

Carlos Martinez

carlos@cmartinez.io

cmartinez.io

928 716 2884

Education

Georgia Institute of Technology

Master of Science
Electrical & Computer Engineering
Aug. 2016 – May 2018
3.6 GPA

New York University

Bachelor of Science
Mathematics
Sept. 2011 – Dec. 2015
3.7 GPA; Magna Cum Laude
Minors: Computer Science, Electrical Engineering,
Nuclear Science & Engineering

Employment

Assistant Research Technician

NYU Langone Medical Center, Cancer Institute
May 2014 – July 2016; New York, New York

Researcher for the Kirchhoff Lab specializing in cancer genetics. Responsible for data pipelines and statistical analysis of genetic sequencing using a high-performance cluster computing environment. Secondary responsibilities include grant and manuscript preparation, project presentations, and digital data storage.

Publications

M. Vogelsang, **C. N. Martinez**, J. Rendleman, A. Bapodra, K. Malecek, A. Romanchuk, E. Kazlow, R. L. Shapiro, R. S. Berman, M. Krogsgaard, et al., "The expression quantitative trait loci in immune pathways and their effect on cutaneous melanoma prognosis," Clinical Cancer Research, 2016.

R. Ferguson, M. Vogelsang, E. Ucisik-Akkaya, K. Rai, R. Pilarski, **C. N. Martinez**, J. Rendleman, E. Kazlow, K. Nagdimov, I. Osman, et al., "Genetic markers of pigmentation are novel risk loci for uveal melanoma," Scientific reports, vol. 6, p. 31191, 2016.

Technical Skills

Core:

- Statistical data analysis and numerical computation: **NumPy, pandas, R, MATLAB, Excel**
- Machine learning libraries: **Scikit, Keras, Tensorflow**
- Interactive and static visualizations with **Dash, plot.ly, matplotlib, seaborn, ggplot2**
- General programming: **Python, C++, shell scripting**
- Equally comfortable in **Windows** or **UNIX**-based OS
- Basic web development and deployment via **Django** and **Heroku**
- Professional communication in technical formats (manuscripts, reviews, poster presentations, slide decks)

Bioinformatics / Genomics:

- **Genomic pipeline development & analysis** for next-generation sequencing data with various software including: **GATK, SAMtools, BWA, Cufflinks, ANNOVAR, Variant Effect Predictor**
- Custom track management for use on **UCSC Genome Browser**
- Querying and investigating public datasets such as **TCGA, Ensembl, 1000 Genomes Project**

Conference Poster Sessions

American Society of Clinical Oncology (ASCO) 2017 Annual Meeting

R. Ferguson, D. Simpson, **C. N. Martinez**, M. Vogelsang, E. Kazlow, U. Moran, J. S. Weber, R. J. Sullivan, K. Flaherty, A. C. Pavlick, A. Ribas, I. Osman, and T. Kirchhoff, "Expression quantitative trait loci (eqtls) as germline determinants of melanoma immunotherapy response.," *Journal of Clinical Oncology*, vol. 35, no. 15 suppl, pp. 3017–3017, 2017.

D. Simpson, R. Ferguson, **C. N. Martinez**, E. Kazlow, U. Moran, A. Heguy, D. Hanniford, E. Hernando, I. Osman, and T. Kirchhoff, "Mutation burden as a potential prognostic marker of melanoma progression and survival.," *Journal of Clinical Oncology*, vol. 35, no. 15 suppl, pp. 9567–9567, 2017.

E. Kazlow, R. Ferguson, D. Simpson, **C. N. Martinez**, M. Vogelsang, U. Moran, Y. Lee, I. Osman, D. Polsky, and T. Kirchhoff, "Novel germline risk loci in familial melanoma (fm).," *Journal of Clinical Oncology*, vol. 35, no. 15 suppl, pp. 1535–1535, 2017.

ASCO 2016 Annual Meeting

(Presented) D. Hanniford, **C. N. Martinez**, I. Dolgalev, M. W. Lattanzi, E. V-S. de Miera, E. M. Robinson, C. Goldman, A. Heguy, T. Kirchhoff, I. Osman, and E. Hernando, "Targeted next-generation sequencing of melanoma patient samples to reveal mutations in non-protein coding regions of targetable oncogenes.," *Journal of Clinical Oncology*, vol. 34, no. 15 suppl, pp. 9559–9559, 2016.

T. Kirchhoff, E. Ucisik-Akkaya, M. Vogelsang, K. Rai, R. Pilarski, **C. N. Martinez**, R. Ferguson, E. Kazlow, I. Osman, F. H. Davidorf, C. M. Cebulla, and M. Abdel-Rahman, "The identification of novel genetic risk loci in uveal melanoma.," *Journal of Clinical Oncology*, vol. 34, no. 15 suppl, pp. 1543–1543, 2016.

S. A. Weiss, **C. N. Martinez**, E. V-S. de Miera, I. Dolgalev, R. L. Shapiro, A. Heguy, E. Hernando, T. Kirchhoff, and I. Osman, "Genomic characterization of acral lentiginous melanoma: Identification of altered metabolism as a potential therapeutic target.," *Journal of Clinical Oncology*, vol. 34, no. 15 suppl, pp. 9524–9524, 2016.

Selected Projects

City Perimeter Detection - cmartinez.io/perimeter-detection/

Automatically detect the perimeters of cities from aerial images. A CNN detects roads in the image followed by image processing to expand the road network into a contour of the city. Tools used include **Keras with Tensorflow** for implementing a CNN, **AWS** for data acquisition, and **OpenCV** for image processing.

Toeing the Party Manifold – cmartinez.io/toeing-party-manifold/

Interactive 2- and 3D visualization of various dimensionality reduction techniques applied to US congressional voting data. Made with **Dash** and deployed using **Heroku**.

Academics & Certificates

Gates Millennium Scholar

2011 - 2018

Full-ride scholarship awarded by the Bill & Melinda Gates Foundation to minority high school students exhibiting academic promise and commitment to community service.

Deep Learning Specialization

March 2018

Deep Learning, a 5-course specialization by deeplearning.ai on Coursera