

Alexej Gossmann

Bioinnovation PhD Program
Tulane University

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AREAS OF INTEREST

Statistical learning with sparsity, mixed effects models, genomics and brain imaging data analysis, 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
Master's Research Project: Analysis of Bone Growth Data with Mixed-Effects Smoothing Spline 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

- 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, L^AT_EX, 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 Malgorzata 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>
- **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.

- 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.