



# Northwestern Public Health Review

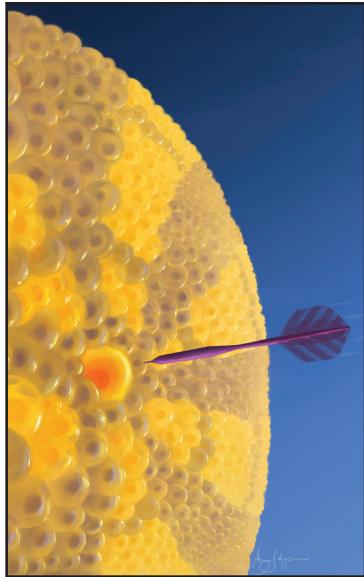
Summer 2018



All of Us

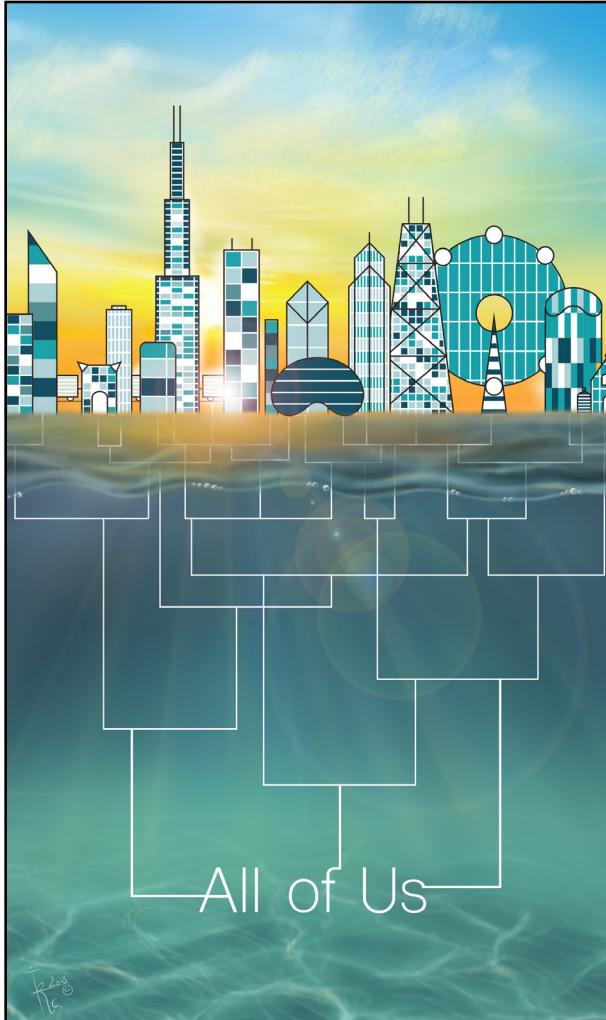
In the Age of Precision Medicine

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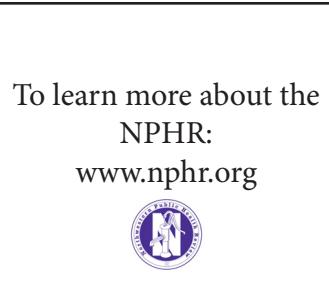
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# Letter From The Editors:

Dear Readers,

We are pleased to bring you the Summer 2018 edition of the NPHR. Dr. James Watson once said that the discovery of DNA is a “giant resource that will change mankind, much like the printing press”. Sixty-five years later genetics, genomics, and metabolomics have very much revolutionized the way we view and use medicine to heal. Precision medicine, or the use of genetic information to tailor treatment and prevention, is only in its infancy. The plethora of data becoming available about the core of what makes us “us” is exciting, but understanding how to use, interpret, and evaluate the consequences of that information is equally important.

In this issue we explore the complex and often contradictory world of genetic health data. First, Makda Zewde takes us through the recently launched, ambitious nation-wide precision medicine ‘All of Us’ program currently conducted at five major health systems across Illinois and Chicagoland, including Northwestern. Grace Bellinger, in an interview with Debra Duquette, the Associate Director of Northwestern’s graduate program in genetic counseling, deep dives into the world of genetic counselors. Duquette explains the challenges facing the genetic counseling profession and the key role they play in communicating the implications of genomic data to clients and patients. Finally, Dr. Paul Burridge explores how precision medicine is being used to predict drug efficacy and toxicity to fight diseases such as cancer. Through these varied perspectives, we seek to understand the ever-changing landscape of *big* genetic data and how it affects our everyday lives.

Sincerely,  
Nelly Papalambros and Simona Morochnik



**Nelly Papalambros**  
PhD/MPH Candidate, NU

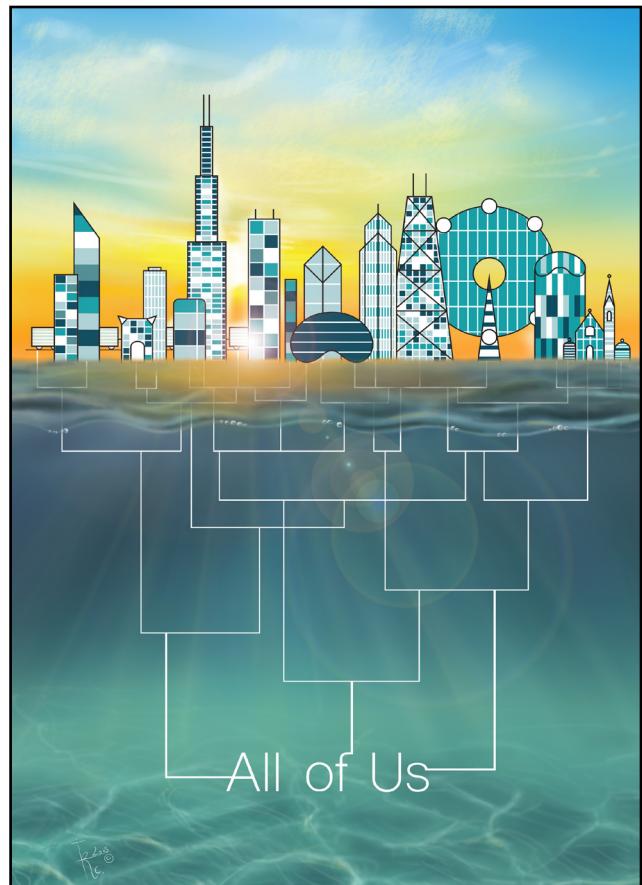


**Simona Morochnik**  
PhD Candidate, NU

# Cover Artist Statement

Creating a scientific cover illustration opened the door to combine my two big passions: art and science. I was inspired by the mission of the “All of Us” program to create the largest national health database in the country, which will ultimately include a variety of data from a million diverse individuals. This data will have the potential to guide the development of personalized medicine for generations to come. The purpose of this cover was to communicate the implementation of this program throughout the greater Chicago area and all of Illinois, as a part of the national effort.

I started by designing the Chicago skyline with heatmap patterns to suggest graphical representations of vast databases that could be created by collecting information from numerous individuals from communities across the city. I added a stylized dendrogram under Lake Michigan to represent the interconnectedness of “All of Us”. The ordered lines of the underwater dendrogram symbolize a unification of the heterogeneous shapes and patterns of the buildings. Finally, I painted a sunrise that reflects through the water as a metaphor of the hope of this ordered information to benefit current and future generations.



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(UIC Biomedical Visualization graduate student)

## About

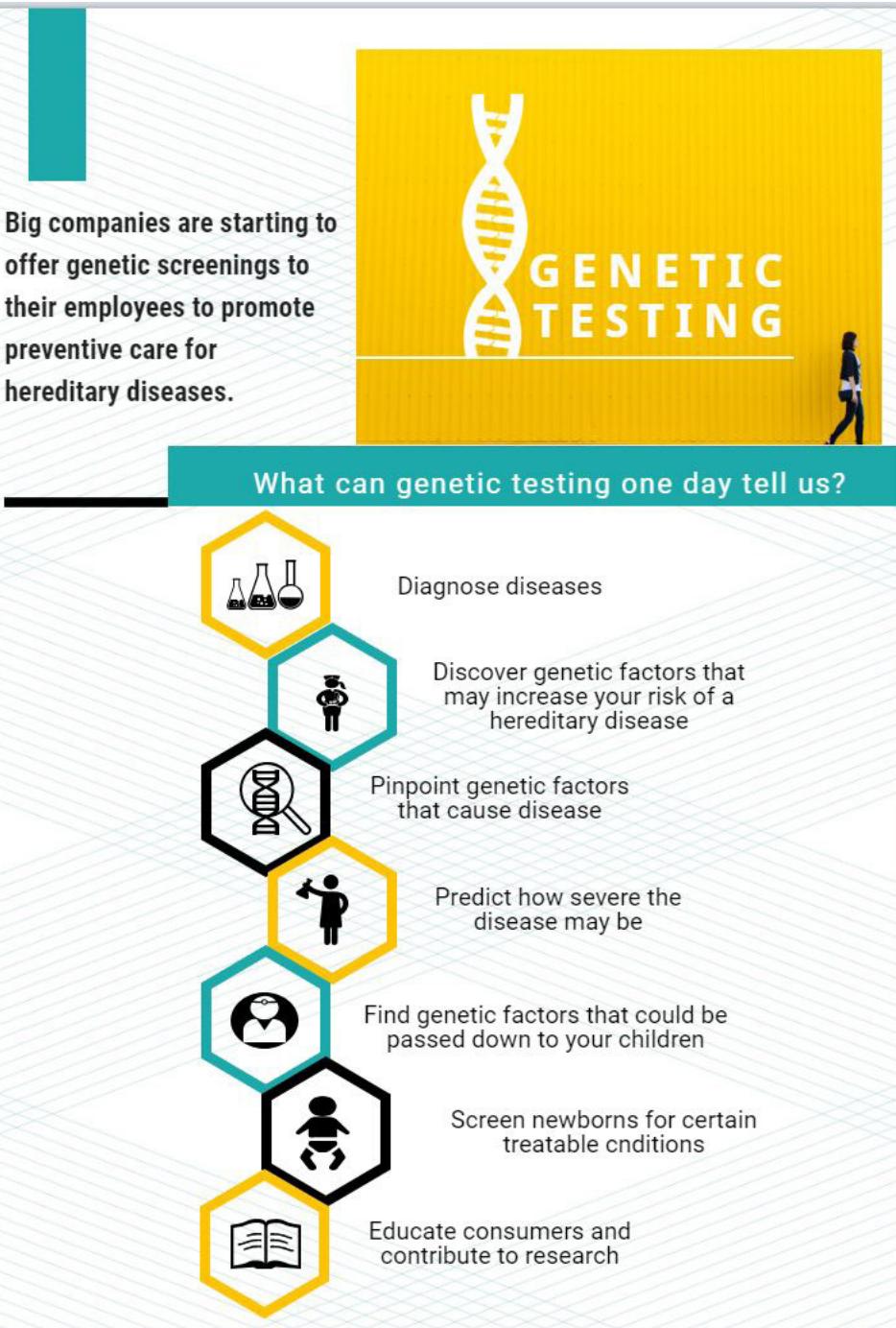


*Dr. Isabel Romero Calvo is a scientific illustrator working out of Chicago. Isabel grew up in the historic town of Granada, Spain. She earned her PhD from the Biochemistry Department of the University of Granada, before moving to the US for her postdoctoral training at the University of Chicago in the field of cancer biology. After her scientific training, Isabel decided to follow her passions for both art and science by combining these fields as a biomedical illustrator. She is currently completing her Master of Science degree in Biomedical Visualization at the University of Illinois at Chicago.*

# Precision Medicine Fact Sheet

*Precision Medicine is a new model for the customization of healthcare that takes into account medical decision making and treatment tailored to the individual patient.*

## One of the arms of precision medicine is Genetic Testing



The National Institutes of Health define precision medicine as "*an emerging approach to disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle.*"

## Tools of Precision Medicine

### Molecular Diagnostics



### Analytics



### Imaging Techniques





By Makda Zewde

## From All of Us to Precision Medicine

In his 2015 State of the Union address, former president Barack Obama announced the launch of the \$215 million dollar Precision Medicine Initiative, a national effort to accelerate biomedical discovery that can better tailor healthcare to the needs of individual patients. This emerging approach to medicine has already shown immense potential in the treatment of certain diseases, such as cancer, where genetic tests are frequently used to identify the most effective treatments for a patient. To expand upon this success, the NIH launched the All of Us Research Program, a longitudinal research program that aims to collect health data on one million or more people living in the United States over many years. Using this broad dataset, the program aims to improve our understanding of a wide range of factors – biology, lifestyle, and environment – that contribute to health, and apply this understanding toward more evidence-based, individualized healthcare.

## All of Us at Northwestern

In 2016, Northwestern University became one of over 50 HPOs across the country to receive the All of Us Health Care Provider Organization Award. The designation involves building research protocols as well as enrolling individuals and collecting health data. Over the next five years, the \$60 million award will be distributed across five medical centers in Illinois: Northwestern University, The University of Chicago, Rush University Medical Center, NorthShore University HealthSystem, and the University of Illinois at Chicago, which together make up the Illinois Precision Medicine Consortium.

So far, more than 3,000 full participants – those who have provided general and electronic health record consent and completed in-person visits for biosamples and physical measurements – have enrolled through the consortium. More than 31,000 have enrolled nationally.

**"[The] All of Us Research Program is a longitudinal research program that aims to collect health data on one million or more people living in the United States over many years."**



## EHRs as Data Source: The Challenges



In addition to its designation as an HPO for the program, the Northwestern center is also involved in developing tools to integrate and curate electronic health record (EHR) data from multiple institutions. Dr. Firas Wehbe, Northwestern Medicine's Chief Research Informatics Officer, explained that this has been a rate-limiting step for the program. In order to facilitate the kind of large scale discovery anticipated from the All of Us program, data from multiple healthcare systems need to be integrated into a common data model. Even EHR systems within the same institution may require integration – Northwestern University's various EHR systems, for example, had not been unified into a common data model until March of this year.

According to Dr. Abel Kho, director of the Center for Health Information Partnerships at Northwestern University, another major challenge

involved in health data analysis is integrating scattered health records from the same patient. Patients often change providers and insurance plans, causing their EHR data to be scattered across multiple institutions.

Further complicating the data retrieval process is the fact that EHR data contains unstructured data such as clinical notes, which are not easily organized into searchable databases. Although EHR systems carry a great wealth of patient data, Dr. Wehbe explains, they are designed primarily as transactional systems to manage workflow, and to serve as legal medical documentation, and thus are not directly amenable to analysis. Significant computing resources are therefore required to process the data and extract necessary information.

Another challenge involved in analyzing EHR data stems from the potential inaccuracy of the data.

For instance, Dr. Kho explains that healthcare providers sometimes input diagnosis codes in order to bill certain procedures rather than to document true diagnoses, making these codes somewhat unreliable. Demographic data may also have inaccuracies, as race and ethnicity is not self-reported in EHRs. Indeed, a 2015 study published in the Journal of General Internal Medicine found that 3% and 6.6% of Hispanic and African American patients, respectively, were not identified correctly in the EHR.



*The All of Us program aims to address these problems by crosswalking self-reported, EHR, survey, and genetic data to verify patient information.*

It is clear that data collection at this scale will be challenging, particularly given that EHRs will serve as a major source of data for the project. On the positive side, Dr. Wehbe highlights how harmonious it has been to work with informaticians from all over the country. “Maybe it’s because there’s been enough work to go around that everyone is busy, but I’m surprised it progressed as it has.”



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(UIC Biomedical Visualization graduate student)

# “Partners” not “Subjects”



The All of Us program has placed a notable emphasis on its recruitment language. Volunteers who enroll in the program are referred to as “participants”, or “partners”, rather than subjects. In addition to providing their health data to the program, which include biosamples, EHRs, physical exams, and surveys, Dr. Wehbe explains that participants will also have a say in the research questions that come out of the program. To facilitate this, the Illinois consortium has created an 11-member Community Participant Advisory Committee (CPAC), which met for the first time this month. Eventually, as the technology evolves and the program builds trust with participants, the program will expand to include data from mobile and wearable technologies.

Another emphasis in recruitment is the enrollment of underrepresented groups in biomedical research (UBR). The program aims to enroll at least 75% from UBR populations, which are broadly defined as people from minority race/ethnicity, low socioeconomic status, or low educational attainment groups. Historically, biomedical studies have failed to reflect the diversity of the US population, thus failing to fully comprehend the factors that affect disease outcomes in all populations. A 2015 study published in PLOS Medicine found that less than 2 percent of clinical cancer trials included enough underrepresented minorities to fulfill the NIH’s own diversity-related criteria. Thus far, however, the Illinois Consortium has successfully oversampled from UBR populations, with over 55% of participants identifying as Black/African American.

*While other biobanks have successfully collected and stored health data in the past, none have attempted to do so at the scale of the All of Us program, making it truly a giant leap forward in the pursuit of precision medicine.*



**Makda Zewde** is a part-time MS in Biostatistics student at Northwestern University and a Research Specialist at the Institute of Molecular Engineering at the University of Chicago, where she studies immunology. She enjoys communicating public health and scientific topics to the public, and is particularly interested in covering the use of big data in improving public health.

# *An Interview with*

## Debra Duquette

Associate Professor of Medicine (Cardiology) and  
Associate Director of the Northwestern Graduate Program in Genetic Counseling

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By Grace Bellinger

We are surrounded by a plethora of genetic health information. Whether we are doing an at-home DNA test or being screened in a clinic for potential inheritance of sickle cell disease, it has become critical to be able to understand and interpret the implications of our own genetic makeup for our everyday lives. In clinical and research settings, genetic counselors at the forefront of this interpretation and dissemination. The mission of the genetic counseling profession has remained consistent since its inception and aligns with the modern implementation of precision medicine. The National Institutes of Health define precision medicine as “an emerging approach to disease treatment and prevention that takes into account individual variability in genes, environment, and lifestyle.”

Historically, clinical genetic counselors worked primarily in the fields of pediatrics, obstetrics, and cancer. However, specialization has recently extended into specialties such as cardiology and neurology. With the development of technologies such as next-generation sequencing, more generalist genetic counselors may be warranted to provide information about the entire genome to patients. I sat down with Debra Duquette to discuss the profession of genetic counseling and its utilization of big data.

**Grace Bellinger (GB):** Could you tell us a little bit about what genetic counseling is and what it entails?

**Debra Duquette (DD):** Essentially, it is trying to help interpret an individual's genetic, scientific, and medical information based on genes and family history as well as lifestyle and behavior. [This can be useful] for patients, families, or providers. The formal definition of genetic counseling is the process of helping people understand and adapt to the medical, psychological, and familial implications of genetic contributions to disease. The process includes three things: 1) interpretation of family and medical histories to assess the chance of disease occurrence or recurrence; 2) education about inheritance, testing management, prevention, resources, and research; and 3) counseling to promote informed choices and adaptation to the risk or condition.

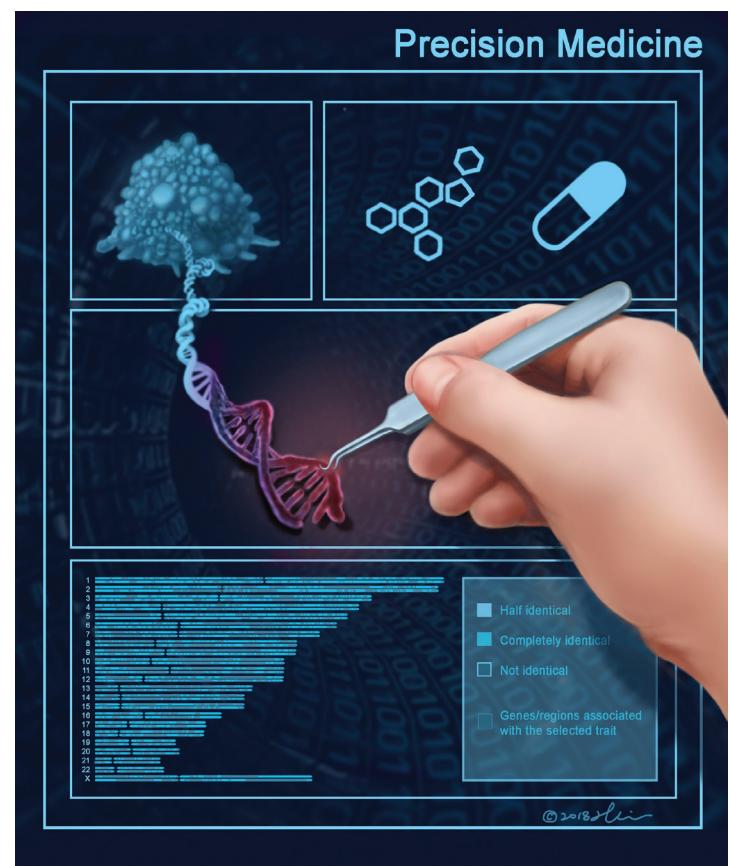
**GB:** What are some common apprehensions or questions people have regarding genetic counseling? What are the typical questions you encounter during a counseling session?

**DD:** There are a variety of different settings genetic counselors [work] in right now. There are genetic counselors in academia and research and in the clinical setting. Interestingly, there are increasingly more genetic counselors in industry with clinical testing laboratories. The setting in which you see a genetic counselor likely determines the most common questions. Traditionally, genetic counselors have been seen mostly in three primary settings: pediatrics, prenatal, and cancer. However, at Northwestern and in the Chicagoland area there are different specialties like cardiology, neurology, etc. Questions may range from issues during pregnancy to pediatric concerns surrounding a child and what a certain diagnosis means for that child's future? There may be family or personal history with cancer, and the question is often the likelihood of inheritance, what it means for other family members, and what can be done to prevent it.

**GB:** Given some of these questions, how does a genetic counselor translate big data information to someone with limited knowledge of the genome?

 “[Common] questions may range from issues during pregnancy to pediatric concerns surrounding a child and what a certain diagnosis means for that child's future.”

**DD:** Most people do not have the knowledge base to really understand what the genome is. I do think with big data, especially with big data in regards to genetics, what often ties things together is precision medicine—or a new term which was recently coined, which I like even more, *precision public health*. Precision medicine and precision public health both have to do with genes—trying to look at genetic interactions with other factors (such as lifestyle) to give people the very best, tailored treatment for them. I think when it comes to big data, it is only with big data that we are going to be able to reach the dreams that are related to precision medicine and precision public health. Genetic counselors are being seen as pivotal [actors] on the frontline in the age of big genomic data. We



can leverage our strong communication skills to provide information tailored to an individual based on their specific risks, family history, and personal history. Genetic counselors are unique in their knowledge base and experiences with providing informed consent for genetic testing.

Interestingly, at Northwestern we have a program called NUgene, which is a biobank of DNA samples and health information. The collected information can then be used by researchers to study the role of genes in the development and treatment of various diseases. NUgene has over 13,500 blood and DNA samples from individuals that have been patients at Northwestern-affiliated outpatient clinics and hospitals. One of the primary investigators on that project is a genetic counselor, Maureen Smith, MS, CGC. I think that really speaks to the leadership and experience that genetic counselors bring to the fields of big data and genomics. Another project is eMERGE. eMERGE just hit a goal by having 3,000 participants in their study. eMERGE uses electronic health records coupled with genetic history to explore the clinical and personal

**“Genetic counselors are being seen as pivotal [actors] on the frontline in the age of big genomic data. We can leverage our strong communication skills to provide information tailored to an individual based on their specific risks, family history, and personal history.”**

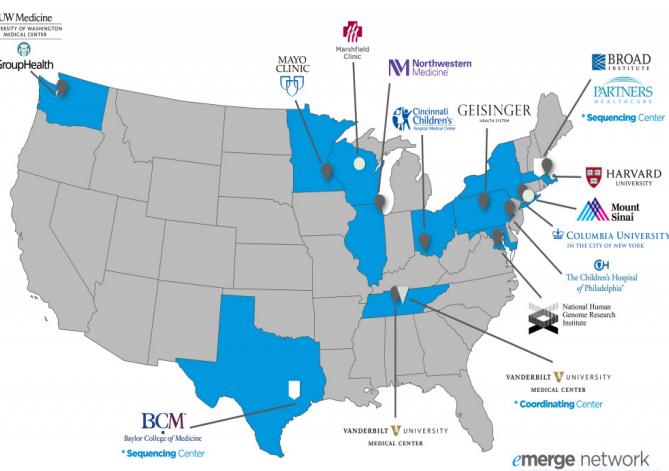
utility of that genetic information. As part of these large studies we find that while we have a lot of information about the genome, we do not yet know what most of it means, often referred to as a “genetic variant of uncertain clinical significance”. Some genetic counselors have full time jobs trying to figure out

what those variants mean and if there is something that is clinically significant or not. That is something that I can see is going to continue to grow and is a new niche for genetic counselors.

**GB:** *What are some of the biggest challenges in genetic counseling and how does one ensure that patients have all of the information that you just listed?*

**DD:** If you ask most counselors right now, the greatest challenge is the shear demand for genetic counselors and how we are going to meet this ever-growing need. For this reason, we have expanded the Northwestern Graduate Program in Genetic Counseling to include 20 students in each cohort. Such growth makes our program the second largest in the world. Additionally, the field is changing rapidly with the advances in technology, the number of genetic tests available, and general awareness due to direct-to-consumer advertising. There has been a lot of hope attached to genetics, yet we are still exploring the true clinical and personal utility of the information. Also, inclusion of underrepresented and minority groups is a challenge that we need to be thinking about.

**GB:** *So how do these types of genetic tests help or hurt disparities already present in healthcare?*



**DD:** We do not know quite yet the answer to that question. I truly believe that any issue for which we know there is a significant health disparity—we have to put that issue front and center. We have to [recognize] those populations first and then think about the technologies and interventions to improve health and reduce health inequities. I really do fear that without putting those populations at the forefront, those who are most likely to receive our services will not be from those populations. Therefore, that could definitely increase health disparities and health inequities.

**GB:** *Do you have any insight into how policy should or should not evolve with the rise of genetic screening?*

**DD:** Policy can take different shapes and forms. A lot of people [ascribe] policy to mean laws. But there are also professional policies, recommendations, a health system policy, or a health plan policy. One of the most critical laws we have right now is a federal law. I don't know how many people are aware, but the Genetic Information Nondiscrimination Act (GINA) was passed in 2008 by President George W. Bush to protect people from genetic discrimination in the workplace and in [health] insurance.

A major concern about pursuing genetic counseling and testing is whether that information could lead to discrimination. Right now GINA does not cover life insurance, but it certainly does cover health insurance and workplace protections. I think that any policy that helps increase access and ensure quality of genetic counseling and testing is critically important. For example, Illinois has genetic counseling licensure, but, believe it or not, not all states in the U.S. do. Kudos to the state of Illinois that genetic counselors are licensed here as this is critical to ensure proper quality of counseling. I also think that it is very important to ensure access for all individuals. For example, right now genetic counseling is not covered under Centers for Medicare and Medicaid Services and this needs to change.

**GB:** *What do you envision as the future of this field?*

**DD:** I think genetic counseling is going to continue to evolve. Our profession started in the prenatal and pediatric realm, where you had to know a lot of things both about prenatal and pediatric genetics, but genetic counselors were not specialized. Now, for instance, we have specialty clinics here at Northwestern for very specific kinds of genetic disorders. People have become specialists in cardiac genetics or neurogenetics. I do not know if that is going to continue. Once we get all of this information that could be cancer-specific, cardiology-specific, or neurology-specific, I do not think that it will be possible that a patient will end up having to see three different genetic counselors. While there may be more specialties developing, I think genetic counseling is going to have to start becoming more general about how this information is conveyed.

Additionally, we have to consider the interface of genetic counseling. It is often done individually on a one-on-one basis. There are new models of delivery being developed such as telemedicine, which is one way to help ensure access to different kinds of populations. It is a way to see more patients. So, I think that there will be innovative and novel methods that genetic counseling can be delivered.

For a long time we have been waiting for the impact of genetic information [to hit]. We thought it was going to happen with the completion of the human genome project—that it was going to be something that affected people's everyday lives, that genomic information was going to be really important for all healthcare providers to know, and the whole public, because it was going to start having a huge impact on their health. I think that is finally going to be very, very true and very, very soon. We have to be ready for this information to make sure that it is used properly, for which genetic counselors are definitely going to be an important part. However, it cannot just be done by genetic counselors alone. It is something that whole populations, whole communities, whole professions are going to have to start getting ready for. That is, perhaps, going to be the biggest challenge.

**For more information on the role of genetic counselors in precision medicine, see a recent article penned by Catherine Wicklund (Director), Debra Duquette (Assistant Director) and Amy Swanson (Assistant Director) referenced below:**

Wicklund CAL, Duquette DA, Swanson AL. Clinical genetic counselors: An asset in the era of precision medicine. Am J Med Genet Part C Semin Med Genet. 2018;178C:63–67. <https://doi.org/10.1002/ajmg.c.31605>  
NIH. (2015). Precision medicine initiative infographic. Retrieved from <https://allofus.nih.gov/about/about-all-us-research-program>

# Using Precision Medicine to Predict Drug Efficacy and Toxicity

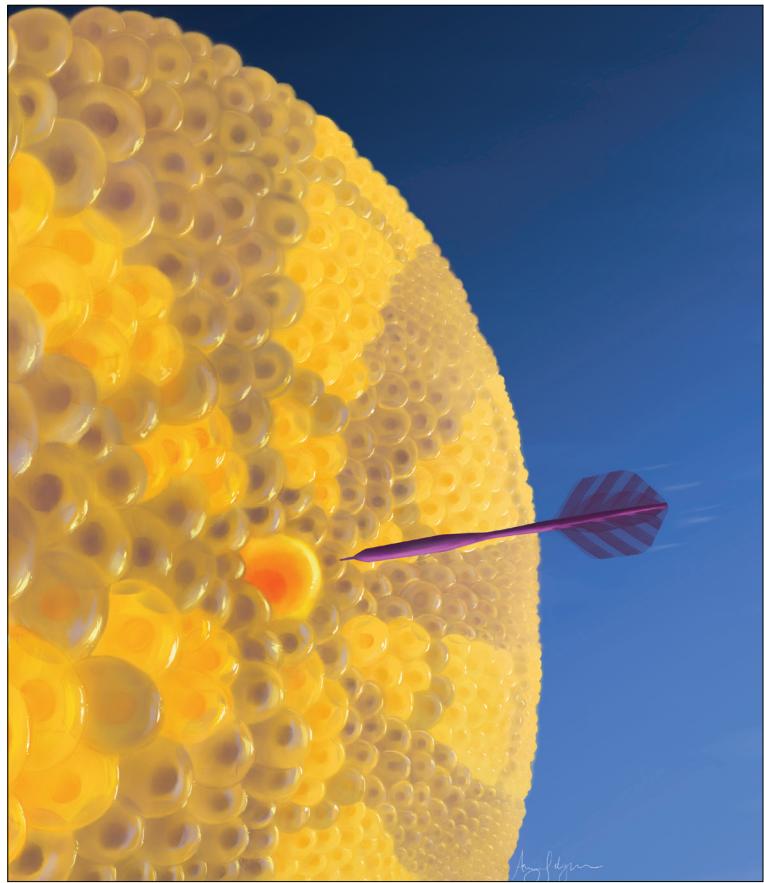
**Paul W. Burridge, PhD**

*Department of Pharmacology, Center for Pharmacogenomics,  
Northwestern University Feinberg School of Medicine.*

The precision medicine revolution is upon us. The ability to collect a variety of patient data, computationally combine and process it, and algorithmically pinpoint a disease management or preventative strategy will profoundly change patient treatment. In the future your doctors will not only know which diseases you are most likely to experience, they will also know how an illness will progress, which drugs should be used for treatment, when and in which combinations, and whether you are likely to suffer side-effects from these interventions.

The wealth of information furnished by a patient's genome makes genomic data a more valuable clinical tool than all other forms of patient information. With advances in DNA sequencing technology, and the cost of research-grade whole-genome sequencing (WGS) now only \$600, there are no other precision medicine tools with such an extreme data-power-to-cost ratio. Genome sequencing is also a one-time cost, as your genome remains essentially the same throughout your life. Although the technology required to read a patient's three billion base-pairs of genomic information is now cheaper and more readily accessible than ever before, our knowledge of how to interpret and act upon this wellspring of data is still profoundly lacking.

The central aim of the field of pharmacogenomics is to investigate the relationship between patient drug response and the genome. The primary pharmacogenomics research method so far has been the genome-wide association study (GWAS), in which DNA is compared from patients who either do or do not have a specific positive or negative drug response. We can then locate single base-pair changes in DNA called single nucleotide polymorphisms (SNPs) that statistically correlate with this difference in drug response. This methodology has been used on a large scale by companies such as 23andMe, where they have collected DNA from millions of subjects and asked them to complete questionnaires to self-identify phenotypes. Conveniently, these participants can be contacted repeatedly to ask questions further clarifying their phenotypes or to collect responses to additional phenotype questions that arise once genotype data have been analyzed. Of course, phenotype-genotype data collected by private companies is proprietary and is therefore not a resource available to the global research community.



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(UIC Biomedical Visualization graduate student)

**“The wealth of information furnished by a patient’s genome makes genomic data a more valuable clinical tool than all other forms of patient information.”**

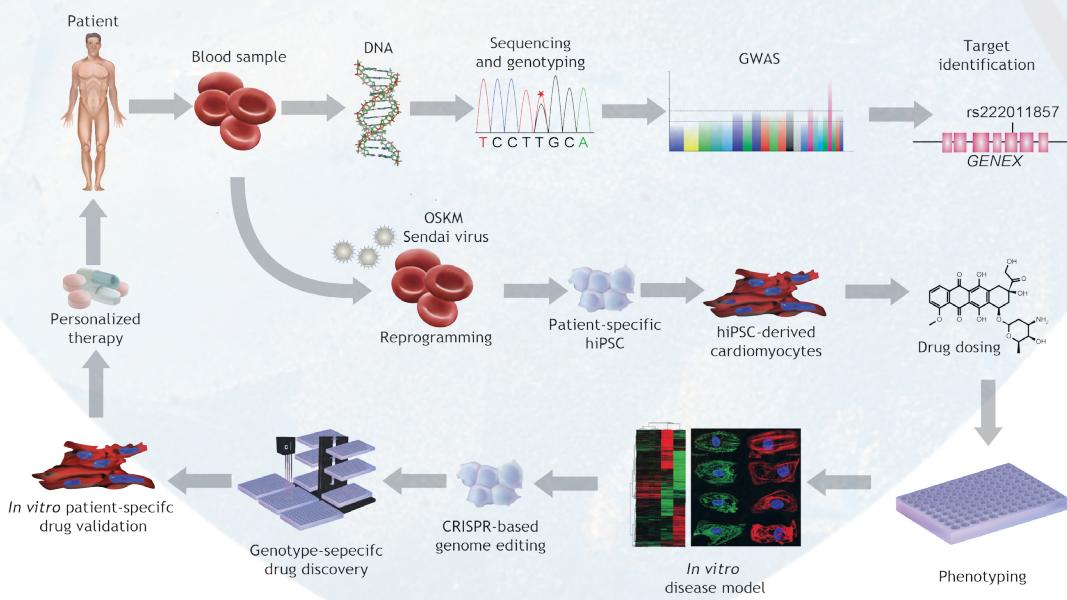
Large-scale academic GWAS studies in the pharmacogenomics field are commonly completed from 300-500 patients, using cost-effective genotyping arrays which assess ~700,000 SNPs and cost as little as \$100 per participant. Although this strategy is useful, the SNPs identified are unlikely to be the true SNP of interest, merely one of the many SNPs co-inherited with it. As the costs of sequencing continue to decline, more of these studies will be completed with WGS, allowing researchers to close this data gap. WGS does have some drawbacks: analyzing 3 billion base-pairs means that each result is less statistically powerful than when measuring 700,000 base-pairs, so even more patients are required to complete a study.

Along with the promise of more readily available WGS, another major area of excitement is progress with the electronic health record (EHR). If all goes as planned, the EHR will be able to store patient data accurately and systematically, in a way that is compatible with the systems of different healthcare providers. Although progress with EHR implementation has been slow, the potential for researchers to recruit patients who have both comprehensive drug response EHR data and their WGSs available would allow GWAS to be performed virtually. This would populate databases with drug-genome correlations with improved statistical quality and eliminate the current substantial costs. The issue

**“[We are] using the human induced pluripotent stem cell (hiPSC) model to take on this question of how to validate human SNPs of interest in drug response [...] looking at why some patients experience toxic damage to the heart as a result of their chemotherapy treatments.”**

with GWAS has always been validation and uncertainty that the correlations identified are real. GWAS findings are commonly not replicated in subsequent studies. Genetic questions have been successfully answered using model organisms, such as the mouse, but animal models are not suitable to experimentally validate human GWAS data, as the majority of GWAS ‘hits’ are not in protein coding regions but in the non-protein coding areas of the genome responsible for modulating gene expression. Non-protein coding areas are not necessarily under the same selective pressure to stay constant as those

coding genes therefore have much more variation between species. In addition, the majority of model organisms are intentionally inbred, making them poor tools to study genetic variability. Therefore, for us to probe how these SNPs function, a human cell type is required, and for gene expression to be accurate this cell type needs to be as similar to the affected cell type as possible, for example if we want to study cardiac myosins, we need functioning cardiomyocytes. Finally, these cells must come from a patient with a specific phenotype, preventing the use of traditional cell lines such as HeLa cells.

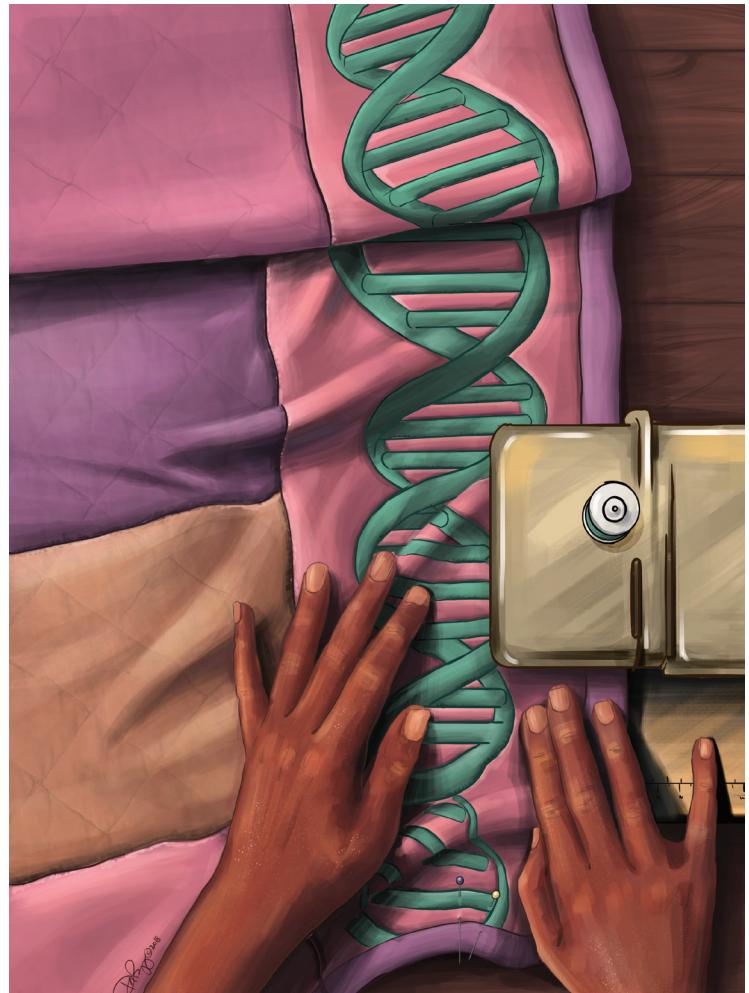


My research group is using the human induced pluripotent stem cell (hiPSC) model to take on this question of how to validate human SNPs of interest in drug response. hiPSCs are made by taking a blood sample from a patient and temporarily inserting four reprogramming genes that cause the cells to switch from one cell type to another. The resulting hiPSC grow rapidly, are essentially immortal, and can theoretically turn (differentiate) into any cell type in the human body. Through years of careful optimization, we have refined our method of differentiating hiPSC to cell types affected by particular drugs, such as heart cells (cardiomyocytes) which contract or “beat” in cell culture, blood vessel lining cells (endothelial cells) that form tubes in culture, and neurons that can be electrically stimulated. Importantly, these cells maintain the genome of the patient from which they were generated and theoretically should also mimic that patient’s drug response.

**“We demonstrated that hiPSC-derived cardiomyocytes from patients who experience chemotherapy-induced cardiotoxicity are in fact more sensitive when treated with the same drug in the lab.”**

We have been looking at why some patients experience toxic damage to the heart as a result of their chemotherapy treatments. For doxorubicin, this cardiotoxicity occurs in ~8% of patients. The heart is a particularly interesting subject for hiPSC modeling because human heart cells are difficult to obtain from patients, as they are generally unwilling to undergo a clinically unnecessary heart biopsy, and heart cells are notoriously difficult to maintain in cell culture. We demonstrated that hiPSC-derived cardiomyocytes from patients who experience chemotherapy-induced cardiotoxicity are in fact more sensitive when treated with the same drug in the lab.

This finding confirms that patient drug sensitivity has a genetic basis because the genetic material is the only factor shared by the *in vitro* cardiomyocytes and the patients from whom the cardiomyocytes were derived. The hiPSC model also allows us to test whether SNPs previously found to be associated with certain effects are in fact causally related to the outcomes in question and to determine whether an effect was in fact caused by a target SNP or merely by a SNP co-inherited with the target. This research can be performed using genome editing tools to correct the SNP in question and see if the patient-specific drug response goes away. The most powerful current genome editing tool is called CRISPR/Cas9, this is a combination of an enzyme that cuts DNA (Cas9) and a guide to tell the Cas9 where to cut. Once the Cas9 has cut, we introduce a small template that the DNA is then tricked into using when repairing the cut, adding or removing our SNP of interest at the same time. We are currently working through massive amounts of GWAS data to experimentally validate previously discovered genome-drug effect relationships.



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(UIC Biomedical Visualization graduate student)

**“This finding confirms that patient drug sensitivity has a genetic basis because the genetic material is the only factor shared by the *in vitro* cardiomyocytes and the patients from whom the cardiomyocytes were derived.”**

Through hiPSC-validation research, it will one day be possible for a clinician to use genetic testing or existing WGS patient data to check whether a patient has genetic variants predicting that a particular drug will work especially well for the patient or will have potentially dangerous side-effects. Over time, the increasing availability of WGS data and EHR infrastructure will allow more SNPs to be discovered and experimentally validated, using hiPSC. A remaining question is whether clinical trials are required to further validate the drug-genome relationship or if the hiPSC-validation will be strong enough to stand alone. The potential elimination or reduction in clinical trials could allow drugs to be brought to market more quickly and reduce overall drug development costs with a substantial potential impact on patient care. Given sufficient availability of paired WGS and EHR data, this crucial validation process could be

completed via efficient computational methods. Another issue will undoubtedly be that database companies may each interpret validated SNP data differently, as is currently the case with disease-related SNPs, making clinicians' responses dependent on their choices of vendor.

In summary, we now have powerful tools to answer pharmacogenomic questions in a thorough and actionable manner. Utilization of this approach will improve drug efficacy, reduce serial testing routine in clinical practice, and minimize unintended drug toxicity. Widespread adoption of precision medicine is not restricted by technological progress but by the uptake of genome sequencing and comprehensive digital health records as standard healthcare practice, both of which are necessary for researchers to vault us into the pharmacogenomic future.



**Dr. Burridge** is an assistant professor in the Department of Pharmacology at Northwestern University Feinberg School of Medicine. Dr. Burridge began his career in genomics and bioinformatics at the Sanger Institute working on the human and mouse genome projects. He completed a PhD in Human Stem Cell Biology at the University of Nottingham before pursuing postdoctoral fellowships at the Johns Hopkins University in Pediatric Oncology and then at Stanford University in Cardiology before becoming an Instructor in Cardiovascular Medicine at Stanford. For more than 15 years, Dr. Burridge has worked on the applications of human pluripotent stem cells (both hESC and hiPSC), concentrating on culture and differentiation methodologies, regenerative medicine, and disease modeling, specifically the pharmacogenomic and molecular mechanisms of chemotherapy-induced cardiomyopathy and heart failure.

# *editorial board*

## **Co Editors-in-Chief**



Nelly Papalambros

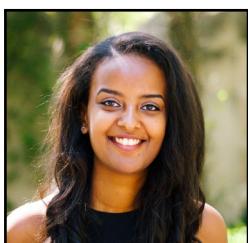


Simona Morochnik

## **Contributing Editors**



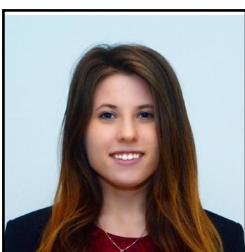
Grace Bellinger



Makda Zewde



Jacqueline Patterson



Jannie Bolotnikov

## **BVIS At University of Illinois, Chicago (UIC)**

Founded in 1921 by Professor Thomas Smith Jones, the Biomedical Visualization graduate program (BVIS) at the University of Illinois at Chicago (UIC) is one of only four accredited graduate programs in North America providing professional training for careers in the visual communication of life science, medicine, and healthcare. The program's unique curriculum attracts graduate students from a variety of disciplines such as medicine, life science, art, digital animation, and computer science.

BVIS utilizes the academic resources of multiple departments throughout the UIC campus to support its interdisciplinary studies. A recently revised curriculum strongly emphasizes effective communication and problem solving and provides a solid foundation in medical science, learning theory, and innovative visualization techniques. In addition to illustration and design, course offerings in visualization technology have been expanded to include animation, interactive media, educational gaming, virtual reality, stereography, haptics, and augmented reality.

Close relationships between UIC BVIS and other prestigious Chicago universities and medical centers provide opportunities for student immersion experiences and effective collaboration with peers. For the sixth consecutive year, BVIS students have contributed editorial illustrations for public health to the Northwestern Public Health Review.



The Northwestern Public Health Review ([nphr.org](http://nphr.org)) was founded in 2013 by Osefame Ewaleifoh and Celeste Mallama, two public health students at Northwestern University. The mission of the NPHR is to stimulate the exchange and cross-pollination of public health ideas, resources and opportunities across the Northwestern community and beyond. Through multiple channels, the student-run NPHR offers opportunities for learning and reporting on public health issues.