

# Markia A. Smith

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**open to relocation**

## SUMMARY

Highly motivated interdisciplinary scientist with 5+ years of experience at a diverse and multidisciplinary interface, integrating genomic and epidemiological approaches with the ethical, legal, and social implications (ELSI) of genomics research. I utilize real world epidemiological and molecular data (SEER, TCGA, ICGC, ClinGen), clinical trials, and population-based studies.

## RESEARCH INTERESTS:

Cancer; Genomics; Epidemiology; Health outcomes; Health disparities; Structural determinants of health; AI/ML; Biostatistics; Risk prediction; Methods development; Bioethics; Ethical Legal and Social Implications (ELSI); Community engagement; Cost effectiveness; Research ethics; Mixed methods; Interdisciplinary research

## RESEARCH SKILLS:

Mixed methods research; Big data analysis; DNA and RNA sequencing methods; Sequencing technologies; Data pre/postprocessing; Data quality control; Data integration; Statistical Analyses; Unsupervised learning; Supervised learning; Linear regression & GLM; Hierarchical clustering; Risk prediction; Survival Analysis; Population based studies; Clinical data analysis; Data sharing and security; Project management

## TECHNICAL SKILLS:

**Programming languages:** Proficient in R, Python, Linux/Unix shell scripting, Matlab

**Programs/Software:** Visual Studio, LaTeX, ImageJ, ChemDraw, Pymol, Vector NTI, FlowJo

## RESEARCH & CLINICAL EXPERIENCE

### Clinical Research Consultant

August 2020-Present

*QuantBio LLC*

- Execute in-depth literature research, data collection, management and analysis, screened data as requested by client
- Convey complex technical insights and create detailed reports based on research findings to clients
- Attention to detail and ability to manage multiple projects and priorities
- Collaborate with consultant team to ensure client's objectives are met

### Graduate Research Assistant

April 2019-Present

Co-Mentors: Katherine Hoadley, PhD & Melissa Troester, PhD, MPH

*Lineberger Comprehensive Cancer Center, University of North Carolina Chapel Hill, Chapel Hill, NC*

- Gain an understanding of interactions between the environment and cancer genomics by integrating genomic data and molecular biology within human studies of cancer pathogenesis and progression
- Determine effects of genomic alterations, and develop/discover genomic, environmental, and molecular determinants to build models of risk, prognosis, and response to therapy
- Develop DNA repair classifiers in the TCGA using gene expression data and machine learning strategies including hierarchical clustering
- Evaluate associations with race, ethnicity, and ancestry in a community-centered ELSI framework, and consider ways to mediate bias in models to improve precision medicine initiatives in historically excluded populations

### Post-baccalaureate Researcher

June 2017-June 2018

Mentor: Cliona Rooney, PhD

*Cell and Gene Therapy, Texas Children's Hospital, Houston, TX*

- Generation of broader repertoire Epstein-Barr virus (EBV)-specific T cells for EBV+ lymphomas
- Construction of constitutive cytokine receptor that potentially improves proliferation, survival, and anti-tumor activity of genetically modified T cells during repeated exposure to tumor cells
- Investigation of ways to render CAR-Ts resistant to immune evasion strategies used by tumor cells to grow in an immunocompetent host

### Undergraduate Researcher

May 2015-May 2017

Mentor: John H. Slater, PhD

*Department of Biomedical Engineering, University of Delaware, Newark, DE*

- Used biomimetic PEG-based hydrogels ranging in stiffness for encapsulation and long-term 3D culture of breast cancer cells
- Investigated cancer cell behavior and disease progression within 3D hydrogel scaffolds

## EDUCATION

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<b>PhD Pathobiology and Translational Science</b> , University of North Carolina Chapel Hill, Chapel Hill, NC	July 2022
<b>Post-baccalaureate</b> , Baylor College of Medicine, Houston, TX	May 2018
<b>Bachelor of Science in Biochemistry, Minor: Chinese Studies</b> , University of Delaware, Newark, DE	May 2017

## SELECTED PUBLICATIONS & PRESENTATIONS

**Invited Speaker.** Opening the gates: a push for inclusion of Black people in genomic medicine. *Gatekeeping Genetics: Towards a More Diverse, Just, and Inclusive Research Enterprise*, American Society of Human Genetics (ASHG) Virtual Meeting, October 22, 2021.

Damrauer, J.S.\*, **Smith, M.A.\***, Walter, V., Thennavan, A., Mose, L.E., Selitsky, S.R., and Hoadley, K.A. (2021) Genomic characterization of rare molecular subclasses of hepatocellular carcinoma. *Commun Biol* 4, 1150. <https://doi.org/10.1038/s42003-021-02674-1>

Damrauer, J.S.\*, Roell, K.\*, **Smith, M.A.\***, Sun, X., Kirk, E.L., Hoadley, K.A., ... Bochner, B., Furberg, H., Troester, M.A., and Pietzak, E. (2021) Identification of a Novel Inflamed Tumor Microenvironment Signature as a Predictive Biomarker of Bacillus Calmette-Guérin Immunotherapy in Non-Muscle-Invasive Bladder Cancer. *Clin Cancer Res.* <https://doi.org/10.1158/1078-0432.CCR-21-0205>

Martschenko, D.O.\*, **Smith, M.A.\***. (2021) Genes do not operate in a vacuum, and neither should our research. *Nat Genetics* 53, 255–256. <https://doi.org/10.1038/s41588-021-00802-5>

Garcia Recio, S., Xia, Y., Hinoue, T., **Smith, M.A.**, Pascual, T., Hughes, N.M., Chandran, U.R., Garrido-Castro, A.C., ... Mardis, E., Laird, P., Hoadley, K.A., Balko, J., and Perou, C.M. Multiplatform Analysis of Primary and Metastatic Breast Tumors from the AURORA US Network finds microenvironment and epigenetics drivers of metastasis. *Accepted, Nature*.

Walens, A.\*, Van Alsten, S.C.\*, Olsson, L.T., **Smith, M.A.** ... Perou, C.M, Hoadley, K.A., Troester, M.A. RNA-based classification of homologous recombination deficiency in racially-diverse patients with breast cancer. *In submission*.

**Markia A. Smith**, Charles M. Perou, Melissa A. Troester, Katherine A. Hoadley. Mutational signature analysis in Black and non-Black women with breast cancer. Komen Annual Breast Cancer Disparities Research Summit. Virtual (2020). *Oral Presentation*.

\*Equal contribution

## SELECTED LEADERSHIP & SERVICE

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<b>ClinGen JEDI Advisory Board</b> <i>NIH Clinical Genome Resource (ClinGen)</i>	2022-Present
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- Contribute resources to the genomic knowledge base that will enhance equity in patient care across populations
- Develop and publish recommendations for the rigorous and responsible use of diverse population descriptors in clinical genetics and genomics practice

<b>EDGE Advisory Committee</b> <i>University of North Carolina at Chapel Hill, Chapel Hill, NC</i>	2020-Present
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- Assist co-PIs and Program Director with guidance, evaluation, and oversight implementation of the training program

<b>BlackInGenetics (BIG)</b> , <a href="https://www.blackingenetics.com/">https://www.blackingenetics.com/</a> <i>President, Co-organizer</i>	August 2020-Present
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- Working to amplify voices and work by Black-identifying geneticists across the U.S. and beyond.

## HIGHLIGHTED AWARDS AND HONORS

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Susan G. Komen TREND Grant	2021-Present
Program in Translational Medicine T32 Training Grant	2019-2020