

Alexej Gossmann

Department of Mathematics
Tulane University
6823 St.Charles Ave.
New Orleans, LA 70118

Web: alexejgossmann.com
Email: agossman@tulane.edu

Updated: May 15, 2016

AREAS OF INTEREST

Sparse Regression, Mixed Effects Models, Computational Statistics, Machine Learning, Application to Genomics

EDUCATION

PhD, Mathematics

Tulane University, New Orleans, Louisiana, expected May 2018

MS, Statistics

Tulane University, New Orleans, Louisiana, May 2014

Master's Research Project: Analysis of Bone Growth Data with Mixed-Effects SS ANOVA Methods (supervised by Dr. Michelle Lacey)

GPA: 3.975

BS, Mathematics

Technische Universität Darmstadt, Darmstadt, Germany, May 2012

Thesis: On disjunction and numerical existence properties of extensions of Heyting arithmetic (supervised by Dr. Ulrich Kohlenbach)

GPA: 4.0

EXPERIENCE

Teaching Experience

- *Instructor*: Calculus 1, Tulane University, Department of Mathematics, Fall 2014.
- *Co-Teacher*: Statistics for Scientists, Tulane University, Department of Mathematics, Spring 2014.
- *Teaching Assistant*: Various Statistics, Calculus, and Real Analysis courses at Tulane University and Technische Universität Darmstadt, Fall 2010 - Spring 2014.

Internships

- *Student developer for Google Summer of Code 2015*. Project: Adding Linear Mixed Effects Models Support to SciRuby. Supervised by the Ruby Science Foundation. May – August 2015.

Professional Service Activities

- *Mentor for Google Summer of Code 2016*. Project: Categorical data support for Daru, Statsample and Statsample-glm. May – August 2016.
- President of the SIAM student chapter at Tulane University. September 2014 – Present.
- Main organizer of the Graduate Student Colloquium at the department of Mathematics, Tulane University. September 2014 – Present.

Summer Schools and Workshops

- *20th Summer Institute in Statistical Genetics*. University of Washington School of Public Health. July 2015.

Modules attended:

- Unsupervised Methods for Statistical Machine Learning
 - MCMC for Genetics
 - Pathway & Network Analysis for Omics Data
- *SAMSI 2014 Mathematical and Statistical Modeling Workshop for Graduate Students*, North Carolina State University. July 2014.
Project: Allergy, Asthma and Exposures in the Homes of the US Population (supervised by scientists from Rho Inc.).

Other

- Kommando 1. Luftwaffendivision, Fürstenfeldbruck. Military service at the department for public relations and press. June 2008 – February 2009.

- PUBLICATIONS**
- [1] Shaolong Cao, Huaizhen Qin, Alexej Gossmann, Hong-Wen Deng, and Yu-Ping Wang. Unified tests for fine scale mapping and identifying sparse high-dimensional sequence associations. *Bioinformatics*, 2015.
 - [2] Mimi C Sammarco, Jennifer Simkin, Alexander J Cammack, Danielle Fassler, Alexej Gossmann, Luis Marrero, Michelle Lacey, Keith Van Meter, and Ken Mu-neoka. Hyperbaric oxygen promotes proximal bone regeneration and organized collagen composition during digit regeneration. *PloS one*, 10(10), 2015.
 - [3] Shaolong Cao, Huaizhen Qin, Alexej Gossmann, Hong-Wen Deng, and Yu-Ping Wang. Unified tests for fine scale mapping and identifying sparse high-dimensional sequence associations. In *Proceedings of the 6th ACM Conference on Bioinformatics, Computational Biology and Health Informatics, BCB '15*, pages 241–249, New York, NY, USA, 2015. ACM.
 - [4] Alexej Gossmann, Shaolong Cao, and Yu-Ping Wang. Identification of significant genetic variants via slope, and its extension to group slope. In *Proceedings of the 6th ACM Conference on Bioinformatics, Computational Biology and Health Informatics, BCB '15*, pages 232–240, New York, NY, USA, 2015. ACM.

TALKS AND COLLOQUIA

- Title: *Identification of Significant Genetic Variants via SLOPE, and its Extension to Group SLOPE*. The 6th ACM Conference on Bioinformatics, Computational Biology, and Health Informatics, Atlanta, GA, 2015.
- Title: *Reproducing Kernel Hilbert Spaces and Smoothing Spline Regression*. Graduate student colloquium, Tulane University, 2014.

POSTER PRESENTATIONS

- A. Gossmann, S. Cao, and Y.-P. Wang, Identification of Significant Genetic Variants via SLOPE, and its Extension to Group SLOPE; (Abstract/Program #1343F). Presented at the 65th Annual Meeting of The American Society of Human Genetics, October 9, 2015, Baltimore, MD.

SOFTWARE

- **grpSLOPE** – Group SLOPE (Group Sorted L1 Penalized Estimation) is a penalized linear regression method that is used for adaptive selection of groups of significant predictors in a high-dimensional linear model. The Group SLOPE method can control the (group) false discovery rate at a user-specified level. Project repository: <https://github.com/agisga/grpSLOPE>. CRAN: <https://cran.r-project.org/web/packages/grpSLOPE/index.html>

- `mixed_models` – Fit statistical linear models with fixed and random effects in Ruby. Project repository: https://github.com/agisga/mixed_models. RubyGems: https://rubygems.org/gems/mixed_models.
- `spitzy` – A toolbox of numerical differential equation solvers written in pure Ruby. Project repository: <https://github.com/agisga/spitzy>. RubyGems: <https://rubygems.org/gems/spitzy>.
- I am an active code contributor to projects of the Ruby Science Foundation (SciRuby), such as `NMatrix` (<https://github.com/SciRuby/nmatrix>), `statsample-glm` (<https://github.com/SciRuby/statsample-glm>), and others.

SKILLS

Computer skills: R, Ruby, C++, Matlab, L^AT_EX, Linux, git and github, HTML, CSS.

Language Knowledge: Bilingual in German and Russian, fluent in English, basic knowledge of French.