

Alexej Gossmann

Bioinnovation PhD Program
Tulane University

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

AREAS OF INTEREST Statistical learning with sparsity, feature selection and prediction on big high-dimensional datasets, mixed effects models, analysis of genomics and brain imaging data, development of scientific software

EDUCATION *PhD*, Bioinnovation
Tulane University, New Orleans, Louisiana, in progress

Doctoral research, Mathematics
Tulane University, New Orleans, Louisiana, through January 2017
GPA: 3.975

MS, Statistics
Tulane University, New Orleans, Louisiana, May 2014
GPA: 3.975

BS, Mathematics
Technische Universität Darmstadt, Darmstadt, Germany, May 2012
GPA: 4.0

EXPERIENCE

- Instructor, co-teacher, or teaching assistant for various undergraduate statistics, calculus, and real analysis courses at Tulane University and Technische Universität Darmstadt, Fall 2010 - Fall 2014.
- 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.
- 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 – September 2016.
- Main organizer of the Graduate Student Colloquium at the department of Mathematics, Tulane University. September 2014 – September 2016.

SKILLS *Computer skills:* R, Ruby, C++, Matlab, \LaTeX , Linux, git and github, HTML, CSS.

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

HONORS & AWARDS

- Reviewers Choice Abstract (top 10% of poster abstracts), 66th Annual Meeting of The American Society of Human Genetics, October 19, 2016, Vancouver, Canada.
- SIAM Student Chapter Certificate of Recognition, SIAM (Society for Industrial and Applied Mathematics), April 2015.

- PUBLICATIONS**
- [1] Alexej Gossmann, Shaolong Cao, Damian Brzyski, Lan-Juan Zhao, Hong-Wen Deng, and Yu-Ping Wang. A sparse regression method for group-wise feature selection with false discovery rate control. *IEEE/ACM Transactions on Computational Biology and Bioinformatics*, 2016 under review.
 - [2] Damian Brzyski, Alexej Gossmann, Weijie Su, and Małgorzata Bogdan. Group slope-adaptive selection of groups of predictors. *arXiv preprint arXiv:1610.04960*, 2016.
 - [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. *Bioinformatics*, 2015.
 - [4] 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.
 - [5] 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.
 - [6] 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.

CONFERENCE PRESENTATIONS

- SlopeCCA and gslopeCCA: sorted L1 penalized canonical correlation analysis (Abstract/Program #2803W). Presented at the *66th Annual Meeting of The American Society of Human Genetics*, October 19, 2016, Vancouver, Canada.
- 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.
- 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, September 2015.

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>.
- **grpSLOPEMC** – This is an extension package to the R package grpSLOPE. It contains Monte Carlo based methods for the estimation of the regularizing sequence. Project repository: <https://github.com/agisga/grpSLOPEMC>.
- **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.
- In my free time I like to contribute to open source software projects. Visit my Github page for the projects that I contribute to: <https://github.com/agisga>.

Updated: March 28, 2017