MARK REPPELL

Address	Cummings Life Science Center 411
	Department of Human Genetics
	University of Chicago
	920 E. 58th Street
	Chicago, IL 60637
Phone	(504) 782-9705
Email	mreppell@uchicago.edu

EMPLOYMENT

2014-Present Postdoctoral Scholar
Department of Human Genetics
University of Chicago, Chicago
Advisor: Prof. John Novembre

EDUCATION

2010-2014 Ph.D. · Biostatistics
University of Michigan, Ann Arbor
Dissertation: *Using rare genetic variation to understand human demographics and the etiology of complex traits*
Advisor: Prof. Sebastian Zöllner

2008-2010 M.S. · Biostatistics
University of Michigan, Ann Arbor
Advisor: Prof. Mike Boehnke

2002-2006 B.S. · Mathematics and Ecology/Evolutionary Biology
Tulane University, New Orleans

PUBLICATIONS

Reppell M, Novembre, J. (2017) Karp: accurate and fast taxonomic classification using pseudoalignment. bioRxiv doi: 10.1101/097949.

Reppell M, Zöllner S. (2017) An efficient algorithm for generating the internal branches of a Kingman coalescent. (*In revision*)

Reppell M, Koch E, Peter BM, Novembre J. (2014) Surfing waves of data in San Diego: sophisticated analyses provide a broad view of human genetic diversity. *Genome Biology.* 15:562

Zawistowski M*,**Reppell M***, Wegmann D, St Jean PL, Ehm MG, Nelson MR, Novembre J, Zöllner S. (2014) Analysis of rare variant population structure in Europeans explains differential stratification of gene-based tests. *European Journal of Human Genetics.* 22, 1137-1144

Reppell M, Boehnke M, Zöllner S. (2013) The impact of accelerating, faster than exponential population growth on genetic variation. *Genetics.* 196, 819-828.

Reppell M, Boehnke M, Zöllner S. (2012) FTEC: a coalescent simulator for modeling faster than exponential growth. *Bioinformatics.* 28, 1282-1283.

PRESENTATIONS

Karp: Accurate and fast classification of microbiome taxonomy using pseudomapping. Midwest Population Genetics Conference. August 2016 (Talk).

Inferring population growth rates in a structured population. Probabilistic Modeling in Genomics Conference. October 2015 (Talk).

The distribution of internal branch lengths in the Kingman coalescent. American Socieity of Human Genetics Annual Conference. October 2014 (Poster).

Incorporating faster than exponential population growth into the coalescent using FTEC. National Center for Integrative Biomedical Informatics Tools & Technology Seminar Series. January 2013 (Talk).

An Assessment of Population Stratification in Rare Variant Association Tests Using an Analytic Model of Joint Site Frequency Spectra. American Society of Human Genetics Annual Conference. November 2012 (Poster).

A Coalescent Simulator Capable of Modeling Faster than Exponential Growth. International Congress of Human Genetics. November 2011 (Poster).

Identification of plausible sets of causal SNPs in GWAS associated regions. American Society of Human Genetics Annual Conference. November 2010 (Poster).

TEACHING	
2015	Workshop · "An introduction to the coalescent." Dordt College.
2014	Guest Lab · "Group-based association testing using EPACTS." University of Chicago. Human Genetics 471: Introduction to Statistical Genetics.
2014	Guest Lecture · "Population structure in the coalescent." University of Michigan. Biostatistics 665: Statistical Population Genetics.
ORGANIZATIONAL SERVICE	
2015-Present	Organizer · Human Genetics Postdoc Society, University of Chicago
	Referee · *American Journal of Human Genetics*, *Bioinformatics*, *Genetics*, *Theoretical Population Biology*, *European Journal of Human Genetics*, *Evolutionary Bioinformatics*
2010-2013	Organizer · Statistical Genetics Journal Club, University of Michigan
HONORS	
2009-2012	NIH Pre-Doctoral Genome Science Training Program, University of Michigan
2008-2014	Graduate Student Research Assistant, University of Michigan Department of Biostatistics
2006	Departmental Honors, Tulane University Mathematics Department
2006	Cum Laude, Tulane University
2002-2006	Deans Honor Scholarship, Tulane University
PROFESSIONAL MEMBERSHIPS	
2010-Present	American Society of Human Genetics
COMPUTATIONAL SKILLS	C++, Perl, R, Latex, Bash, Linux, Microsoft Office Suite, Coalescent simulation, Genetic association testing
GITHUB	https://github.com/mreppell