Axel S. Martin

Work and Research Experience

2021–present   **New York University Langone Health**, *Division of Biostatistics*
PhD. Student
— Under the mentorship of Michele Santacatterina and Ivan Diaz
— Machine learning causal inference methodology for doubly robust estimators
— Generalization and transportability of time-to-event causal estimators

2017–2022   **Memorial Sloan-Kettering Cancer Center, 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

2016–2017   **University of Michigan, MI**
Graduate Teaching/Research Assistant
— First semester - Teaching assistant in introductory class for statistics at the school of public health
— Second semester - Research Assistant under the supervision of Dr. Saun Lee, GWAS for BMI and height

Summer 2016   **University of Michigan, MI**
Summer Research Assistant at Jeffrey Kidd's lab
— Building a Python/UNIX pipeline to download and process dog genomes data into analysis ready format
— Work on mapping, imputation problems and haplogroups creation
— Analysis of the canid 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
— Use of principle component analysis and correlation heatmaps
— Web-based applications development

Education

M.S. Biostatistics, *University of Michigan*, Ann Arbor
Coursework in : Statistical Theory, Generalized Linear Regression, Statistical Computation and Genetics

B.S., *McGill University*, Montreal, CA
Degree in Mathematics with a minor in Computer Science. 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

Computer languages and tools

Advanced, R, RShiny, UNIX

Basic Knowledge, C, C++, Python, MatLab, LaTeX

Selected Publications

1. Ronglai Shen, Axel Martin and al. Harnessing Clinical Sequencing Data for Survival Stratification of Patients with Metastatic Lung Adenocarcinomas. JCO Precision Oncology 2019 :3, 1-9.

2. 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 : 10.1186/s12864-018-4749-z.

3. Sam Whipple, Axel Martin and al. Validation of broad panel clinical sequencing-based genomic risk stratification in patients with advanced lung adenocarcinomas. DOI : 10.1200/JCO.2019.37.15-suppl.9113 Journal of Clinical Oncology 37, no. 15-suppl (May 20, 2019) 9113-9113.

4. DD Correa, J Satagopan, A Martin, E Braun, M Kryza-Lacombe, ..., Genetic variants and cognitive functions in patients with brain tumors. Neuro-oncology 21 (10), 1297-1309

5. GZ Li, T Okada, YM Kim, NP Agaram, ..., Axel Martin,..., Rb and p53-Deficient Myxofibrosarcoma and Undifferentiated Pleomorphic Sarcoma Require Skp2 for Survival Cancer Research

Presentations

JSM (2019)   Presentation and poster on how to use clinical sequencing data for survival stratification with metastatic lung cancer.

ISMCO (2019)   Talk presenting the OncoCast R package which is a flexible ensemble machine learning framework for survival prediction.

Languages

Bilingual, French and English

Intermediate, German

Beginner, Spanish, Japanese

Further Information

Website   https ://axelmartin.netlify.app/

GitHub   https ://github.com/AxelitoMartin