

## Alexej Gossmann

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### 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](https://github.com/agisga/mixed_models). RubyGems: [https://rubygems.org/gems/mixed\\_models](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<sup>A</sup>T<sub>E</sub>X, Linux, git and github, HTML, CSS.

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