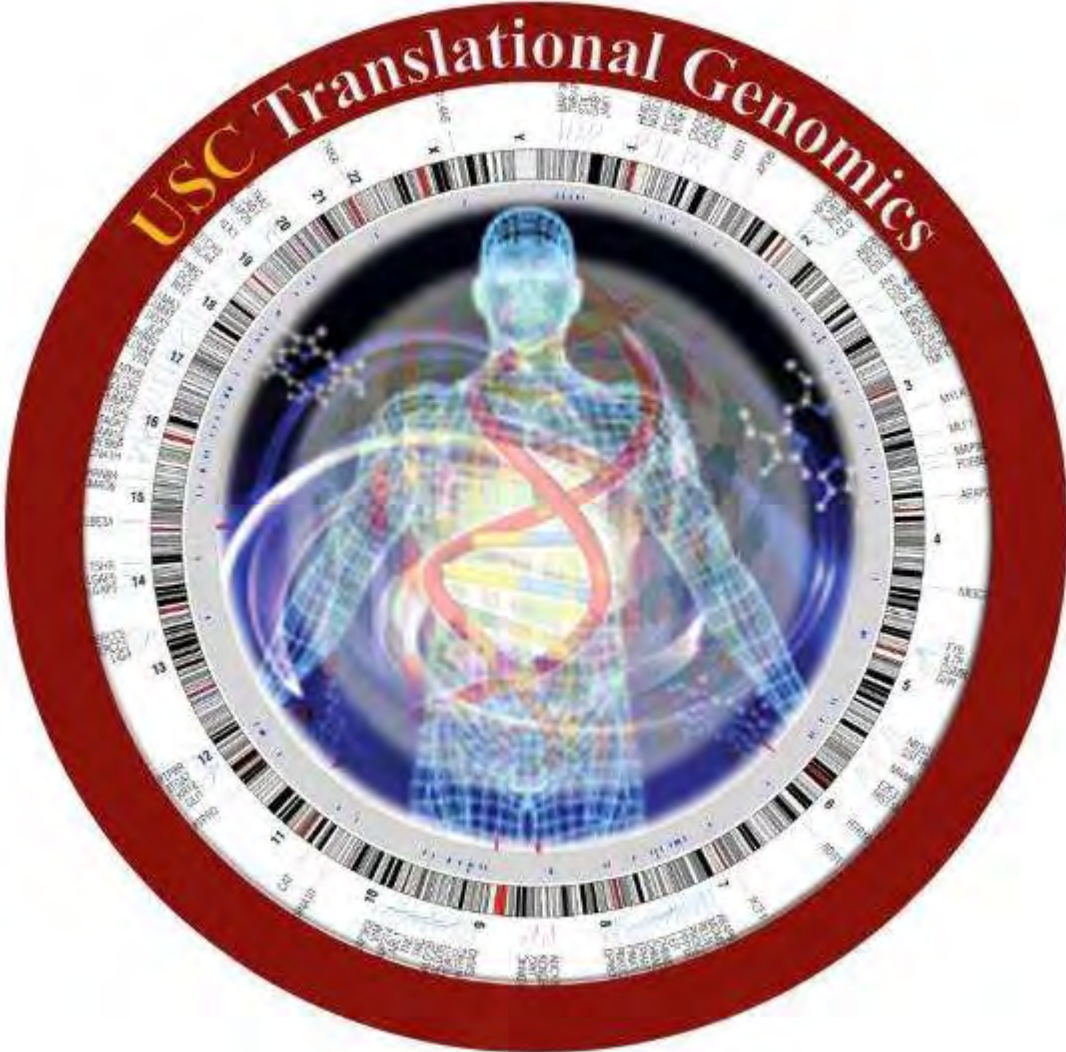


Accelerating improvements in healthcare at USC KSOM through intentional integration between basic discovery research and clinical science!





Education/Training

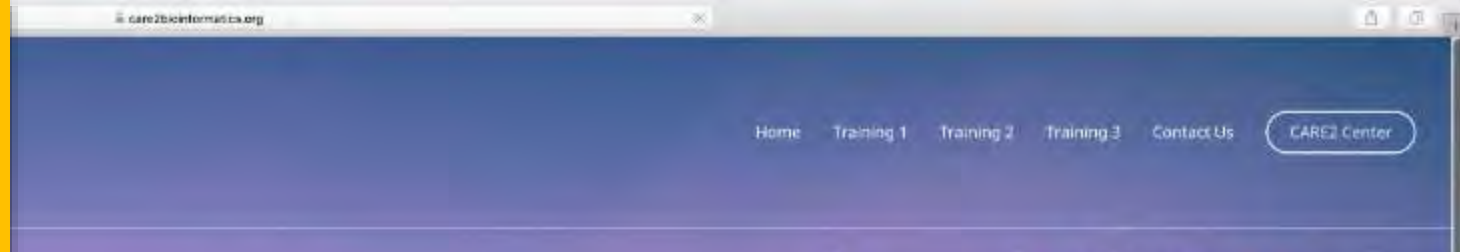
Carol Lin, Ph.D.
Associate Professor
Masters in Translational Biotechnology



David Craig, Ph.D.

Professor

Masters in Translational Biomedical Informatics



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BIOINFORMATICS

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A Password must always be 8 to 32 characters in length. Special characters that are not allowed are: !, @, #, \$, %, ^, &, *, (,), =, +, -, ~, {, }, [,], \, |, /, <, >, ~, `.

Allowed Special Characters: !, @, #, \$, %, ^, &, *, (,), =, +, -, ~, {, }, [,], \, |, /, <, >, ~, `.

Remember to save the information and changes.

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Remember to save the information and changes.

"I'm proud that we will be helping lead the way nationally toward advancing cancer health equity"

- John D. Carpten, Ph.D.

"MORE-MATERIAL" RELATED WITH BIOINFORMATICS & CANCER HEALTH DISPARITIES

CARE2 Bioinformatics "More-Material" series is a collection of video resources that will help you understand the role of bioinformatics in cancer health disparities research. The series includes a video on the role of bioinformatics in cancer health disparities research, a video on the role of bioinformatics in cancer health disparities research, and a video on the role of bioinformatics in cancer health disparities research.

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CARE2 BIOINFORMATICS TRAINING MODULES

by Drs. Enrique I. Velazquez-Villareal and David W. Craig

CARE2 Bioinformatics modules were developed to provide health care training to address genomic diversity (GVD) in cancer health disparities research that promotes their individual career development toward conducting translational cancer research focused on the cancer disparities among Black and Latin populations.

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FOUNDATIONS IN BIOMEDICAL INFORMATICS (PART 1)

Webinar by Enrique I. Velazquez-Villareal, M.D., Ph.D., M.P.H., M.S. February 2020 Date and Time TBA

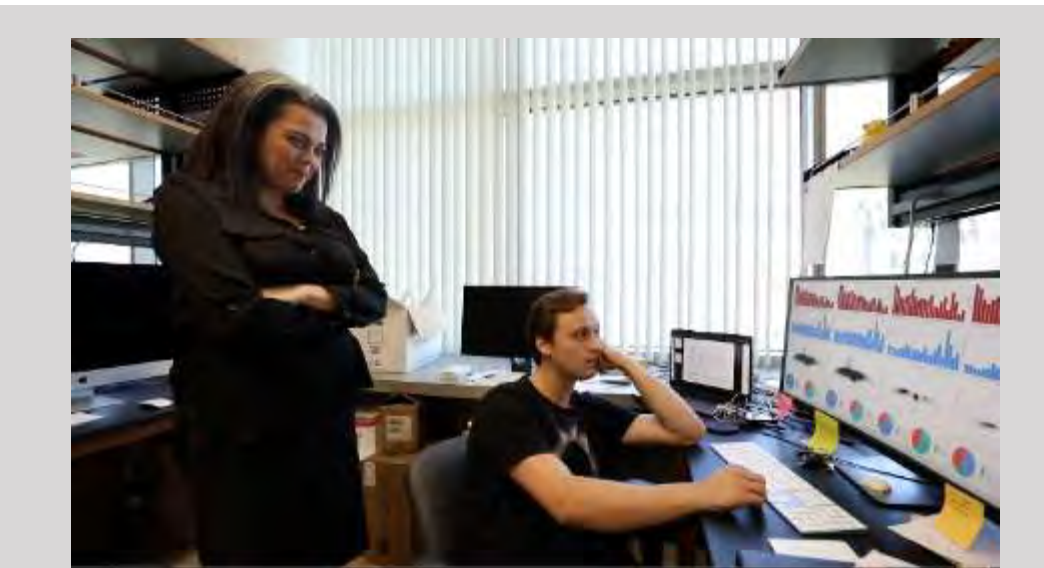
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FOUNDATIONS IN BIOMEDICAL INFORMATICS (PART 2)

Webinar by Enrique I. Velazquez-Villareal, M.D., Ph.D., M.P.H., M.S. March 2020 Date and Time TBA

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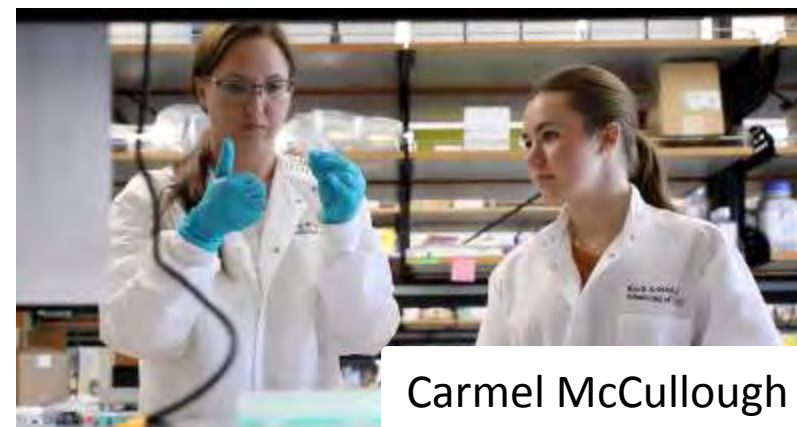
Ben Tew, PhD



Lee Gibbs, PhD



Fullbright Fellow
Solomon Rotimi, PhD
Covenant University, Nigeria



Carmel McCullough



Heather Miller, MD



Rania Bassiouni, PhD



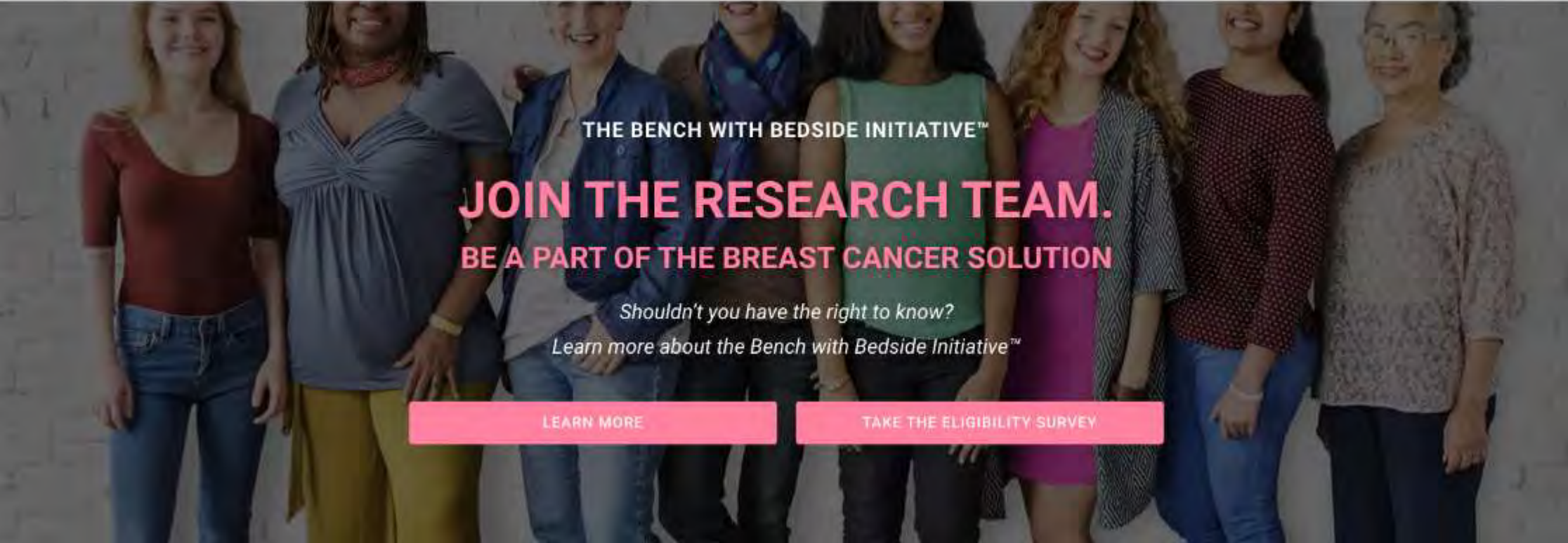
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SPOTLIGHT ON NEUROSCIENCE

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Unlocking the Aging
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SPOTLIGHT ON NEUROSCIENCE

Finding Missing Pieces in the Brain

BROOKE E. HJELM

*Assistant Professor of Clinical Translational
Genomics
Department of Translational Genomics
Keck School of Medicine of the University of
Southern California*



After creating a new method for identifying large mitochondrial genome deletions, Brooke Hjelm now investigates the connections between mitochondrial dysfunction and neurological disorders in unique ways.

What drew you to genomics and neuroscience?

I am obsessed with technology applications, so I have experience in a lot of different fields: plant biology, infectious disease, vaccine development, stem cells, genomics, and neuroscience. I am fascinated with the inner workings of living organisms and manipulating them into laboratory tools.

Going into neuroscience was a happy accident. Initially, my interest was in genomics. Genomics technology is such a fast-moving field that it changes dramatically within months. It is an exciting area because scientists are always discovering something new. My graduate work was in neurogenomics at the Translational Genomics Research Institute. In David Craig's lab, I learned both the wet lab and the dry lab components of genomics research. I ended up falling in love with the brain, but probably for different reasons than a lot of other neuroscientists.

What do you love about the brain?

I like that neurons are post-mitotic, so every cell has its own fixed genome; if something goes wrong, there is almost no opportunity to fix it. Additionally, different neurological diseases may have the same phenotype because they converge at the circuitry level, rather than the molecular level, which makes the genomics data complex.

Another thing that interests me is the differences throughout tissues of the body and how those differences can determine what part of the body gets a disease. Because of that, I have been involved in a lot of RNA work focusing on different

brain regions, including single cell RNA sequencing and spatial gene expression profiling.

What is your current research focus?

My most recent research has been on complex neurological disorders. I have been working on Alzheimer's and Parkinson's diseases since I was in graduate school, and diseases related to psychiatric disorders, such as schizophrenia and major depression, since my postdoctoral fellowship at the University of California, Irvine. I am also studying the mitochondrial genome, which has led my research into new areas both within and outside the brain.

How do mitochondrial genomes affect brain function?

The tricky thing about mitochondria is that they are polyploid, so every cell can have thousands of mitochondrial DNA molecules. This is a backup system. If you have a problem with one molecule, the cell will tolerate it as long as the "bad genomes" are kept at a low threshold. However, mitochondrial genomes with deletions are smaller, so they have a replication advantage. The "bad" proportion can get larger over time to the point where the cell cannot generate enough energy. If you get these cells in certain parts of the brain, you may get a phenotype like depression. Although we typically think of DNA as something that is the same throughout the body, the structure of the mitochondrial genome can change a lot from one tissue to another. I looked at this variation to determine what tissue-specific diseases might be caused by mitochondrial dysfunction.

During my postdoctoral fellowship in Manjiv Vawter's lab, I analyzed next-generation sequencing (NGS) data from mitochondrial PCR amplicons to find large deletions. We knew that the deletions existed, but no one had a good way to get at the bulk of this information from NGS data. DNA



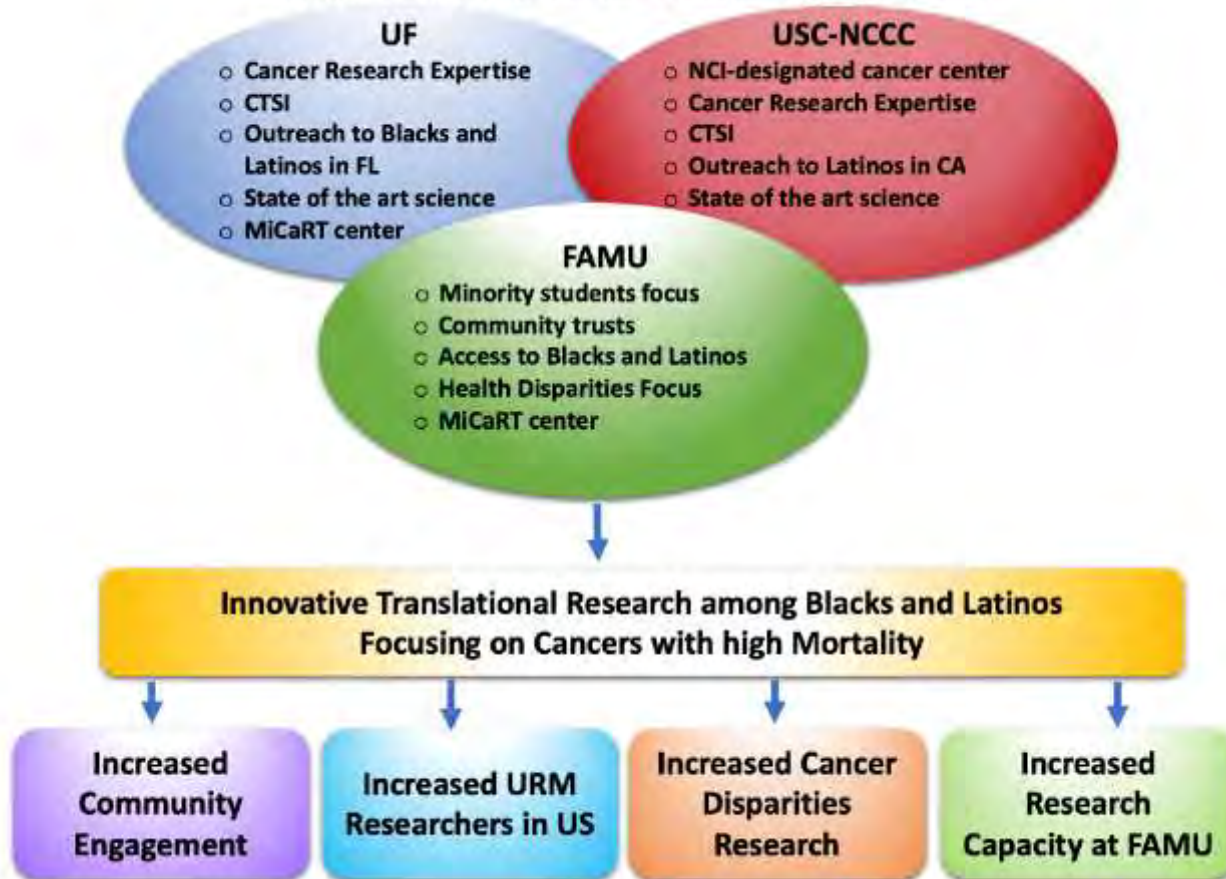
AACR 110th
Annual Meeting
Program Chair,
Atlanta, GA, April
2019



The National Cancer Institute awarded a five-year, \$16 million U54 grant to create a cancer health equity center through a Triad partnership between USC, FAMU, and the University of Florida that will conduct research on cancer health disparities, train underrepresented minorities and perform community outreach among underrepresented minorities and the medically underserved.



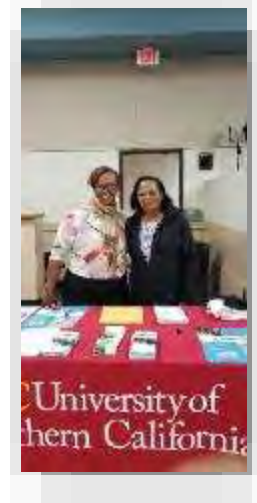
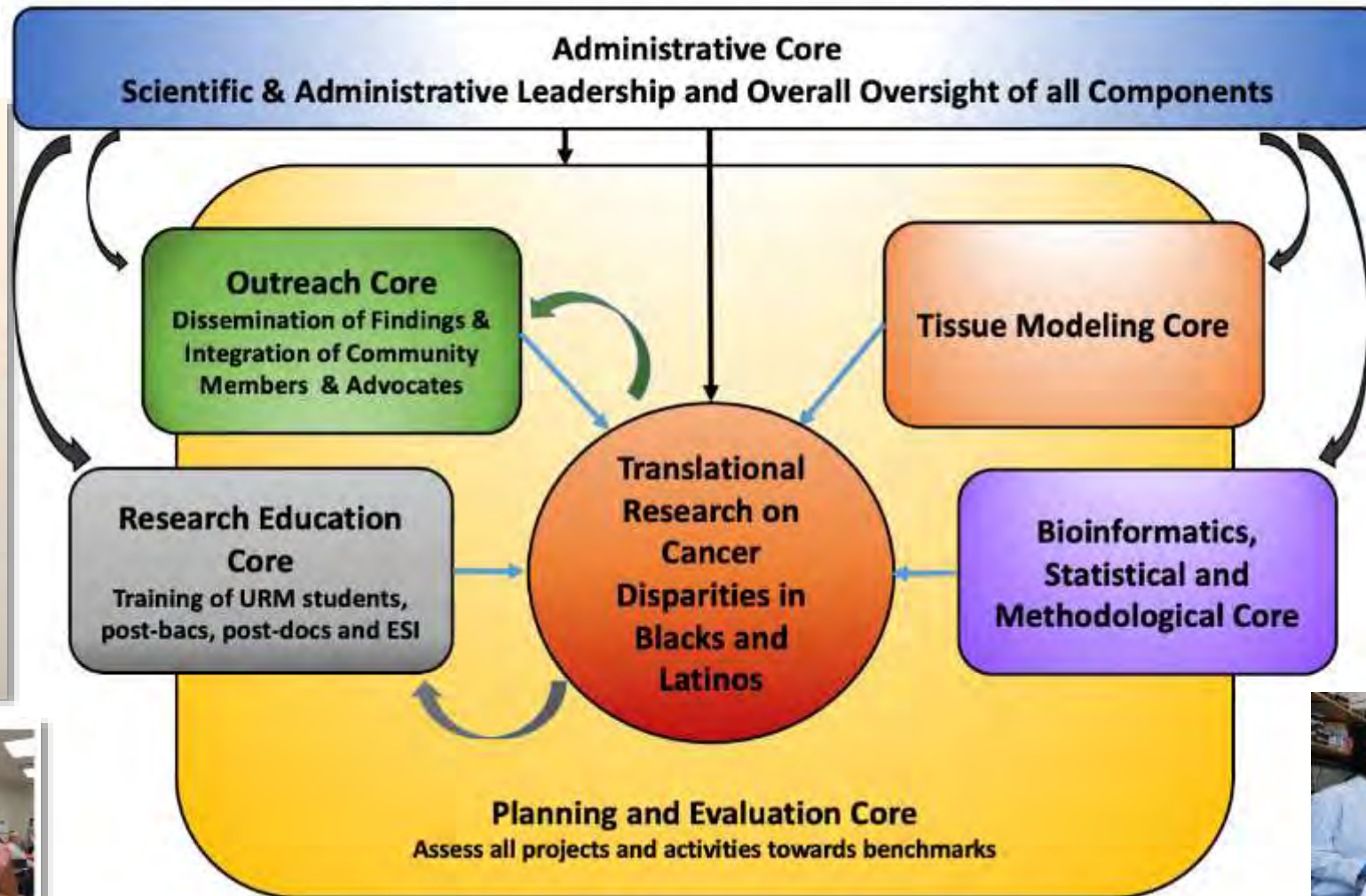
Florida-California CaRE² Health Equity Center





CaRE² Partnership Structure and Workflow

Florida-California CaRE² Health Equity Center





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