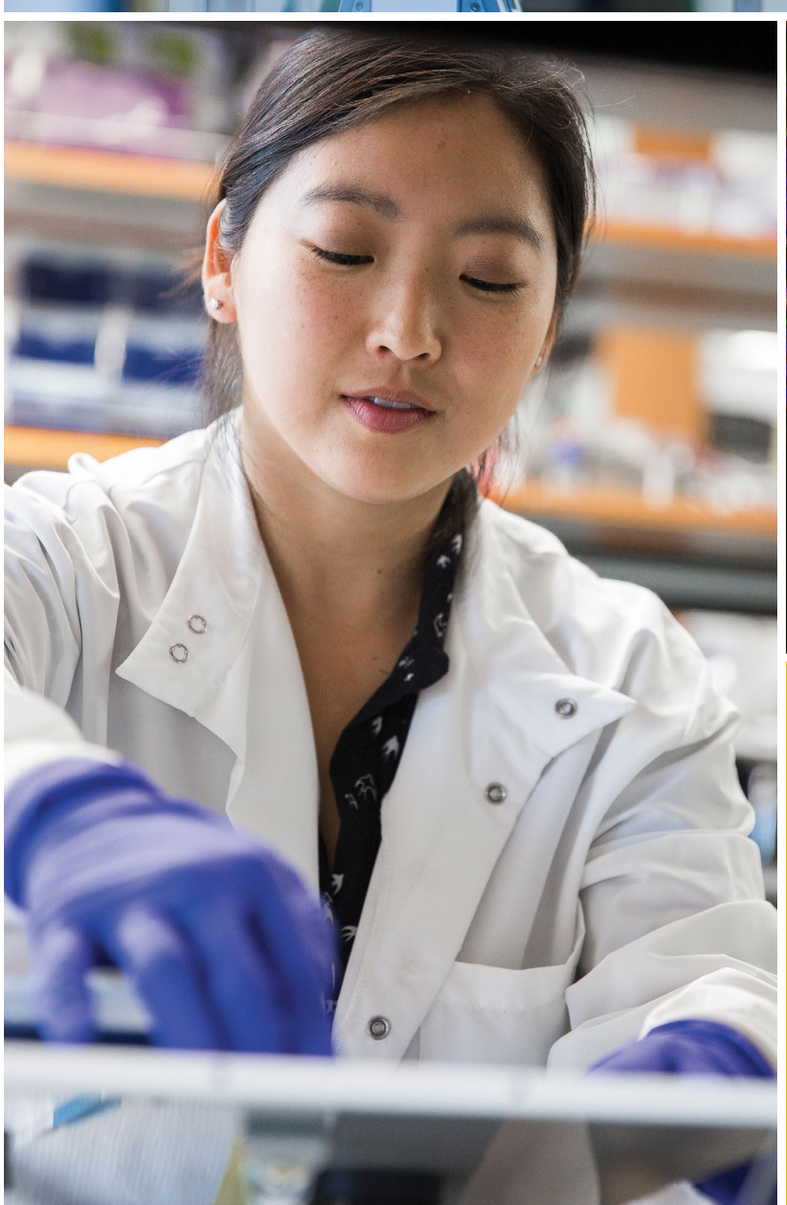
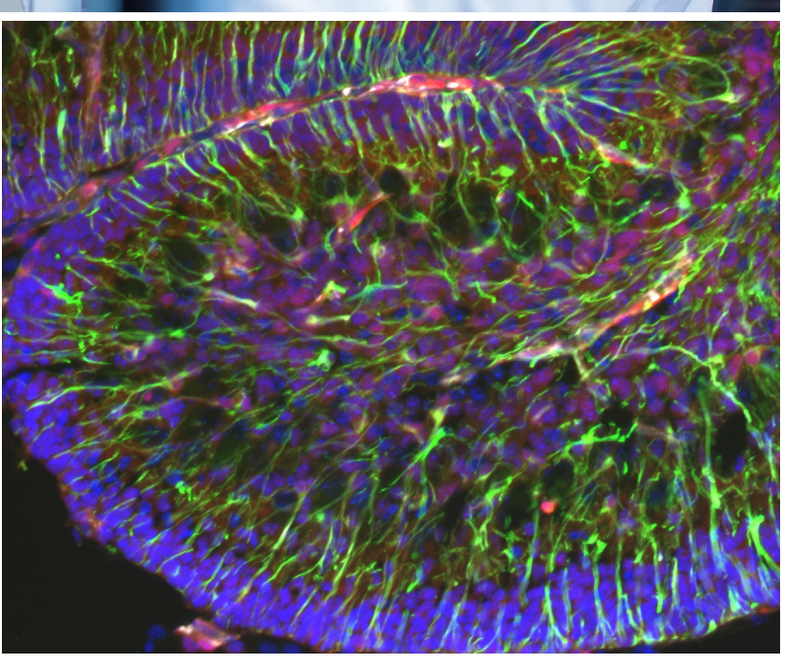
Keck School of Medicine of USC





# Translational Genomics

Keck School Medicine of USC

# Master of Science in Translational Biomedical Informatics

USC Department Of Translational Genomics

## Get on the right track

### Move from the wet-lab to the dry-lab through applied bioinformatics

Keck's MS in Translational Biomedical Informatics can be your career at the intersection of health, science, and informatics. Whether you are a lab technician hoping to take your career to the next level, or a recent graduate looking for an alternative career in the biomedical sciences, our hands-on learning program can help you find your path. You'll learn how to apply and use existing biomedical informatics tools to solve complex biomedical problems. You'll learn how to work within complex regulatory environments developing solutions to improve human health and disease from datasets that are both small and massive.

*Students in this program will gain an understanding of:*

- Best practices for using existing tools and bioinformatics datasets together to better understand biomedical problems;
- Analysis of next-generation sequencing (NGS) including whole-genome, exome, and transcriptome sequencing (RNA-seq), as well as emerging methods in single-cell sequencing;
- Project management and requirements in bioinformatics gathering skills to allow them to interface and interact with computational and engineering expertise to help design solutions;
- Experience and training utilizing modern frameworks for rapid prototyping, and how to extract information from a wide variety of databases;
- Core responsibilities towards data security, privacy, and data sharing spanning open access frameworks to restricted and regulated frameworks;

## Bridging The Gap

USC's Department of Translational Genomics at Keck's School of Medicine is offering an intensive two-year MS program in biomedical informatics focusing on bioinformatics within health-related fields. The goal of this program is to train applied bioinformaticians, providing students with the training, skillsets, and best practices for applying and integrating existing bioinformatics tools in the study of human health and disease.

**Translational:** Translating laboratory data to bedside or clinic

**Biomedical:** Relating to human biology, medicine, and disease

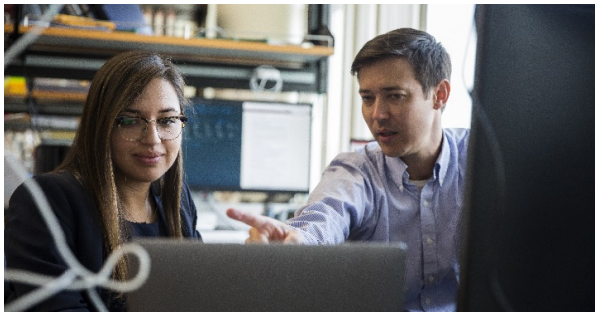
**Informatics:** Applied processing and analysis of data

This program uses both traditional class-room based teaching, an applied in silico laboratory for assignments that is coupled with additional on-line materials. Bioinformatics after all is about world for help.

## Training In Applied Bioinformatics

This program uses both traditional class-room based teaching, an applied in silico laboratory for assignments that is coupled with additional on-line materials. Bioinformatics after all is about working mostly on computers with a community that spans the world for help.

Courses alternate between online interactions with faculty followed by in-class lectures and laboratories. Class is often focused on helping students apply concepts that were made available outside of the classroom. Fundamentally, this is an applied program where the focus is on learning to become independent and solve new problems as they emerge. It teaches processes, though in a way that is effectively learning by example. For example, several courses have a strong inclusion of R, R-markdown, and R-shiny, where students develop web-applications to complete homework by submission via GitHub. These applications may include a biomedical research or clinical problem commonly seen in the field. Classroom time is often used for working with teams of students on their solutions and suggesting paths through obstacles. In person classes are often interactive with students and lectures engaged in ongoing dialogue where lecture materials were already made available and reviewed prior to the course. Students who succeed use both online resources and the in-person classroom time.



## Courses

General requirements include at least 28 units of required courses and the Master's in Translational Biomedical Informatics can be completed typically in 2 years. Courses include:

- *Foundations in Biomedical Informatics*
- *Genomic Analysis Methods I and II*
- *Genomic Technology in Biomedical Research I and II*
- *Translational Genomics Databases and Data structures*

Additional curriculum options include programming and informatics courses taught within other departments upon approval. New courses to be introduced include Clinical Bioinformatics in 2018 & 2019.

## Ideal Candidates

This program is tailored for individuals with laboratory-based biomedical experience and whom have bachelors in biomedical sciences or biomedical engineering. This program focuses on tool application and integration along pipelines, will scripting emphasized over coding. This program is not for existing software engineers, computational biologist interesting in developing novel algorithms, but rather on the use and application of existing tools and standards within human health and disease. Graduates will have the analytical capabilities for analyzing datasets across molecular biology, systems biology, structural biology, and genomic datasets. They'll understand complex regulatory environments and the unique requirements for working in a biomedical setting.

- Biologists
- Biomedical engineers
- Medical students
- Industry professionals

## Career Options

Biomedical Informatics is an exploding field that can lead to careers in hospitals, clinical labs, research institutes & companies, and biotechnology companies. Bioinformatic hiring initiatives can be found in such as Illumina, AstraZeneca, Covance, Eli Lilly, Genentech, Invitae, Johnson and Johnson, Loreal, Pfizer, Roche.

Bioinformaticians are in high demand in most research institutes and medical schools with focuses in life sciences. Hospitals and clinical labs – particularly those introducing high-complexity molecular testing – are part of a new opportunity supplementing existing tracks within hospital laboratory IT tracks.

**MS in Translational Biomedical Informatics**
Keck School of Medicine of USC
1450 Biggy Street, NRT G517F
Los Angeles, CA 90033

http://dtg.usc.edu

**Program Director**
David Wesley Craig, Ph.D.
Phone: 323.442.7784
Email: davidwcr@usc.edu

Keck School of Medicine of USC

# Welcome to USC's Institute and Department of Translational Genomics

**Where our team strives to make healthcare smarter, based on a vision that future advances in personalized medicine will build from, benefit, and ultimately serve an incredibly diverse set of individuals.**

Medicine is undergoing one of its biggest transitions in recent history. For the first time, we can treat patients based not on what works best for an average person in the population, but based on what will work best for each individual patient.

Personalized medicine, also known as precision medicine, has been enabled by game-changing discoveries in genomics. Our deep understanding of DNA and how it varies from person to person is powering a new golden age of diagnostics and treatment, as well as predictive and preventive medicine. In areas like cancer and rare disease, however, it is just the starting point as we utilize high-throughput technology to integrate information from the molecular and systems level to ultimately improve patient outcomes.

To realize the promise of precision medicine, we need to understand the molecular and genetic diversity across all individuals. We believe that precision medicine doesn't build or benefit from focusing on one population, but instead requires studies involving diverse populations.

The diversity of Los Angeles in many ways mirrors the future diversity of healthcare across America, highlighting its challenges and opportunities. We launched USC Translational Genomics to serve as a catalyst for precision medicine — a home for scientific and medical experts dedicated to challenging the status quo in healthcare by implementing and advancing precision medicine across all populations.

With a foundation of cutting-edge scientific facilities at the USC Keck School of Medicine, our renowned team of researchers and physicians is collaborating to realize the potential of genome-based medicine with the understanding that these

**"We are deeply committed to excellence in translational genomics research, bringing to bear vast experience and expertise in molecular genetics, genome science, biomedical informatics, translational science, and molecular medicine."**

**John D. Carpten, Ph.D.**
Director, Institute of Translational Genomics

advances will be made from and serve the diverse clinical populations that will make up the future of healthcare.

We also believe that advancing precision medicine to affect a diverse set of populations requires diversity in leadership. Our faculty span diverse backgrounds and experience, and collectively we are committed to integrating these together to improve lives by combining the best genome science with the best clinical care.

**"By developing new tools for integrative analysis of genomic, epigenetic, proteomic, and clinical data and assimilating them into the clinic, we can enhance treatment decisions and make a real impact on the future of medicine."**

**David W. Craig, Ph.D.**
Co-Director, Institute of Translational Genomics

# What is translational genomics?

## ge·no·mics

**noun**
the branch of molecular biology concerned with the structure, function, evolution, and mapping of genomes.

## pre·ci·sion med·i·cine

**noun**
an emerging approach for disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle to tailor care for each person.

**Translational genomics: telling each patient's unique story building from diverse populations.**

The story of each person is a saga, comprised of the tales of ancestors, the history of the species, and the collection of vignettes that makes everyone unique. Encoded in our DNA is a manual with 46 chapters called chromosomes that hold about 20,000 genetic instructions in sequences of four letters — A-T-C-G. Written out, each DNA strand would be 30 million letters long. These instructions are read by RNA, which in turn tells proteins to carry out all the essential functions of our bodies.

How do we translate such an immense source of data into something useful?

At USC Translational Genomics, our researchers speak the language of DNA, RNA, and proteins.

As pioneers of precision medicine, we have dedicated our careers to deciphering the genetic code, harnessing the latest technology to comb through the deluge of data, and interpret the results to create breakthroughs in medicine.

We are now poised to translate those discoveries in ways that will directly benefit patients.

By studying each patient's unique genetic signature and interpreting the biological and environmental events that have shaped their stories, we can more precisely diagnose disease, predict risk, and tailor therapies to improve outcomes.

**"The future of medicine requires groundbreaking research, with rapid translation to the operating room and the clinic. USC Translational Genomics and the USC Institute of Urology epitomize this synergy. Together, we are unlocking the secrets of cancer at the genome level and developing new, cutting-edge treatments personalized to each patient."**

**Inderbir Singh Gill, M.D.**
Chair and Distinguished Professor of Urology
Shirley and Donald Skinner Chair in Urologic Cancer Surgery
Executive Director, USC Institute of Urology
Associate Dean For Clinical Innovation

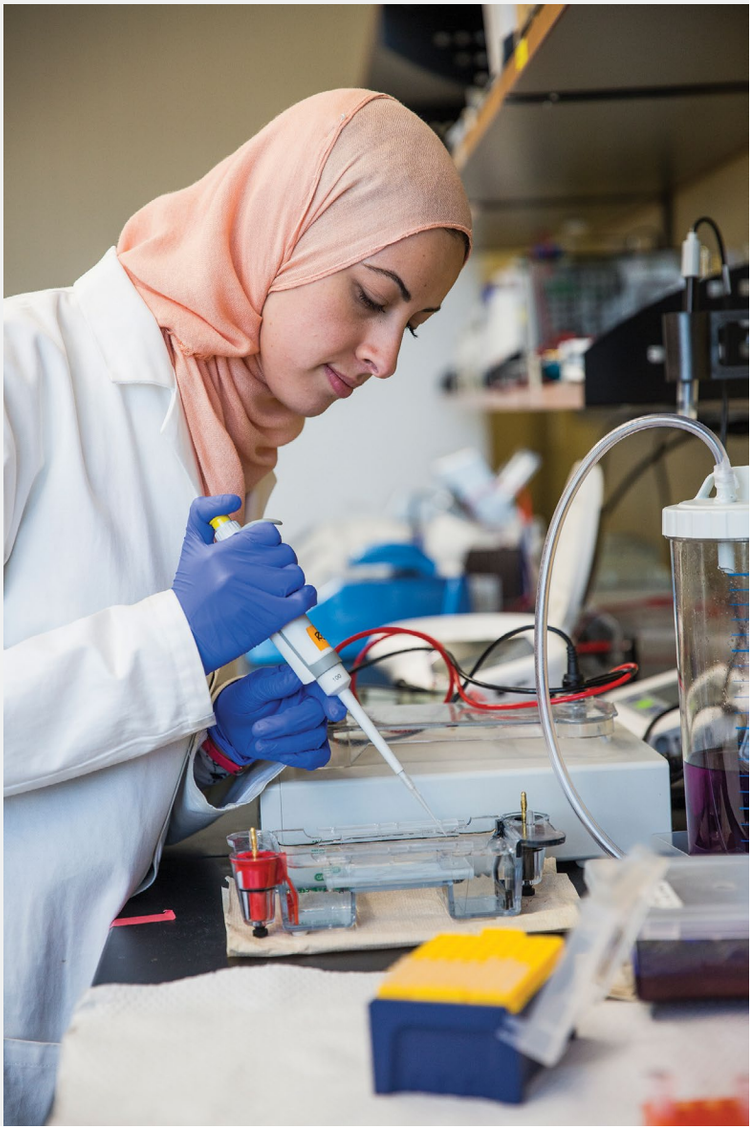

# Our story

USC Translational Genomics was founded in January 2016 under the leadership of John Carpten, Ph.D., and David W. Craig, Ph.D., who both came to Keck School of Medicine from TGen in Arizona.

USC Translational Genomics includes a truly transdisciplinary team of biologists, geneticists, and data scientists working hand in hand with engineers, chemists, and clinicians across USC departments, campuses, and hospitals.

Together, we work in the lab and behind the computer to advance our understanding of a range of diseases and disorders — from neurological diseases and rare genetic syndromes to adult and pediatric cancers — and in the clinic to produce practical applications. We are also committed to understanding why certain diseases and disorders are more prevalent among different populations.

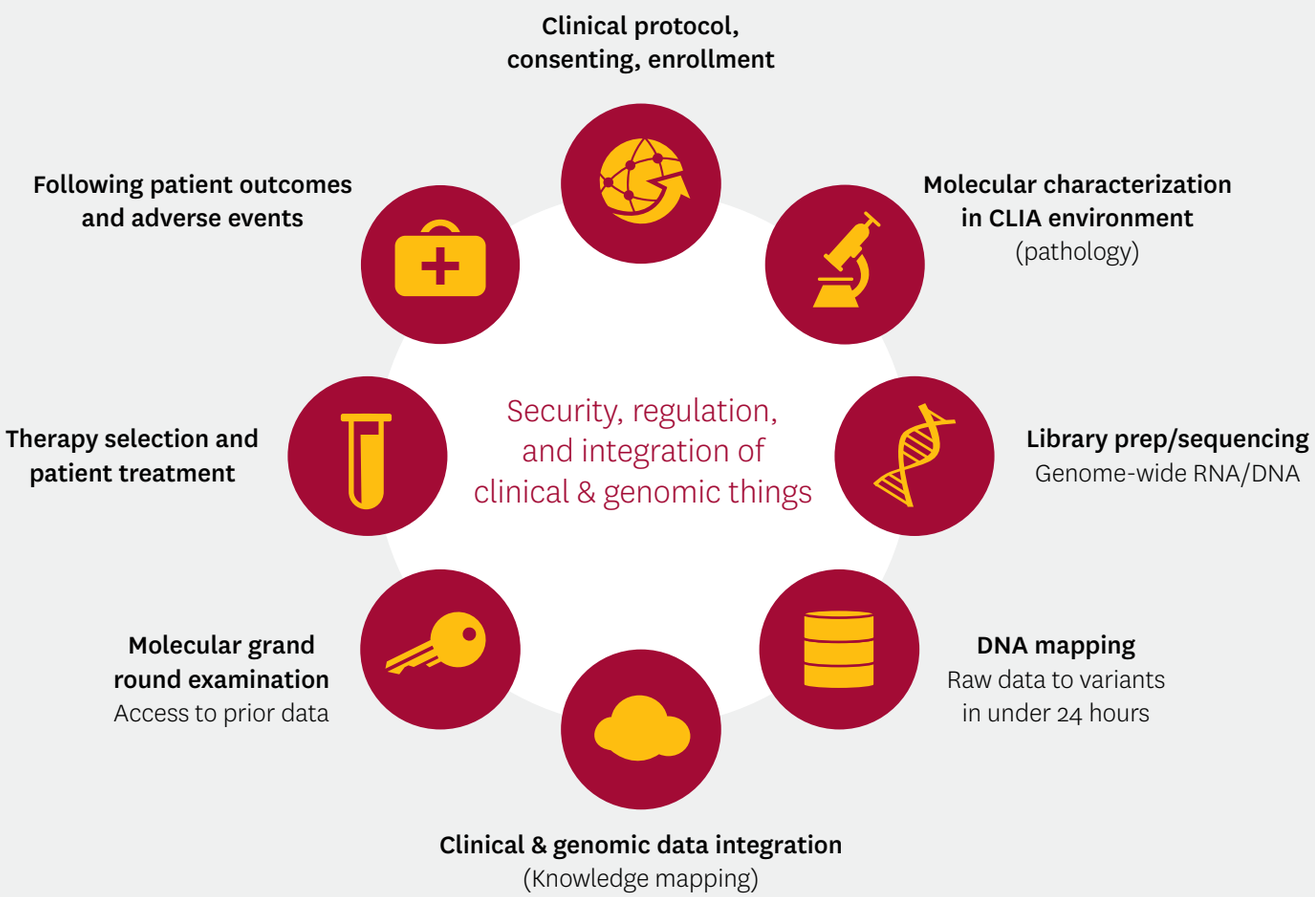
In addition to our research and clinical efforts, USC Translational Genomics began to offer degree programs in innovative areas of biomedical research in 2017. We are dedicated to training the field's next generation of leaders in genomics, biotechnology, and biomedical informatics.



# What we do

**The USC Translational Genomics faculty have helped write the book of precision medicine. Not only have we penned hundreds of defining publications, but we have also created many of the technological tools that have enabled the field to progress. Today, our discoveries continue to move precision medicine forward.**

## Clinical and genomics data integration




## Data management platform supporting complex regulatory environment

| | | |
|---|---|---|
| Regulation by CMS, FDA, and IRBs | Clinical utility requires turnaround in days not months | Utilizing a rapidly updated, growing body of knowledge |

## ’Omics

Our scientists are utilizing next-generation genomic (DNA), transcriptomic (RNA), and proteomic (protein) sequencing technologies to shed light on a variety of diseases, and were among the first to prospectively apply these to improving patient care and treatment. For example, David W. Craig and John Carpten helped lead one of the first studies of whole-genome and transcriptome sequencing for the treatment of triple negative breast cancer. This foundational work led to other studies in late-stage metastatic oncology including melanoma, pediatric oncology, pancreatic cancer, glioblastoma, and colorectal cancer.

As part of their efforts, they helped establish standards and frameworks by which groups across the world apply clinical medicine. They led the development of one of the first CAP/CLIA certified laboratories focused on integrated analysis of whole-genome and transcriptome data, working with the FDA and others on establishing best practices for applying these approaches in clinical studies. They have helped lead the establishment of standards and references for other laboratories to implement similar approaches, partnering with researchers at healthcare systems across the country.

As part of the new department and institute, they are building and expanding such efforts to tackle integration across multiple scales and systems. They are using the latest methods and technology, and integrating these directly within the Keck healthcare system from the ground up.

## Precision diagnostics

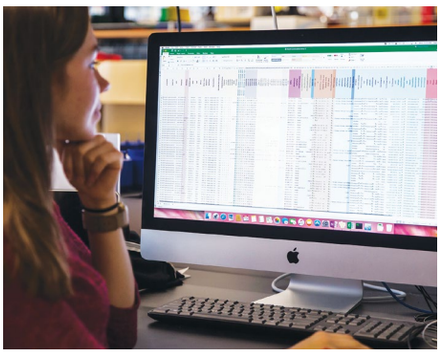
These technologies can treat, and they can also diagnose from a molecular and genetic level. Bodour Salhia, Ph.D., has developed a way to test for the presence of gene modifications via circulating tumor DNA taken from blood samples. The hope is that these could be used as biomarkers to find previously undetectable evidence of breast cancer that is likely to return or spread to other parts of the body. This could be transformative for the 234,000 Americans who develop breast cancer annually, 41,000 of whom die from the disease, usually due to metastasis that is detected too late for effective treatment.

David W. Craig has utilized integrated analysis of DNA and RNA to improve diagnosis in children with rare neurological conditions. He helped to establish a research clinic enrolling thousands of individuals across hundreds of families, developing approaches that improved diagnosing children at a genetic level from 5% to nearly 50%. He is now partnering with Keck leaders in cardiothoracic surgery to apply these methods in new populations and conditions.

**Bodour Salhia, Ph.D.**
Assistant Professor of
Translational Genomics

## Data integration

Advancing precision medicine means building and creating the informatics systems to gather, integrate, and analyze patient data at massive scales, across multiple dimensions and time points in decision making, for clinical value and utility. The scale of data our scientists sift through on each patient is massive and requires integration of bioinformatics, statistics, genetics, epidemiology, clinical medicine and public and global health reports. Working with David W. Craig, Enrique I. Velazquez-Villarreal, M.D., Ph.D., M.P.H., M.S., is integrating clinical and genomic data from a variety of technologies to assemble a more complete reference library in hopes of developing machine-learning tools that more rapidly help physicians access the critical decision-making datapoints they need.



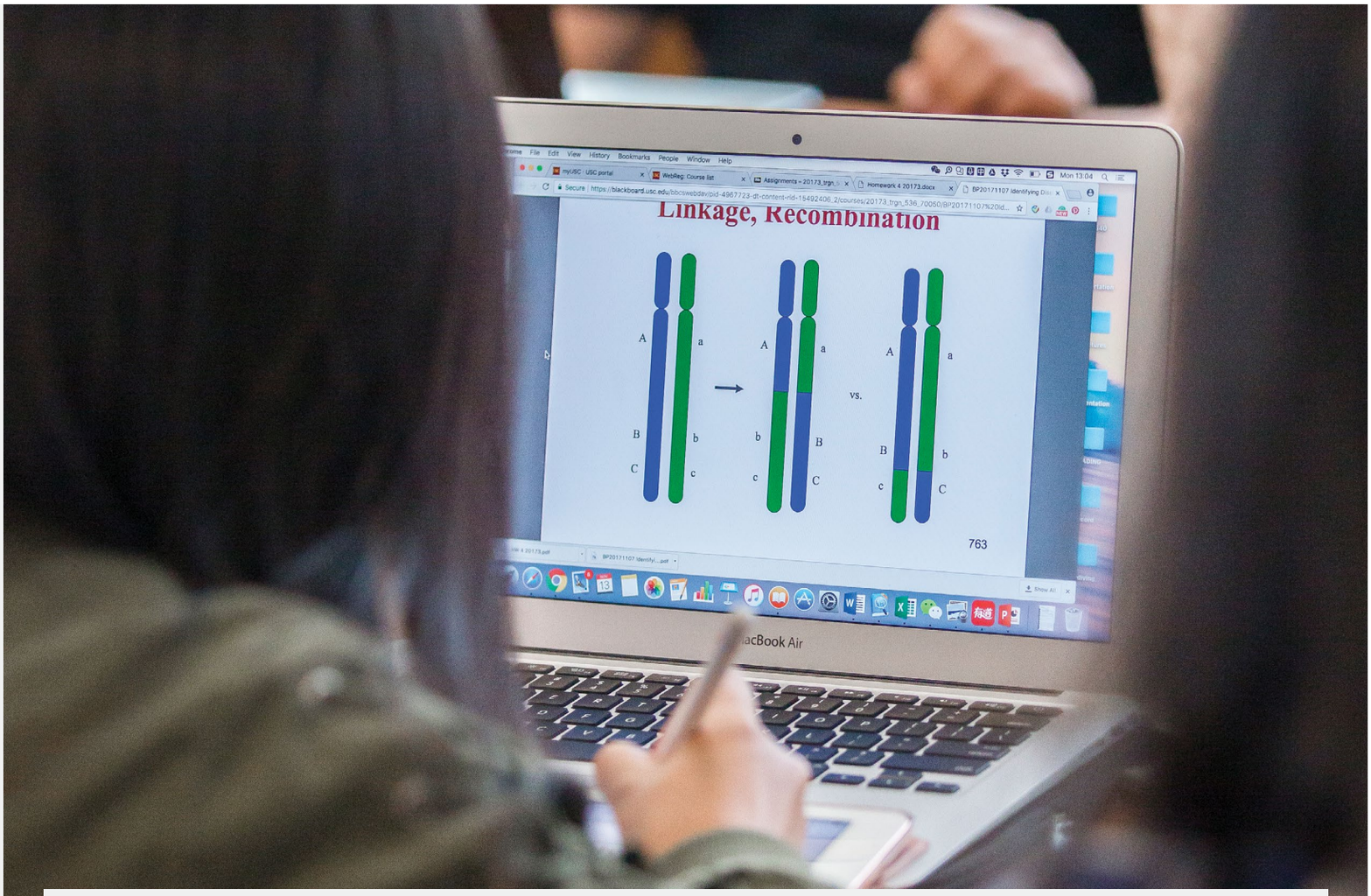
We are building transformative data-driven discovery platforms where researchers can collaborate daily and make discoveries that would not otherwise be possible under the current paradigm of fragmented research groups working in isolation. These platforms are mission-driven around principles of linked data, integrative analysis, structured curation, inherent sharing, and data harmonization across researchers and environments.


# Education

There is a skills gap in trained individuals within biotechnology, genomics, and bioinformatics that is significant and cannot be overstated. Within laboratories across academia, healthcare and industry, researchers are finding themselves lacking the ability to analyze or understand the next generation of genomics technology, its data, and how it can be interpreted. This is affecting the field's ability to make new biomedical discoveries and translate these from bench to bedside. In many cases, the tools exist — it is the expertise to use and apply them to a specific biomedical problem that does not. Bridging the gap will require interdisciplinary training that explores business as well as biology, and fosters collaboration at the bench, the bedside, and the boardroom. We are committed to addressing these problems by training biomedical students, technicians, and other healthcare scientists in the application of bioinformatics and biotechnology tools and translational research focused on moving biomedical research from bench to bedside.

**"Meeting the world's healthcare demand will require a new workforce beyond theoretical knowledge and research skills. It must be interdisciplinary with strong training in biomedical sciences coupled with sufficient proficiency in economics, business, and law terminologies."**

**Carol Lin, Ph.D.**
Associate Professor of Clinical Medical Education and Biochemistry & Molecular Biology




**We have created two master's level programs to arm biomedical scientists with additional skills for analyzing, processing, and managing large-scale data, and to provide students with strong knowledge and procedural road maps of the entrepreneurial process in biotechnology from idea generation through economic viability.**

## Master of Science in Translational Biomedical Informatics

This program will take scientists' knowledge of bioinformatics to the next level, enabling them to analyze, apply, and integrate the latest data tools in the laboratory. They will be able to extract information to better understand biomedical problems, and to design experiments to address those problems. In preparation for a spectrum of careers that span from research to the clinic, students will understand their critical role in working with data under a bevy of regulatory bodies. Graduates of the two-year program will be well suited to work as applied bioinformaticians within academic and clinical research laboratories, pharmaceutical companies, and biotechnology companies.

## Master of Science in Translational Biotechnology

This program combines a unique curriculum of foundational learning and practical training, teaching students to translate genomic and molecular insights into the creation and application of biotechnology in the research and medical sciences industries. Bioscience-based courses are integrated with entrepreneurial elements that explore the economic and regulatory frameworks that impact the development and use of new interventions. This program is ideal for biologists, medical students, investors, industry professionals, and all those who are passionate about biomedical sciences and would like a career in biotechnology beyond laboratory research.


# Clinical collaboration

**Ewing sarcoma, the second most common bone cancer in children, adolescents, and young adults, is an extremely enigmatic tumor with no known viable therapeutic drug targets. Luckily, DNA detective Troy McEachron, Ph.D., is on the case, along with pathologist Timothy Triche, M.D., Ph.D., and oncologists James Hu, M.D., and Lee Helman, M.D.**

"Sarcoma is one of the last frontiers in cancer. There aren't too many people who have dedicated their careers to it and there have been no blockbuster drugs or modalities that have changed the landscape for sarcoma sufferers in the last few decades. We still don't have any targeted therapies for this disease," McEachron says. "But with the team we have here, I feel like there is a genuine opportunity to do something great for the patients and learn more about the underlying biology of this disease."

McEachron began chasing sarcoma-causing culprits as a postdoctoral researcher at the Translational Genomics Research Institute in Arizona. "The disease appears to be driven by oncogenic fusion genes, and we know that if we inhibit them, the cancer dies. But we don't yet know how to target them, and we have to better understand how they work," McEachron says. "My laboratory is dedicated to developing new biological tools and approaches to investigate these mechanisms."

McEachron has weekly meetings with his clinical counterparts at the Children's Hospital of Los Angeles (CHLA) to understand clinically relevant issues that he might be able to incorporate into his research. He also relies on physicians to identify patients, provide samples, and eventually validate his research findings in the clinic.

"Working directly with the clinical teams helps scientists know that we are asking the right questions and doing the right experiments," McEachron says. "It's a critical feedback loop to make sure our results have the best chance of being meaningful for improving patient outcomes."

"Ewing sarcoma is unique among cancers in the young for many reasons, and remains one of the most devastating cancers in that age group. This is particularly vexing, as we have known for over 30 years that the tumor is driven by a fusion gene that occurs in essentially all cases, but we don't know how," says Triche, co-director of CHLA's Center for Personalized Medicine Program and one of the foremost Ewing sarcoma researchers.

"Troy brings a fresh approach to deciphering the enigma, and working with him and the new techniques he brings to bear on the problem will hopefully allow us to finally put all the pieces together into an understanding of how the fusion gene causes the cancer," Triche adds. "Once we know that, we can also begin to craft specific therapy that blocks that mechanism, and perhaps improve the current 50% survival rate for the first time in 30 years."

The collaboration is just one of many taking place among USC Translational Genomics faculty with researchers and clinicians around USC, in the greater Los Angeles community, across the nation, and around the world.

"As new medical approaches and technology become available, we have a unique opportunity to work with our colleagues in this diverse clinical setting to ensure they are available to everybody, including the underrepresented and underserved," says Director John Carpten.

**"The Translational Genomics program can play a critical role in helping clinicians identify patients who are at increased risk to develop specific diseases or complications related to treatment."**

**Jay R. Lieberman, MD**
Chair and Professor of Orthopaedic Surgery
Chief of Orthopaedic Surgery Service, Keck Medical Center
President of USC Care

**"While the development of chemotherapeutic agents has made a significant impact on treatment for patients with cancer, the ideal approach would be to fingerprint each tumor to allow us to target its weaknesses and thus potentially make a lasting impact. Our Division plans to work closely with the Institute to put the magnifying glass on gynecologic cancers with the hope of developing more individualized and less toxic treatments."**

**Lynda Diane Roman, MD**
Associate Professor of Obstetrics & Gynecology
Division Chief, Gynecologic Oncology

# Caring for community, building on diversity

Truly effective personalized therapies must be based on sound science that reflects the diversity of the population it will serve. Cancer is unique to each individual. In some cases, it also presents itself differently within different populations. The blood cancer multiple myeloma, for instance, disproportionately affects African Americans and often leads to worse outcomes for those patients.

Researchers at USC Translational Genomics are committed to finding out why — and to ensuring that these populations are included in the large-scale genomic databases used for most research studies, which overwhelmingly contain samples from Caucasian patients. Out of 5,729 samples in The Cancer Genome Atlas, for instance, 660 were African-American, 173 were Asian, and 149 were Hispanic, compared with 4,389 from white patients.

"There is a significant paucity in our understanding of molecular factors that may be driving these cancers and leading to disparities among underrepresented populations," says Director John Carpten.

By creating a more diverse collection of cell lines and animal models — and contributing them to the National Cancer Institute's database — the team hopes to improve the entire scope of cancer care for everyone.

Carpten was an early pioneer in the study of cancer disparities among underrepresented populations.


He conceived the African American Hereditary Prostate Cancer Study (AAHPC) Network, which has become a model for genetic linkage studies in underrepresented populations and led to the first genome-wide scan for prostate cancer susceptibility genes in African Americans.

**"Building upon previous work done at USC, we want to draw upon our unique and diverse catchment area to ensure we include a multiethnic cohort in research and clinical care that will better benefit everyone. We want to do this in a culturally sensitive manner that will truly engage the community."**

**John D. Carpten, Ph.D.**
Director, Institute of Translational Genomics

Triple negative breast cancer is next in his sights. Together with colleague Bodour Salhia (left) and a team of collaborators across the United States, Nigeria, and Ghana, Carpten is tracing the biology of breast cancer across the African diaspora. Whereas the incidence of the aggressive triple negative form of the disease among women diagnosed with breast cancer hovers around 12% among Caucasian women, it is 25-30% among African-American women and 70-75% among African women.

“We want to better understand the ancestral genetic differences that seem to be a factor in some of the aggressive breast cancers we are seeing in young black women,” Carpten said.

Salhia has already collaborated with oncologists and pathologists in Egypt to uncover the molecular uniqueness of breast cancer subtypes among that population, and she has worked with underserved Native American populations, including the Navajo Nation in Arizona.

Other researchers at USC Translational Genomics are also conducting clinical and epidemiological studies in the community.

For Troy A. McEachron, the incredibly rich cultural tapestry is particularly valuable in his study of rare bone and connective tissue cancers, or sarcomas. “With the diversity that is intrinsic to LA, we are able to ask and answer a lot of important questions.”

Enrique Velazquez-Villarreal agrees that LA is an amazing place to study the same disease in different populations. “Gene expression and disease prevalence often differ across populations. Receptors are also different, which can affect drug discovery and development.”

## All about integration

Once a week, Enrique Velazquez-Villarreal crosses the border on a mission: to bring precision medicine to Mexico. He’s starting in one clinic in Tijuana, where he delivers primary care to about a dozen patients who have had their genetic data examined and integrated into their clinical care and records.


**Enrique Velazquez, M.D., Ph.D., M.P.H., M.S.**
Assistant Professor of Research
Translational Genomics

It’s a miniature real-world implementation of work Velazquez-Villarreal does on a much larger scale. At USC, the bioinformatician interrogates and integrates huge databases and computational systems from different branches of medicine to create tools and libraries for both research and clinical applications. Earlier in his career, he worked with millions of records on the world’s largest supercomputer at Carnegie Mellon. Later, he used artificial intelligence and machine learning to predict biological processes and the effect of behavioral interventions in neurological conditions, such as autism.

A man of many hats — and five degrees — Velazquez-Villarreal uses his vast knowledge across the entire spectrum of care, discovery, and teaching.

As a teacher, he leads classes in statistics, data analytics, and bioinformatics, and as a bench scientist, he has studied neurological conditions, transplantation immunology, and basic cell biology and mechanisms.

As an epidemiologist, he’s committed to delivering precision public health, using genetic data to assess risk and inform prevention strategies for individuals and communities. The Mexican native is currently canvassing Latino neighborhoods in San Diego to collect data and educate residents about positive family dynamics as part of a project with the University of California, San Diego.

“There’s a lot of biology and behavior that you can understand by linking information,” Velazquez-Villarreal says. “I think in the future, if we can find a way to integrate clinical and genetic information, it will be a great opportunity to advance the medical field.”

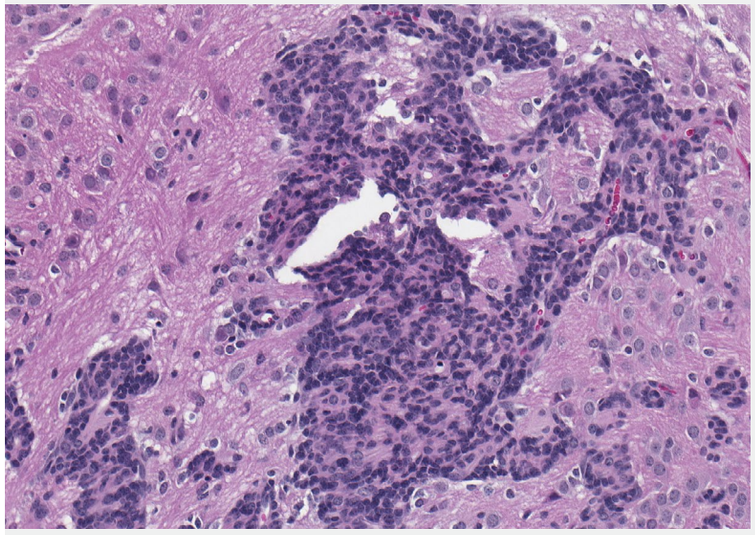
# Here to help: Empowering users through genomics and bioinformatics

The plating prowess and bioinformatic brains in the halls of Norris are available for the entire Keck academic and clinical community.

“We want to leverage our strengths to increase the research potential of departments in a variety of disciplines, and to assist patients across the disease spectrum,” says Director John D. Carpten.

One of the ways this will be achieved is through the newly launched Keck Genomics Platform. Under the direction of Zarko Manojlovic, Ph.D., the service offers a range of high-tech, high-throughput sequencing, as well as the bioinformatic backbone and support to be able to interpret the data generated. Technicians at the center also have expertise in preparing complex and fragile samples, allowing researchers and physicians to test materials that have previously been considered unusable.

“We can truly help the individual understand the sequencing of the data and the data itself, as well as the analysis,” Manojlovic says.



**“We want to connect as many scientists and physicians as we can to bring unity and centralization. We need to play to each other’s strengths to achieve the best outcomes.”**

**Zarko Manojlovic, Ph.D.**
Assistant Professor of Research Translational Genomics,
Director of Keck Genomics Platform

Manojlovic partners with physicians to bring precision medicine to the clinic in a way that’s not just a data dump. He learns from the physicians—about their needs, challenges, and the day-to-day impacts of precision medicine on their clinical practice—and educates them about what kind of data they can get from samples, how to collect and prepare them, and the relative costs.

Together with David W. Craig, his team is working to create a cradle-to-grave next-generation sequencing data management and bioinformatics platform that focuses on downstream interpretation and accelerates discovery though close collaborations between experimental and informatic groups.

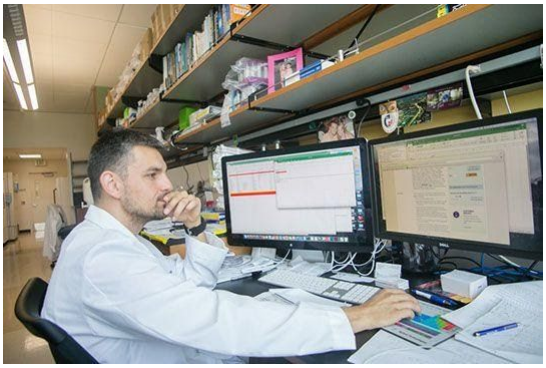
## How to get involved

To learn more about Translational Genomics @ USC research, education, and clinical services:

**Visit:** dtg.usc.edu **E-mail:** dtg@usc.edu **Call:** (323) 865-1591 **Fax:** (323) 442-2490

## Program & Curriculum

### OVERVIEW



USC's Department of Translational Genomics at Keck's School of Medicine is offering an intensive two-year MS program in biomedical informatics focusing on bioinformatics within health-related fields. This program is focused on training individuals who have strong backgrounds in laboratory-based biomedical sciences and seek the bioinformatic skills for analyzing, processing, and managing large-scale data. Graduates will be suited to work as applied bioinformaticians within academic research laboratories, clinical research laboratories, pharmaceutical companies, and biotechnology companies.

**WHAT IS TRANSLATIONAL BIOMEDICAL INFORMATICS?**

The goal of this program is to train applied bioinformaticians, providing students with the training, skillsets, and best practices for applying and integrating existing bioinformatics tools in the study of human health and disease.

- Translational: Translating laboratory data to bedside or clinic
- Biomedical: Relating to human biology, medicine, and disease
- Informatics: Applied processing and analysis of data

This program is tailored for individuals with laboratory-based biomedical experience, biomedical sciences, or biomedical engineering. This program focuses on tool application and integration along pipelines, will scripting emphasized over coding. Graduates will have the analytical capabilities for analyzing datasets across molecular biology, systems biology, structural biology, and genomic sequencing datasets. A major emphasis is on data analysis and data processing associated with next-generation sequencing (NGS) data, understanding that the goal is to build core skill sets that remain relevant as new technologies emerge and change.

**LEARNING OBJECTIVES**

- Understand best practices for putting existing tools and bioinformatics datasets together to better understand biomedical problems;
- Be able to analyze next-generation sequencing (NGS) including whole-genome, exome, and transcriptome sequencing (RNA-seq), as well as emerging methods in single-cell sequencing;
- Understand project management and requirements in bioinformatics gathering skills to allow them to interface and interact with computational and engineering expertise to help design solutions;

- Have experience and training utilizing modern frameworks for rapid prototyping, and how to extract information from a wide variety of databases;
- Understand core responsibilities towards data security, privacy, and data sharing spanning open access frameworks to restricted and regulated frameworks;

### Learning Environment

This program uses both traditional classroom-based teaching and applied in-silico laboratory for assignments that are coupled with additional online materials. Bioinformatics, after all, is about working mostly on computers with a community that spans the world for help. Within the program, each class varies.

Most courses alternate between online interactions with faculty followed by in-class lectures and laboratories. The class is often focused on helping students apply concepts that were made available outside of the classroom. Fundamentally, this is an applied program where the focus is on learning to become independent and solve new problems as they emerge. It teaches processes, though in a way that is effectively learning by example. For example, several courses have a strong inclusion of R, R-markdown, and R-shiny, where students develop web-applications to complete homework by submission via GitHub. These applications may include biomedical research or clinical problem commonly seen in the field. Classroom time is often used for working with teams of students on their solutions and suggesting paths through obstacles. In-person, classes are often interactive with students and lectures engaged in an ongoing dialogue where lecture materials were already made available and reviewed prior to the course. Students who succeed use both online resources and in-person classroom time.

## Courses and example schedule

*Students are expected to become involved in rotations to identify a lab to embed in or other internship opportunities during their first year. Some students may want to wait a few months to develop stronger bioinformatic skills, though all students should be actively working with an advisor by spring of the 2nd semester.*

General requirements include at least 28 units of required courses as follows:

### CORE LECTURE COURSES (REQUIRED: 24 UNITS)

#### Typical Fall First Semester

**TRGN-510. BASIC FOUNDATIONS IN TRANSLATIONAL BIOMEDICAL INFORMATICS (4 UNITS).**

The goal of this introductory platform course is to teach core fundamentals that will allow a someone trained in biology or medicine how to use modern computing and bioinformatics tools to rapidly and reproducibly answer biological questions within an applied setting. The focus is significant on how researchers can use existing tools together to explore novel biomedical questions in ways that retain reproducibility. This course is for all students to have the core fundamentals for the rest of the program and will have bridge together courses that form the Masters in Translational Biomedical Informatics program. Please be aware the students are expected to have a Mac laptop with Sierra or later operating system installed for enrollment.

This course is a core requirement but may be substituted with INF 510 Principles of Programming for Informatics. The INF510 course provides a more focused training specific to python whereas the TRGN510 focuses more on the use of R, bash, and other scripting languages including python in the context of biomedical applications. For more information on INF510, please see https://classes.usc.edu/term-20161/course/inf-510/

**TRGN-514. INTRODUCTION TO HUMAN GENOMIC ANALYSIS METHODS (4 UNITS).**

This course is part of a two-course series and complements courses offered as part of a master's in biomedical informatics. This course is necessary to both teach modern genomics analysis, but to provide students with the broader skillset to adapt and grow in the field as technologies change. More than most fields, they will frequently change tools and frequently build single-use solutions. This course will focus on implementing, versioning, best practices, planning, and delivery specific to translational research by example using a series of emerging methodologies. Please be aware the students are expected to have a Mac laptop with Sierra or later operating system installed for enrollment. This course is a core requirement

TYPICAL SPRING SEMESTER, FIRST YEAR

**TRGN-515. ADVANCED HUMAN GENOMIC ANALYSIS METHODS (4 UNITS).**

This course is part two of a two-course series and complements courses offered as part of a master's in biomedical informatics. This course will continue the process of both teaching modern genomics analysis while providing students with the broader skillset to adapt and grow in the field as technologies change. Students will learn the fundamentals of genomics, transcriptomics, proteomics, and epigenomics technologies and will learn how their application and use drive analytical problems. Students will be expected to be familiar with and now experienced with many foundational skillsets introduced in earlier courses that are necessary for biomedical informatics. This course continues to build those by reinforcement with an increased focus on timeliness and flexibility within the more complex analysis. Please be aware the students are expected to have a Mac laptop with Sierra or later operating system installed for enrollment. This course is a core requirement

**TRGN-516. TRANSLATIONAL GENOMICS, APPLIED DATABASES AND DATA STRUCTURES (4 UNITS)**

The objective of this course is to provide advanced bioinformatics training in the use of databases and development of databases for sharing results and tracking information. The course will cover how to work with databases and understanding the regulatory environment around their use. A major part of this course will be on applied projects wherein teams students will be asked to use a case-study based approach to identify appropriate datasets, use analytic tools to analyze data, evaluating hypotheses, and interpret results. The first major foci are the current standards and key resources in human annotation and gene ontology. Please be aware the students are expected to have a Mac laptop with Sierra or later operating system installed for enrollment.

This course is a core requirement but may be substituted with INF 550 Overview of Data Informatics in Large Data Environment with prior permission. The TRGN516 course is focused

on biomedical applications and the management of biomedical data, particularly within a healthcare context. INF550 provides a deeper technical view using applications that are much broader. In that context, TRGN has a narrower focus on healthcare applications and the associated regulated frameworks, whereas INF550 provides a deeper technical basis within databases and data structures.

TYPICAL FALL/SPRING SEMESTER, SECOND YEAR

**TRGN-524. APPLICATIONS OF GENOMIC TECHNOLOGY IN BIOMEDICAL RESEARCH I (4 UNITS)**

This course is an introductory level course and necessary for Masters of Science (MS) degrees in both Biomedical Informatics and Translational Biotechnology. This course is necessary to build a foundational understanding of modern molecular genetic technologies and the evolution of next-generation technologies. At its core, this course teaches the principles of conducting large-scale data analysis and appreciating how the nature and type of data impact the analysis approach. Next-generation sequencing data is at its nature pseudo-single molecule and analysis approaches treat error differently, and this has implications towards interpretation. Through these courses, students will understand the inherent challenges and opportunities by bridging analysis together to uncover new discoveries, through integration across genomics, transcriptomics, proteomics and epigenomics technologies. Students will learn how these tools are developed and how they are impacting both the laboratory and the clinical setting. Through this course, students will also learn how biotechnology leads to commercialization and gain an understanding of governmental regulations and ethics surrounding hot topic issues such as cloning, stem cells, and genome sequencing.

*This course is a recommended elective, but may be substituted for one of the electives below*

**TRGN-520. TRANSLATIONAL BIOMEDICAL INFORMATICS CAPSTONE PORTFOLIO**

This course will provide students the opportunity to build a portfolio in the form of a web-based application that can capture the projects developed and completed through this course, and also show-cases one larger cap-stone project. The overall objective is to provide students provides the culminating, integrative curricular experience and an overarching project tailored to the career direction they are targeting and build a reactive widely accessible “WebApp” that showcases their project.

ELECTIVES (AT LEAST 4)

- TRGN 525. Foundations, Concepts, Core Principles In Biotechnology II
- PM 570 Statistical Methods in Human Genetics.
- PM 538 Introduction to Biomedical Informatics.
- BME 528 Medical Diagnostics, Therapeutics and Informatics.
- PM 570 Statistical Methods in Human Genetics.
- INF 510 Principles of Programming for Informatics.

- INF 550 Overview of Data Informatics in Large Data Environments.
- NIIN 500 Neuroimaging and Systems Neuroscience.
- NIIN 540 Neuroimaging Data Processing Methods.

## Capstone Project

### Overview

The capstone project is the culmination of your master's degree in translational biomedical informatics.

There are four aspects:

1. Identifying a Lab
2. Proposal
3. Capstone Enrollment
4. Presentation/Delivery

Importantly, it is the vehicle to gain applied experience working within the research field, and ideally, it will aid in future career steps. There is flexibility in the format and deliverables, though a requirement of a capstone proposal is required to enroll in the course.

### Tools for Identifying A Lab

There is no single best way to find a mentor, though it is recommended you start the process after becoming nominally proficient in basic bioinformatic and computing tools. For many students, this will be after there the first semester, though for some it may be sooner depending on their individual backgrounds. Your department will be able to give some advice on this topic, and the process can vary tremendously depending on your long term goals. While for most the mentor will be a USC faculty member, it is possible for the mentor to be an outside individual to be considered on a case-by-case if certain requirements can be made (such as the ability to share openly your work and work product).

The starting point for many emails to prospective labs. You will want to introduce yourself and have a short 1 to 2 paragraph query and introduction. You will want to mention some of your bioinformatics expertise or focus (R/R Shiny, Databases, Unix, Next-generation Sequencing).

## Department

There is no single way to identify a mentor, but utilizing colleagues, the internet and going to presentations are foundational. Clearly, starting by looking at the research and faculty within the Department of Translational Genomics is a great starting point. The research faculty are:

- Brooke Hjlem, Ph.D.
- Troy McEachron, Ph.D.
- David Craig, Ph.D.
- Bodour Salhia, Ph.D.
- Enrique Velazquez, Ph.D. MPH
- John Carpten, Ph.D.
- Zarko Manolojvich, Ph.D.
- Xiaowu Gai, Ph.D.

## Keck School of Medicine

There are many faculty that work closely with the department and many faculty at USC who would make excellent mentors. Collaboration is at the heart of translational genomics. Departments indicating strong interest in Translational Biomedical Informatics Students:

- Department of Medicine
    - Best initial contact is Matthew Salomon who leads informatics and is aware of different groups who have needs
- Department of Psychiatry
    - Specific requests for those interested in databasing with genomics by Steven Siegel
- Stem Cell
    - Various individuals, but Andrew McMahon has opportunities both in his lab and in others. RNA-seq, ChIP-seq, ATAC-seq, single-cell RNA-seq, single-cell-ATAC-seq, and Hi-C to identify the molecular mechanisms regulating maintenance and commitment of stem/progenitor populations in generation and repair of the mouse and human kidney
- Zilka Institute
    - Berislav V. Zlokovic or individual labs may be the best approach
- CHLA
    - Xiaowu Gai is a great contact who may be aware of many opportunities

## Proposal

After working some time in your lab or research environment, you'll want to start defining what will be your Capstone deliverable. Remember, in the beginning, you want to learn and develop from the lab. The right capstone deliverable will typically be pretty clear after a few months, but it should be something that really showcases what you are learning and the experience you are gaining.

Your proposal will be turned in as a Github titled “capstone” in markdown format as the initiating Readme.md. You will create the course PI as a collaborator. There is purposeful flexibility in the type of capstone projects & its deliverable. In the end, they should be done with a mentor. The experience of working within a lab is critical and the deliverable may vary. There will be some back-and-forth on the proposal to make sure expectations are clear. You will be notified by the program director by email when the proposal is accepted.

It is important to understand that the deliverable and timing of the capstone course can capture your entire time within the master’s program. For example, if you are presenting at a conference, you would include work done in all the semesters within the program.

Example deliverables include:

- Publications (e.g. Journal)
- Scientific Poster at a Major Conference
- Technical White Paper, e.g. Biorxv
- GitHub Repositories
- Web-sites

There is not a requirement for a traditional academic style presentation, and various forms can be used including video, websites, the publication (PDF), and other media. Ideally, the presentation can be done in a way that retains your ability to show people the work in the future.

`Readme.MD`

```
#Title
Proposed Title
#Student
#Mentor
John Doe, Ph.D.
john.doe@usc.edu#Proposed Work
150 to 250 Words
#Proposed Deliverable
  150 to 250 Words
```

## Faculty Collaborators

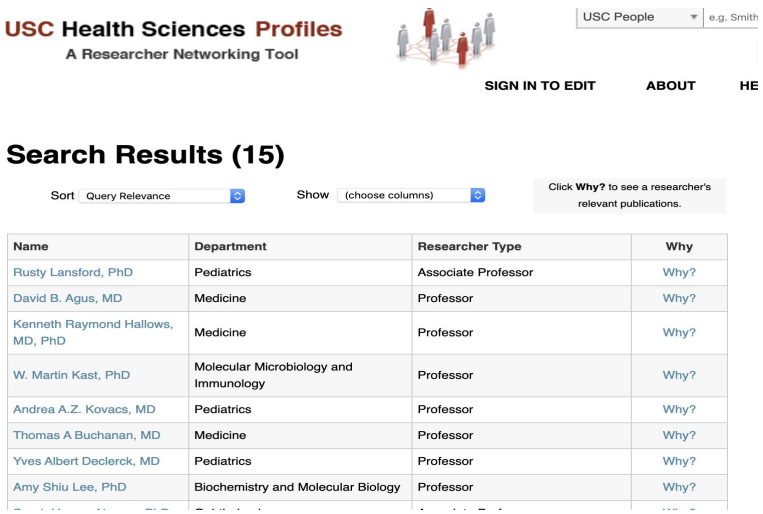
Faculty who have expressed interest in bioinformatic students:

| Faculty/Link | Department | Position |
|---|---|---|
| Adam de Smith, PhD | Genetic Epidemiology | Assistant Professor |
| Andrew P. McMahon, PhD | Stem Cell | Professor |
| Caryn Lerman | Cancer Center | Professor |
| Dana Goldman, PhD | Public Policy | Professor |
| Daniel J. Weisenberger, PhD | Medicine | Associate Professor |
| Daniella Meeker, PhD | Preventive Medicine | Assistant Professor |
| Darcy Spicer, MD | Medicine | Associate Professor |
| Darryl Shibata, MD | Pathology | Professor |
| Jaclyn A. Biegel, PhD | Pediatrics | Professor |
| Jerry SH Lee, PhD | Medicine | Associate Professor |
| Jonathan David Buckley, MD, PhD | Preventive Medicine | Professor |
| Juan Pablo Lewinger, PhD | Preventive Medicine | Assistant Professor |
| Julie E. Lang, MD | Surgery | Associate Professor |
| Juliet Ann Emamaullee | Surgery | Assistant Professor |
| Justin Ichida, PhD | Stem Cell Biology | Assistant Professor |
| Kimberly Siegmund, PhD | Preventive Medicine | Professor |
| Linda Michelle Polfus, PhD | Genetic Epidemiology | Assistant Professor |
| Matthew Salomon | Medicine | Assistant Professor |
| Michael Anthony Bonaguidi, PhD | Stem Cell Biology | Assistant Professor |
| Michael R. Lieber, MD, PhD | Pathology | Professor |
| Paul Marjoram, PhD | Preventive Medicine | Professor |
| Peter Kuhn, PhD | Broad CIRM Center | Professor |
| Pinchas Cohen, MD | Gerontology | Professor |
| Rangasamy Ramanathan, MD | Pediatrics | Professor |
| Ricky Bluthenthal, PhD | Institute for Health | Associate Professor |
| Sarah Hamm-Alvarez, PhD | Ophthalmology | Associate Professor |
| Shahab Asgharzadeh, MD | Pediatrics | Associate Professor |
| Steve Kay, PhD | Zilkha Neurogenetic | Professor |
| Steven Siegel, MD, PhD | Psychiatry | Chair |
| Timothy J Triche, MD, PhD | Pediatrics | Professor |
| W. Martin Kast, PhD | Molecular Microbiology | Professor |
| Wendy Cozen, DO, MPH | Preventive Medicine | Professor |

## USC Health Science Profiles - Learn about Keck Faculty

An automated tool that has information about each faculty. This tool is great for doing searches within areas!

https://profiles.sc-ctsi.org/search/




| Name | Department | Researcher Type | Why |
|---|---|---|---|
| Rusty Lansford, PhD | Pediatrics | Associate Professor | Why? |
| David B. Agus, MD | Medicine | Professor | Why? |
| Kenneth Raymond Hallows, MD, PhD | Medicine | Professor | Why? |
| W. Martin Kast, PhD | Molecular Microbiology and Immunology | Professor | Why? |
| Andrea A.Z. Kovacs, MD | Pediatrics | Professor | Why? |
| Thomas A Buchanan, MD | Medicine | Professor | Why? |
| Yves Albert Declerck, MD | Pediatrics | Professor | Why? |
| Amy Shiu Lee, PhD | Biochemistry and Molecular Biology | Professor | Why? |

## NIH Reporter: Identifies labs with funding

Often the labs with the greatest opportunities have NIH grants. This database is great - remember to limit to USC to see all the different labs with substantial NIH funding.


| T | Act | Project | Year | Sub # | Project Title | Contact PI/ Project Leader | Organization | FY | Admin IC | Funding IC | FY Total Cost by IC | Sim Proj |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| 5 | R01 | DC003552 | 19 | | HUMAN COCHLEAR FUNCTION: A CONTINUUM OF MATURATION AND AGING | ABDALA, CAROLINA | UNIVERSITY OF SOUTHERN CALIFORNIA | 2019 | NIDCD | NIDCD | $455,237 | |
| 5 | K01 | AG051756 | 03 | | HEALTHCARE STEREOTYPE THREAT, HEALTH DISPARITIES, AND MINORITY AGING | ABDOU, CLEOPATRA MIRIAM | UNIVERSITY OF SOUTHERN CALIFORNIA | 2019 | NIA | NIA | $129,492 | |
| 1 | R01 | AG064491 | 01 | | THE IMPORTANCE OF THE NEIGHBORHOOD ENVIRONMENT IN DETERMINING HEALTH AND WELL-BEING AMONG PERSONS WITH DEMENTIA AND THEIR CAREGIVERS | AILSHIRE, JENNIFER A | UNIVERSITY OF SOUTHERN CALIFORNIA | 2019 | NIA | NIA | $423,998 | |
| 5 | R01 | AG053798 | 02 | | GLOBAL ALZHEIMER'S PLATFORM TRIAL-READY COHORT FOR PRECLINICAL/PRODROMAL ALZHEIMER'S DISEASE | AISEN, PAUL S. et al. | UNIVERSITY OF SOUTHERN CALIFORNIA | 2018 | NIA | NIA | $4,967,947 | |
| 5 | U24 | AG057437 | 03 | | ALZHEIMER'S CLINICAL TRIALS CONSORTIUM (ACTC) | AISEN, PAUL S. et al. | UNIVERSITY OF SOUTHERN CALIFORNIA | 2020 | NIA | NIA | $14,925,844 | |
| | | | | | COMBINATION ANTI-AMYLOID | | UNIVERSITY OF | | | | | |

Keck School
of Medicine
of USC

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