# Work and Research Experience

#### 2017-present Memorial Sloan Kettering Cancer Center, NY, NY.

#### Research Biostatistician

- Survival prediction and risk stratification Ensemble Machine Learning algorithms for cancer
- Genomic data processing and analysis software development
- Web-based application development, design and maintenance for statistical analysis
- GENIE multi-center genomic study, regimen-specific progression-free survival analysis
- Optimized sequential treatment regimes for advanced cancer patients based on actionable genomic targets

## Winter 2017 University of Michigan, Ann Arbor, MI.

Graduate Research Assistant under the supervision of Dr. Shawn Lee

Performed a Genome-Wide Assocation Study on BMI and height

## Fall 2016 University of Michigan, Ann Arbor, MI.

Graduate Teaching Assistant

— Teaching assistant for an introductory class on probability and statistical theory at the School of Public Health

## Summer 2016 University of Michigan, Ann Arbor, MI.

Summer Research Assistant at Dr. Jeffrey Kidd's lab

- Built a Python/UNIX pipeline to download and process dog genomes data into analysis ready format
- Worked on mapping, imputation problems and haplogroups creation
- Analyzed canines Y-chromosome phylogeny

#### 2015-2016 MiRCore, Ann Arbor, MI.

Data Analyst at MiRCore

- MicroRNA and RNA data analysis in order to study the link between AXIN2 gene and 3 microRNAs in colon cancer patients
- Used principle component analysis and correlation heatmaps
- Web-based applications development

## Education

#### M.S. Biostatistics, University of Michigan, Ann Arbor, MI.

Coursework in : Probability Theory, Statistical Theory, Generalized Linear Regression, Statistical Computation, Statistical Genetics, Population Genetics and Genetic Epidiomology.

## B.S. Mathematics, Minor in Computer Science, McGill University, Montreal, CA.

Coursework in: Probability Theory, Non-parametric Statistics, Stochastic Processes, Algorithm Design and Dynamic Programming.

French Baccalauréat, Lycée Blaise Pascal, Orsay, France, Degree in Science with a focus in Mathematics.

# Computing Proficiency

Statistical R, Python, MatLab.

Software

Programming UNIX, Shell scripting, C, C++.

Document LATEX, Rmarkdown, Rshiny.

Preparation

## Selected Publications

- Matthew T Oetjens, Axel Martin, Krishna R Veeramah, Jeffrey M Kidd. Analysis of the canid Y-chromosome phylogeny using short-read sequencing data reveals the presence of distinct haplogroups among Neolithic European dogs. BMC Genomics. 2018 May 10;19(1):350. doi: https://doi.org/10.1186/s12864-018-4749-z
- 2. Ronglai Shen, **Axel Martin**, Ai Ni, Matthew Hellmann, Kathryn C Arbour, Emmet Jordan, Arshi Arora, Ryan Ptashkin, Ahmet Zehir, Mark G Kris, Charles M Rudin, Michael F Berger, David B Solit, Venkatraman E Seshan, Maria Arcila, Marc Ladanyi, Gregory J Riely. Harnessing Clinical Sequencing Data for Survival Stratification of Patients with Metastatic Lung Adenocarcinomas. JCO Precision Oncology 2019:3, 1-9. https://doi.org/10.1200/PO.18.00307
- 3. Sam Whipple, **Axel Martin**, Michael Martinec, Kathryn Cecilia Arbour, Venkatraman E Seshan, Gregory J Riely, Gracy Crane, Ronglai Shen. Validation of broad panel clinical sequencing-based genomic risk stratification in patients with advanced lung adenocarcinomas. Journal of Clinical Oncology 37, no. 15-suppl (May 20, 2019) 9113-9113. https://doi.org/10.1200/JCO.2019.37.15suppl.9113
- 4. Denise D Correa, Jaya Satagopan, **Axel Martin**, Erica Braun, Maria Kryza-Lacombe, Kenneth Cheung, Ajay Sharma, Sofia Dimitriadoy, Kelli O'Connell, Siok Leong, Sasan Karimi, John Lyo, Lisa M DeAngelis, Irene Orlow. Genetic variants and cognitive functions in patients with brain tumors. Neuro-oncology 21 (10), 1297-1309. https://doi.org/10.1093/neuonc/noz094
- George Z Li, Tomoyo Okada, Young-Mi Kim, Narasimhan P Agaram, Francisco Sanchez-Vega, Yawei Shen, Norifumi Tsubokawa, Jordan Rios, Axel S Martin, Mark A Dickson, Li-Xuan Qin, Nicholas D Socci, Samuel Singer. Rb and p53-Deficient Myxofibrosarcoma and Undifferentiated Pleomorphic Sarcoma Require Skp2 for Survival Cancer Research. https://doi.org/10.1158/0008-5472.CAN-19-1269
- 6. Gregory D. Jones, Whitney S. Brandt, Ronglai Shen, Francisco Sanchez-Vega, Kay See Tan, Axel Martin, Jian Zhou, Michael Berger, David B. Solit, Nikolaus Schultz, Hira Rizvi, Yuan Liu, Ariana Adamski, Jamie E. Chaft, Gregory J. Riely, Gaetano Rocco, Matthew J. Bott, Daniela Molena, Marc Ladanyi, William D. Travis, Natasha Rekhtman, Bernard J. Park, Prasad S. Adusumilli, David Lyden, Marcin Imielinski, Marty W. Mayo, Bob T. Li, David R. Jones, MD. A Genomic-Pathologic Annotated Risk Model to Predict Recurrence in Early-Stage Lung Adenocarcinoma: A Prospective Observational Cohort Study. JAMA Surgery, In press.
- 7. Saptarshi Chakraborty, **Axel Martin**, Zoe Guan, Colin B. Begg, and Ronglai Shen.Mining the Hidden Genome to Map Tumor Site of Origin. Nature communication, under revision.

## Contributed Oral Presentations

- MSKCC (2018) Ronglai Shen, **Axel Martin**, Mithat Gonen, "Risk prediction and stratification of metastatic lung adenocarcinoma patients using clinical sequencing data." Memorial Sloan Kettering Cancer Center, New York, New York.
  - JSM (2019) **Axel Martin**. "OncoCast: an improved interface for survival analysis using genomic data". Joint Statistical Meetings, Denver, Colorado.
- ISMCO (2019) **Axel Martin**. "OncoCast: an improved interface for survival analysis using genomic data". International Symposium on Mathematical and Computational Oncology, Lake Tahoe, Nevada.
  - ICEC (2020) Patil SM, **Axel Martin**, Satagopan JM. Democratizing statistics education using free interactive applications. International Cancer Education Conference, Virtual, October 2020 (invited)
  - JSM (2020) Patil SM, Neill U, **Axel Martin**, Satagopan JM. Developing and implementing a statistics curriculum for pre-clinical scientists at a free-standing cancer center. JSM 2020 (virtual)
  - ICEC (2019) Patil SM, Neill U, **Axel Martin**, Satagopan JM. Developing and implementing a statistics curriculum for pre-clinical scientists at a free-standing cancer center. International Cancer Education Conference, Salt Lake City UT, September 2019 (invited)

Workshops

- MSKCC (2018) **Axel Martin**. "Introduction interactive web applications with RShiny." Memorial Sloan Kettering Cancer Center, New York, New York.
- MSKCC (2020) **Axel Martin**, Karissa Whiting, Arshi Arora. "Downloading, processing and analysing genomic data with gnomeR." Memorial Sloan Kettering Cancer Center, New York, New York.
- MSKCC (2020) **Axel Martin**, "O-Learning for Individualized Treatment Rules." Memorial Sloan Kettering Cancer Center, New York, New York.
- MSKCC (2020) **Axel Martin**, "Causal inference in time-to-event outcome datasets." Memorial Sloan Kettering Cancer Center, New York, New York.

## Software

OncoCast is an ensemble learning R package for delayed-entry survival prediction and stratification with high-dimensional data. Developed with multiple machine learning algorithms, multi-threading functionality and interactive components for exploration.

gnomeR is an R package providing a consistent framework for genetic data processing, visualization and analysis. The primary target of the package is the MSKCC's IMPACT sequencing platform, handling mutations, fusions and copy number data. It can also be used with other genomic datasets such as TCGA.

gnomeVerse genomeVerse is an umbrella package for genomic data processing and analysis with the genomic ecosystem of R packages developed in the Department of Epidemiology and Biostatistics at Memorial Sloan Kettering Cancer Center.

genieBPC is an R package to efficiently create cohorts of interest from the clinically annotated GENIE dataset by letting the user select regimens, regimen lines, histology or stage of interest. genieBPC will automatically select the appropriate samples for these patients and generate an analysis-ready genomic dataset.

OncoCast online is the web version of the OncoCast package integrating all the major computing Online and exploratory features of the package online for users not familiar with R. Application

Interactive As part of a grant with Dr. Jaya Stagopan and Dr. Sujata Patil, we developed a series of online statistical RShiny applications with objective to create a didactic and interactive experience for medical students to learn about rudimentary statistical processes. These are hosted on a publically available server, such as this introductory class.

## Languages

**Bilingual**, French and English. **Intermediate**, German. **Beginner**, Spanish, Japanese.

## Further Information

Personal www.axelitomartin.github.io Website

GitHub Profile www.github.com/AxelitoMartin
Google scholar Google Scholar - Axel S. Martin
profile