouse genome.*
PI: Aaron Quinlan
Source: NIH/NHGRI (F32 HG005197-02)
Period funded: 01-Aug-2009 - 31-Dec-2010

INVITED LECTURES	<p><i>Towards a map of structural variation in the Exome Sequencing Project.</i> NHLBI Exome Sequencing Project In-Person Meeting, March 28, 2012</p> <p><i>Exploring the origin and extent of structural variation in human genomes.</i> Deans New Faculty Seminar Series, University of Virginia School of Medicine, Jan 19, 2012</p> <p><i>ESP Structural Variation Project Group: goals, initial results, and future work.</i> NHLBI Exome Sequencing Project In-Person Meeting, June 9, 2011</p> <p><i>Large-Scale Characterization of SV Breakpoints in Cancer.</i> Keystone Symposium on The Functional Impact of Structural Variation, Jan. 11, 2011</p> <p><i>Efficient discovery of structural instability in repetitive regions of mammalian genomes.</i> Advances in Genome Biology and Technology, Feb. 2009</p> <p><i>Approaches to rare allele discovery: More samples or more depth per sample?</i> 1000 Genomes Analysis Meeting, Cold Spring Harbor Laboratories, May 2008.</p>
ACADEMIC SERVICE	<p>Member of the Univ. of Virginia Bioinformatics Core Advisory Committee. 01-Nov-2011 - Present.</p> <p>Served on the Univ. of Virginia Bioinformatics Core Director Search Committee. Summer 2011.</p>
TEACHING	<p>Instructor for CSHL Advanced Sequencing Technologies Course. 2009 - Present</p> <p>Guest Lecturer for graduate course in genomics (BIOCH 5080). 15-Feb-2011</p>
THESIS COMMITTEES	<p>Current Michael Lindberg (Ph.D., Biochemistry and Molecular Genetics, qualified 2012)</p>