Imagine a world in which you can input your age, lifestyle, and genetic information into an app and obtain personalized recommendations about the food you should eat or avoid and behaviors you should modify to help maintain your health. Moreover, imagine that when you are sick, your physician inputs the same information to determine your customized treatment plan. That world is not 50 years into the future; it is beginning to unfold now.

At the Stanford Center for Genomics and Personalized Medicine (SCGPM), we are applying our expertise on the science and ethics of genomics to build a new collaborative model of science focused on transforming the practice of medicine. This creates a new paradigm of patient-centered medicine that can monitor the entire genome of individuals to vastly improve disease prediction, prevention, and treatment of conditions such as cancer, diabetes, heart disease, asthma, schizophrenia, and many others.

Stanford is uniquely positioned to drive such an endeavor. We have extraordinary talent in science, engineering and medicine; our location in Silicon Valley provides unique opportunities for technological collaborations; our faculty are highly successful at obtaining competitive funding for their research; and we are leaders in the ethics of personalized medicine and in training physicians to help patients understand their genetic information. Genomics, in particular, requires technologically advanced facilities, and computational infrastructure and benefits from an economy of scale that can only be achieved in center settings like the SCGPM. Our Center offers an omics driven biomedical platform composed of state-of-the-art laboratory and computational facilities to an interdisciplinary research community.

**OVERVIEW OF SCGPM**

**Michael Snyder, PhD,** is the Stanford Ascherman Professor, Chair of the Department of Genetics, and the Director of SCGPM at Stanford University. In 2012, he used his own genome sequence to predict and help diagnose his own metabolic disorder, a story that received international attention and shines a light on the promise of genomics.

“Michael Snyder is my go to guy in genomics, and this book is an invaluable and comprehensive breakdown of a complex and rapidly moving field. This is where medicine is headed, and this book is the way for you to get up to speed.”

Eric Topol, Professor of Genomics, Scripps Research Institute
SCGPM’s Genome Sequencing Service Center (GSSC) is a state of the art genomics facility granting Stanford researchers access to cost-effective high throughput sequencing. At the GSSC we offer library preparation and sequencing services from a variety of sequencing technologies (Illumina, PacBio, 10X Genomics). Our library offerings include preps for whole genome sequencing, exome sequencing, RNA-Seq, Methyl-Seq, ATAC-Seq, and single cell sequencing. GSSC is a key contributor to the sequencing efforts of large-scale sequencing studies including the ENCODE Consortium and the NASA Twins Study. Recently, the GSSC has served as the sequencing hub for CIRM’s Center of Excellence in Stem Cell Genomics, a multi-institutional collaboration funding the stem cell genomic research of seven major California research institutes (Stanford, UCSF, UCSC, UCLA, UCSD, UC Berkeley, Salk Institute, JCVI, and Scripps Research Institute).

Why does SCGPM use the DNAnexus Cloud?
DNAnexus is a trusted Cloud partner for NIH and FDA - DNAnexus is the informatics platform for the prestigious Encyclopedia of DNA Elements (ENCODE) and PrecisionFDA projects. By embracing a trusted genomics Cloud, we can share in the fruits of a larger collaborative ecosystem.

DNAnexus has committed to providing a single pane of view to multiple Clouds - currently supporting Amazon Web Services and Microsoft Azure. This streamlines and simplifies researcher’s experience on the analysis platform while supporting a larger collaboration suite.

Scale to Big Data
Using a cloud platform provides limitless storage capacity and the ability to immediately apply vast and parallel computing resources to analyze data.

Clinical grade security
Our research participants trust us to keep their data secure. End to end data handling on our informatics platform is specifically designed to provide highest standard of security as recommended by NIH.

Take your data out of silos
Generating and storing data on a cloud genomics platform provides the ability to share projects with collaborators around the world, with the click of a button. Seamlessly bring together data generators and analyzers.
NASA Twins Study attempts to study two NASA astronauts, twin brothers Scott and Mark Kelly, with a goal to understand long duration space flight challenges such as Mars mission. Study was undertaken during a 340 day long International Space Station (ISS) Expedition in 2015 when Scott was on ISS and Mark was on earth. The data is being analyzed by 10 investigators spanning aspects of human physiology, behavioral health, gut health and omics. The omics portion of this study is designed following the footsteps of Michael Snyder's integrated Personal Omics Profiling (iPOP) studies. An iPOP study combines multiple high-throughput methods to track the genomic, transcriptomic, proteomic, metabolic, and antibody profiles of an individual through health and disease. Analyzing this data allows for interpretation of how personal omics changes affect health, and is an important step in personalized medicine. Prof Snyder was the first subject, hundreds have followed this path since. The molecular/omics portion of the NASA Twins study is being undertaken by Michael Snyder on SCGPM infrastructure.

NASA Twins Study

Cloud Security Paradigm
Security is fundamental to protecting patient data. Our Center has devoted significant effort towards establishment of a secure Cloud. We published our recommendations in Nature Biotechnology: http://go.nature.com/2frHos4

Real time query engine
To meet the Big Data challenges that genomics brings, we co-developed a low cost scalable data query engine with Google engineers utilizing BigQuery, Spark, and Dataflow. Pre-print available at bioRxiv: http://bit.ly/2fQp4WC

Loom – a workflow engine
Loom is an open source, platform agnostic tool to create, execute, track, and share workflows. It uses modern approaches to code and stack sharing via github and Dockerhub and is written ground up for clinical requirements. Hithub link: http://bit.ly/1WPv/g7D

Data Commons at Stanford
Our vision of a biomedical platform and data sharing is not unlike NIH Data Commons - an ecosystem that brings computing environment together with API centric access to data and software services. With biomedical data there is, correctly so, significant concern around privacy. So how do we navigate the challenge of building a meaningful data commons that not only enables timely research but respects patient privacy? First, we are committed to standards of interoperability (e.g., Global Alliance for Genomics and Health, Observational Medical Outcomes Partnership Common Data Model). Second, we rely on advances in technology to create scalable software services (e.g., Dockerhub). Third, we build a policy driven trusted framework where the research community can get access to data in a timely but secure manner. Finally, we work closely with privacy research experts to bring advances in technology to build software based solutions to insight sharing when data sharing is not timely. In this complex multi-pronged effort, we are aided not only by funding agencies who support implementation of various Data Coordination Centers (e.g., ENCODE, TCGA), we are also blessed by private companies and non-profit agencies who impact the data sharing vision with their own actions (e.g., Ambry, Sage Bionetworks).
BIOINFORMATICS AT SCGPM: BRINGING SCIENTIFIC INSIGHTS

Microbiome Conference
In 2016, SCGPM hosted Stanford’s first microbiome conference with focus on computational solutions for complex metagenomic problems.

The purpose of the conference was to bring together leading minds looking to catalog the human microbiome using modern genetics tools and especially those looking to apply new computational technologies to solve complicated problems in metagenomics to answer such questions such as: a) How are changes in the microbiome associated with diseases in the population, b) How can you identify novel microbes using sequence-based analysis, c) How can you improve patient outcomes by characterizing microbiome dynamics, d) How can you better understand host-microbiome symbiosis to be able to understand and target microbial vulnerabilities, e) How can you track dynamic microbiome shifts during disease, etc.

To check out the videos from this conference, visit: http://stan.md/1YVV6gi

Case Study: Huntington’s Disease
Huntington’s disease is a progressive, fatal neurological disorder with no cure. It’s genetic, and a child of an affected parent has a 50 percent chance of also developing the condition. In an international collaboration, researchers at the National Yang-Ming University in Taiwan and Stanford’s School of Medicine discovered a protein that may one day be a viable therapeutic target for those afflicted with the condition. Our bioinformatics service provided insights into a possible mode of action in a RNA-Seq study comparing gene expression patterns in healthy individuals and Huntington’s disease patients with and without drug treatment.

More at: http://stan.md/2hc36lp

Case Study: Atherosclerosis
Deposition of fatty substances along arterial walls form atherosclerotic plaques that become brittle and vulnerable to rupture, and ultimately cause heart attack and stroke. In collaboration with investigators at the David Geffen School of Medicine at UCLA and the Icahn School of Medicine in New York City, Stanford has discovered anti-tumor antibodies that could counter atherosclerosis. Our bioinformatics service provided insights into vascular biology in a study involving single-cell RNA-Seq data.

More at: http://stan.md/2gX2PQ2

Case Study: Skin Cancer
Immune suppressing drugs are taken during transplant, and for chronic autoimmune disorders, such as celiac disease, Crohn’s disease, Graves’ disease, lupus and rheumatoid arthritis. These drugs can increase risk of skin cancer. Stanford High-Risk Skin Cancer Clinic, serves as an early-warning system, a frontline defense and, if need be, an all-hands-on-board diagnosis and treatment center. Our bioinformatics service is supporting physicians at the Clinic analyze data from whole exome sequencing of squamous cell skin cancer to detect causal variants and implicated genes.


A MESSAGE FROM THE DIRECTOR

W e are seeking the support of individuals who want to become part of the revolution in personalized medicine. Your support can come in various ways:

- Attend or sponsor a conference: Stanford conferences are well attended and present a unique networking opportunity to get to know exceptional researchers, and innovative industry participants. In the serene ambience of Stanford campus, spend an hour or a day with foremost researchers and practitioners.

- In-kind contributions: We strongly appreciate contributions in the form of servers, laboratory products and software. These contributions are immediately made available to a large research community via our bioinformatics and sequencing cores.

- Support research projects: Your gift will have a direct benefit on multidisciplinary science, disease-specific studies, student and faculty support, and developing the technologies and tools needed to advance the goal of more precise and personalized medical care.

Please contact us at medicalgiving@stanford.edu if you would like to learn more about SCGPM and how you can contribute to our efforts. Online giving is available at http://stanford.io/2fY8bd2. You can also contact me at mpsnyder@stanford.edu or our senior staff members directly at somalee@stanford.edu (Somalee Datta, PhD, Director of Bioinformatics), hchaib@stanford.edu (Hassan Chaib, PhD, Director of Sequencing). Thank you for your interest and support.

— Michael Snyder, Stanford Ascherman Professor, Chair of the Department of Genetics, and the Director of SCGPM

GET INVOLVED