| Contact<br>Information                       | E-mail: ranolaj@uw.edu<br>www.john.ranola.org  |
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| About Me                                     | I am a statistical geneticist with a PhD in biomathematics from UCLA with extensive experience<br>programming in R including the creation and development of new analysis packages. I am adept at<br>performing standard statistical analyses on many types of genetic data including SNP chip, whole<br>genome sequencing, and pedigree data. Furthermore, I also excel at adapting methods or creating<br>new ones to answer more unique questions. Although my recent experience focuses on genetic<br>analyses, I have extensive training in statistics and mathematics which may be applied anywhere. |
| Education                                    | University of California Los Angeles, Los Angeles, CA  |
|  | Ph.D. Biomathematics, December 2013  |
|  | <ul> <li>Dissertation Topic: "Probability Models for High-dimensional Spatial and Network Genetic Data"</li> <li>Advisor: Konneth Lange</li> </ul>   |
|  | • Advisor. Remetin Lange<br>M.S. Biomathematics, May 2008  |
|  | M.S. Diomaticinatics, May 2000   |
|  | University of Portland, Portland, OR   |
|  | B.S. Mathematics and Biology, May, 2006  |
| Professional<br>Appointments &<br>Employment | Statistical Geneticist       Jan 2016 - Present         Department of Laboratory Medicine University of Washington, Seattle, WA       Advisor: Brian Shirts  |
|  | • Was the only statistician and thus a key figure in the analysis endeavors of the group.  |
|  | • Developed analytical tools, based on published literature, to perform cosegregation analysis to aid in the classification of variants of uncertain significance. This included development of the R package CoSeg and the website http://analyze.myvariant.org/.   |
|  | • Assisted with the training of students rotating through the lab.   |
|  | • Developed novel tools to assist in the classification of variants of uncertain significance including one which determines the most informative relative for genotyping.   |
|  | • Analyzed genetic data from colleagues to answer their specific questions.  |
|  | • Created figures and graphs to showcase various aspects of datasets.  |
|  | Postdoctoral Scholar in Statistical GeneticsJan 2014 - Dec 2015Department of Statistics University of Washington, Seattle, WAAdvisor: Elizabeth Thompson   |
|  | • Wrote an R package called OriGen used in the geographical localization of individuals or their ancestry using their genetic information.   |
|  | • Published a paper in Bioinformatics titled Fast Spatial Ancestry via Flexible Allele Frequency Surfaces.   |
|  | • Presented the work in an International Center for Mathematical Sciences workshop in Edin-<br>burgh Scotland titled "Statistical and Computational Methods for Relatedness and Relation-<br>ship Inference from Genetic Marker Data".   |
|  | Math Teacher and Private TutorSept 2006 - Dec 2013Renaissance Kids, Los Angeles, CA• Taught preparatory classes for SAT and ISEE.  |

- Gave private lessons in math subjects ranging from Pre-Algebra to Calculus.
- Prepared individual students for standardized tests such as the SAT and ISEE.

| Selected Honors<br>and Awards | <ul> <li>International Biometric Conference Best Poster 2016</li> <li>Genome Training Grant UW 2014-15</li> <li>Chancellor's Prize UCLA 2007-8</li> <li>Passed Actuarial Exam P/1 (2006)</li> <li>Scored in the 99th percentile Putnam Exam 2005 (8 points)</li> </ul>   |
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| Software                      | <ul> <li>http://analyze.myvariant.org/ - A website designed to help clinicians and genetic counselors with the classification of variants of uncertain significance.</li> <li>CoSeg - An R package available on R-Forge that generates historically accurate U.S. and Chinese pedigrees based on population census data. It also simulates pedigrees with realistic cancer causing mutations and contains functions to analyze the mutation in the pedigree for pathogenicity.</li> <li>OriGen - An R package available on R-Forge and CRAN for estimating the geographical origin of an individual based off their DNA. Along with unmixed individuals, the package can also</li> </ul> |
|                               | <ul> <li><b>PropClust</b> - An R package available on CRAN for implementing propensity clustering and decomposition. Propensity decomposition can be viewed on the one hand as a generalization of the eigenvector-based approximation of correlation networks and on the other hand as a generalization of random multigraph models and conformity-based decompositions.</li> </ul>   |
| Selected<br>Publications      | Ranola John Michael, Tsai Ginger, and Shirts Brian. Exploring the Effect of Clinical Ascertain-<br>ment Bias on Genetic Studies that use Clinical Pedigrees. In Review.  |
|                               | Roberts Maegan, <b>Ranola John Michael</b> , Marshall Megan, Susswein Lisa, Graceffo Sara, Bohnert Kelsey, Tsai Ginger, Klein Rachel, Hruska Kathleen, and Shirts Brian. <i>CDH1 Penetrance Estimates are Lower than Once Thought</i> . In Review.   |
|                               | <b>Ranola John Michael</b> , Pearlman Rachel, Hampel Heather, and Shirts Brian. Modified Capture-<br>Recapture Estimates of the Number of Families with Lynch Syndrome in Central Ohio. Familial<br>Cancer 2018.   |
|                               | Tsai Ginger, <b>Ranola John Michael</b> , Smith Christina, Garrett Lauren, Bergquist Timothy, Casadei Silvia, Bowen Deborah, and Shirts Brian. <i>Outcomes of 92 patient-driven family studies for reclassi-fication of variants of uncertain significance</i> . Genetics in Medicine. 2018.   |
|                               | Ranola John Michael, Liu Quanhui, Rosenthal Elisabeth, and Shirts Brian. A Comparison of Cosegregation Analysis Methods for the Clinical Setting. Familial Cancer 2018.  |
|                               | Rosenthal Elisabeth, <b>Ranola John Michael</b> , and Shirts Brian. Power of Pedigree Likelihood<br>Analysis in Extended Pedigrees to Classify Rare Variants of Uncertain Significance in Cancer Risk<br>Genes. Familial Cancer 2017.  |
|                               | Ranola John Michael, Novembre John, and Lange Kenneth. Fast Spatial Ancestry via Flexible Allele Frequency Surfaces. Bioinformatics 2014; 30(20).  |
|                               | Chen Gary, Chi Eric, <b>Ranola John Michael</b> , and Lange Kenneth. <i>Convex Clustering: An Attrac-</i><br><i>tive Alternative to Hierarchical Clustering.</i> PLOS Computational Biology 2015; 11(5).   |
|                               | Blue EM, Brown LA. Conomos MP, Kirk J, Nato AQ, Popejoy AB, Raffa J, <b>Ranola J</b> , Thorn-<br>ton T and Wijsman EM. <i>Estimation of Relationships between Subjects and Phenotypes in Admixed</i><br><i>Families.</i> In Proceedings of the 19th Genetics Analysis Workshop, 2014, Vienna, AT.  |
|                               | Ranola John Michael, Langfelder Peter, Lange Kenneth, and Horvath Steve. Cluster and Propen-<br>sity Based Approximation of a Network. BMC Systems Biology 2013; 7(21).  |
|                               | Ranola John Michael, Ahn Sangtae, Sehl Mary, Smith Des, and Lange Ken. A Poisson Model for Random Multigraphs. BMC Bioinformatics 2010; 26(16):2004-11.  |

Ranola John, Tobalske Bret, Warrick Douglas, and Powers Donald. Circulation in the Wake of the

| Presentations | American Society of Human Genetics Annual Conference  |                 |
|---------------|---|-----------------|
|               | San Diego Convention Center, San Diego CA   | Fall 2018       |
|               | • Presented a poster on ascertainment bias when using clinically ascertained pedigrees.   |                 |
|               | American Society of Human Genetics Annual Conference  |                 |
|               | Vancouver Convention Center, Vancouver BC   | Fall 2016       |
|               | • Presented a poster on cosegregation analysis methods.   |                 |
|               | International Biometrics Conference   |                 |
|               | Victoria Convention Center, Victoria BC Spri  | ing 2016        |
|               | • Presented a poster on mapping worldwide human populations back into the central po<br>Africa.   | ortion of       |
|               | • Won a prize for best poster presentation.   |                 |
|               | Mathematical Modeling in Biomedicine: The Carol Newton Legacy Symposium   | n               |
|               | University of California Los Angeles, Los Angeles CA Win  | ter 2015        |
|               | • Presented a poster on finding the spatial ancestral origin of samples.  |                 |
|               | ICMS: Statistical and computational methods for relatedness and relationship in from genetic marker data  | ference         |
|               | University of Edinburgh, Edinburgh Scotland Summ  | mer 2014        |
|               | • Presented a poster on finding the spatial ancestral origin of samples.  |                 |
|               | WNAR/IMS Student Speaker  |                 |
|               | University of California Los Angeles, Los Angeles CA Summ   | mer 2013        |
|               | • Presented a student paper on Cluster and Propensity-based Approximation of a Netw   | work.           |
|               | Biomathematics 210: Optimization Methods in Biology Guest Speaker   |                 |
|               | University of California Los Angeles, Los Angeles CA  | Fall 2009       |
|               | • Presented research in Random Multigraphs.   |                 |
|               | • Presented current papers on Vertex Discriminant Analysis.   |                 |
|               | Systems & Integrative Biology Retreat Speaker   |                 |
|               | University of California Los Angeles, Los Angeles CA Win  | ter 2009        |
|               | • Presented research on Random Multigraphs.   |                 |
|               | Biomathematics 206: Mathematical Oncology Guest Speaker   |                 |
|               | University of California Los Angeles, Los Angeles CA Win  | ter 2008        |
|               | • Presented research on optimization in time, dosage, and respite periods of chemother immunotherapy treatments using an ODE model presented by De Pillis and Radunsk | apy and<br>aya. |
|               | Systems & Integrative Biology Retreat Speaker   |                 |
|               | University of California Los Angeles, Los Angeles CA Win  | ter 2007        |
|               | • Presented research on a Lotka-Volterra 4-species food chain.  |                 |
|               | Student Presenter for the Society of Integrative and Comparative Biology Annua ing  | l Meet-         |
|               | Buena Vista Palace Resort, Orlando FL Win   | ter 2006        |
|               | • Presented research on the mechanics of bird flight, particularly on issues of threshold wake decay.   | ling and        |

## Student Speaker for the Mathematical Association of America Northwest Regional Meeting

University of Puget Sound, Tacoma WA Spring 2005

• Presented research on a Lotka-Volterra 4-species food chain in the northwest regional meeting.

## Student Speaker for 14th Regional Conference on Undergraduate Research of the Murdock College Science Research Program

Northwest Nazarene University, Nampa ID

• One of two groups chosen to represent the University of Portland to speak about summer research on the mechanics of bird flight, particularly on issues of thresholding and wake decay.

## Student Speaker for Portland Area Undergraduate Mathematics Conference

University of Portland, Portland OR

Spring 2005

• Presented summer research in mathematical biology dealing with a Lotka-Volterra 4-species food chain.

References Available upon request

Fall 2005