

Alexej Gossmann

Bioinnovation PhD Program, Tulane University, New Orleans

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AREAS OF INTEREST

Development of statistical and machine learning techniques for feature selection and prediction on big high-dimensional datasets, with focus on understanding how false positive findings can arise, and how they can be avoided; applications in genomics and neuroimaging, and other medical applications of machine learning; translation of the statistical and machine learning methodology into a useful (software) product.

EDUCATION

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

Doctoral research, Mathematics
Tulane University, New Orleans, Louisiana, through January 2017
GPA: 3.978

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

BS, Mathematics
Technische Universität Darmstadt, Darmstadt, Germany, May 2012
GPA: 3.7 (1.54 German grade)

SKILLS

Software & programming: R, Ruby, C++, Python, Matlab, L^AT_EX, Linux/Unix, git and github, HTML, CSS.

Domain knowledge: Genomics and medical imaging

Language Knowledge: Bilingual in German and Russian, fluent in English.

EXPERIENCE

- Research assistantship in The Multiscale Bioimaging and Bioinformatics Laboratory at Tulane University under the supervision of Dr. Yu-Ping Wang. Spring 2015 – present.
- Student Intern doing machine learning research in the Division of Imaging, Diagnostics, and Software Reliability (CDRH/OSEL/DIDSR) at the U.S. Food & Drug Administration (FDA). May – August 2017 and Jan – Feb 2018.
- 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.

- Mentor for Google Summer of Code 2017. Project: Creating the fastest math libraries for Ruby by using the GPU through OpenCL and ArrayFire. May – August 2017.
- Research assistantship under the supervision of Dr. Oleksandr Gromenko at the Department of Mathematics, Tulane University, working on novel statistical methods for the analysis of spatio-temporal processes. June – August 2014.
- President of the SIAM student chapter at Tulane University, and organizer of the Graduate Student Colloquium at the Department of Mathematics, Tulane University. September 2014 – September 2016.

PUBLICATIONS

- [1] Alexej Gossmann, Aria Pezeshk, and Berkman Sahiner. Test data reuse for evaluation of adaptive machine learning algorithms: Over-fitting to a fixed “test” dataset and a potential solution. In *Proceedings of SPIE: Medical Imaging 2018*, 2018.
- [2] Alexej Gossmann, Pascal Zille, Vince Calhoun, and Yu-Ping Wang. FDR-corrected sparse canonical correlation analysis with applications to imaging genomics. *arXiv preprint arXiv:1705.04312*, 2017 **under review**.
- [3] A Gossmann, S Cao, D Brzyski, L J Zhao, H W Deng, and Y P Wang. A sparse regression method for group-wise feature selection with false discovery rate control. *IEEE/ACM transactions on computational biology and bioinformatics / IEEE, ACM*, PP(99):1–1, 2017.
- [4] Damian Brzyski, Alexej Gossmann, Weijie Su, and Małgorzata Bogdan. Group SLOPE-adaptive selection of groups of predictors. *Accepted for publication in the Journal of the American Statistical Association Theory and Methods Section*, 2017.
- [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. *Bioinformatics*, 2015.
- [6] 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.
- [7] 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.
- [8] 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>.

EXTRA-CURRICULAR ACTIVITIES

Elected *President* of the SIAM student chapter at Tulane University, September 2014 – September 2016. Organized the Graduate Student Colloquium at the Department of Mathematics, Tulane University, September 2014 – September 2016.

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.