BIOGRAPHICAL SKETCH

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NAME: **Michael P. Snyder**

eRA COMMONS USER NAME (credential, e.g., agency login): mpsnyder

POSITION TITLE: Stanford W. Ascherman Professor, Chair, Department of Genetics and Director, Center for Genomics and Personalized Medicine

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.)*

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
University of Rochester, Rochester, NY	B.A.	05/1977	Chemistry/Biology
California Institute of Technology	Ph.D.	09/1982	Biology
Stanford University, Palo Alto, CA	Postdoc	01/1986	Molecular Genetics

A. Personal Statement

We are presently in an big data revolution in which omic and other data (wearables) can be used to characterize biological systems and health. My lab uses and invents a variety of omics approaches including genome sequencing, transcriptomics, proteomics, metabolomics, DNA methylation and microbiome assays to the analysis of complex systems. For example, we carried out the first longitudinal profiling of individuals using multi-omics technologies (genomics, transcriptomics, proteomics, metabolomics, etc.) to track human health, and we also demonstrated using wearable sensors can be used for monitoring health and detecting illness presympthomatically. Furthermore, I have run an independent lab for 34 years and trained approximately 170 postdoctoral fellows and 65 graduate students. Nearly all (>95%) have gone onto successful research careers in academia or industry. For the past 25 years I have run many diversity programs serving underrepresented groups—presently a R25 summer research program. I have hosted many high school, undergraduate, and graduate students as well as postdoctoral fellow in my lab from underrepresented backgrounds. As department chair I have helped build two highly successful departments (Yale Univ., Dept. of Molecular Cellular and Developmental Biology) and (Stanford Univ., Dept. of Genetics). I have written one book for the layperson, *Genomics and Personalized Medicine: What Everyone Needs to Know.*

Ongoing and recently completed projects I would like to highlight include:
RM1 HG007735
(PI: Chang) Role: Co-Investigator
07/01/19 - 06/30/24
Center for Personal Dynamic Regulomes

U54 MD010724
(PIs: Cullen/Maldonado) Role: Project 1 PI
4/11/16 – 3/31/22
Stanford Precision Health for Ethnic and Racial Equity (SPHERE)

U24 DK112348
(PI: Snyder)
12/13/16 – 11/30/22
MoTrPAC Center for Genomics, Transcriptomics and Epigenomics

R01 HL074186
(PI: Rabinovitch) Role: Co-Investigator

02/01/19 – 01/31/24
Pulmonary Hypertension In Genetically Modified Mice

P30 DK116074
(PI: Kim) Role: Co-PI
09/15/17 – 06/30/22
Stanford Diabetes Research Center

P01 HL108797
(PI: Rabinovitch) Role: Co-Investigator
09/15/17 – 06/30/22
Elafin Therapy for Pulmonary Arterial Hypertension

U54 HG010426
(PI: Snyder)
09/19/18 – 06/30/22
Stanford Tissue Mapping Center

R01 AT010232
(PI: Snyder)
09/20/18 – 08/31/22
Multiomic Signature of Microbial Metolites following Prebiotic Fiber Supplementation.

U2C CA233311
(PI: Snyder)
09/30/18 – 06/30/23
Precancer Atlas of Familial Adenomatous Polyposis.

U01 MH1165290
(PI: Urban) Role: Co-PI
06/20/19 – 03/31/24
Integrated, cell type specific functional genomics analyses of regulatory sequence elements and their dynamic interaction networks in neuropsychiatric brain tissues.

R01 HL141105
(PI: Nicolls) Role: Sub-recipient
01/21/19 – 12/31/21
PAVIR; Prime: National institutes of Health / NHLBI
A Critical Role for Leukotriene B4 in Lymphedema.

R25 HG010857
(PI: Snyder)
09/01/19 – 08/31/24
Genomics diversity Summer Program (GDSP) at Stanford.

Leona & Harry B. Helmsley Foundation, Inc.
(PI: Snyder)
09/15/19 – 09/14/24
Investigating the role of human exposome in Crohn's diseases.

B.Positions, Scientific Appointments, and Honors

Positions and Scientific Appointments

2009-	Chair of Genetics and Director of Center of Genomics and Personalized Medicine, Stanford University School of Medicine
2002-2009	Director, Yale Center for Genomics and Proteomics
1998-2004	Chair, MCDB Yale University
1986-2009	Assistant, Associate Full Professor, Department of (MCD) Biology, Yale University, CT
1982-1986	Postdoctoral Fellow, Dept. Biochemistry, Stanford University, Advisor: Dr. Ronald Davis,
1978-1982	Graduate Student, California Institute of Technology, CA Advisor: Dr. Norman Davidson

Other Experience and Professional Memberships

2019	GSA George Beadle Award
2015	Elected American Academy of Arts and Sciences
2014-present	High Impact/Highly Cited Scientists
2011	Named Stanford B.Ascherman Professor
2009	Pioneer Award (HUPO)
2007	CT Medal of Science
2002	Named Lewis B. Cullman Professor
2000	Burroughs Wellcome Scholar Award
1989	Yale Junior Faculty Fellowship
1987-1991	Pew Scholar Award
1982-1985	Helen Hay Whitney Postdoctoral Fellowship

Selected Recent Advisory Committees

Presently	Editor: Genes & Devel., PloS Genetics, Drug Discov., Mol. Systems Biol., Proteomics, Clinical Proteomics
2011-2019	EMBL, Scientific Advisory Committee
2008-2012	Member, NIH MABS study section (Chair, 2010-2012)
2019-	NIDDK, Council Member
2016-	Scripps CTSA, Scientific Advisory Board.Chair since 2019
2001-2010	P.I. Yale Center of Excellence in Genome Sciences
2001-2009	Member Institute of Genetics Advisory Board, CIHR Canada

Commercial

I have founded/cofounded several Biotechnology companies: Excelexis, Protometrix (Purchased by Life Tech, now Thermo), Affomix (Purchased by Illumina), Personalis, SensOmics, Iollo, RTHM, Marble Therpeutics. I have served on Scientific Advisory Boards of many companies.

C. Contributions to Science

1. Personal omics profiling, big data and systems medicine: Although many people talk about personalized medicine, prior to our effort little was happening except in the context of severe diseases. We established the first longitudinal detailed *omics* (genomics, proteomics, metabolomics, autoantibodyomics) profiling of a human for personalized health and medicine. We showed that genomic sequencing can be used to predict disease risk and that, by subsequent monitoring of appropriate markers, the onset of the predicted disease can be readily detected. We have recently performed related integrative omics studies to generate new concepts for autism, and we have used multiomics profiling to examine the effect of weight gain and loss on people with insulin resistance. Finally, we have developed novel machine learning methods for identifying the genetic basis of complex disease, and through their application identified much more of the genetic heritability of AAA, ALS and severe COVID.

a. Schüssler-Fiorenza Rose SM, Contrepois K, Moneghetti KJ, Zhou W, Mishra T, Mataraso S, Dagan-Rosenfeld O, Ganz AB, Dunn J, Hornburg D, Rego S, Perelman D, Ahadi S, Sailani MR, Zhou Y, Leopold SR, Chen J, Ashland M, Christle JW, Avina M, Limcaoco P, Ruiz C, Tan M, Butte AJ, Weinstock GM, Slavich GM, Sodergren E, McLaughlin TL, Haddad F, **Snyder MP**. A longitudinal big data approach for precision health. *Nat Med*. 2019 May;25(5):792-804. PMID: 31068711.
b. Ahadi S, Zhou W, Schüssler-Fiorenza Rose SM, Sailani MR, Contrepois K, Avina M, Ashland M, Brunet A, **Snyder M**. Personal aging markers and ageotypes revealed by deep longitudinal profiling. *Nat Med.* 2020 Jan;26:83-90. PMCID: PMC7301912
c. Chen R, Mias GI, Li-Pook-Than J, Jiang L, Lam HY, Miriami E, Karczewski KJ, Hariharan M, Dewey FE, [30 authors], **Snyder M**. Personal omics profiling reveals dynamic molecular and medical phenotypes. Cell. 2012.148(6): 1293-307. PMID 22424236.
d. Zhang S, Cooper-Knock J, Weimer AK, Shi M, Moll T, Marshall JNG, Harvey C, Nezhad HG, Franklin J, Souza CDS, Ning K, Wang C, Li J, Dilliott AA, Farhan S, Elhaik E, Pasniceanu I, Livesey MR, Eitan C, Hornstein E, Kenna KP; Project MinE ALS Sequencing Consortium, Veldink JH, Ferraiuolo L, Shaw PJ, **Snyder MP.** Genome-wide identification of the genetic basis of amyotrophic lateral sclerosis. Neuron.

2022 Mar 16;110(6):992-1008.e11. doi: 10.1016/j.neuron.2021.12.019. Epub 2022 Jan 18.PMID: 35045337

2. Invention of high throughput gene/protein characterization/Systems Biology: Scientists used to study genes one at a time: *e.g.* one gene, one PhD. We established the first large-scale gene/protein characterization project (prior to DNA microarrays) that involved the characterization of thousands of genes and proteins at once. This project launched the fields of functional genomics and systems biology. It also generated community reagents (transposon libraries) and datasets that were, and still are, valuable resources for the entire scientific community. It led to the invention of protein microarrays by our laboratory and enabled the first large-scale characterization of proteins.

a. Burns N, Grimwade B, Ross-Macdonald PB, Choi EY, Finberg K, Roeder GS, **Snyder M**. Large-scale analysis of gene expression, protein localization and gene disruption in *Saccharomyces cerevisiae*. *Genes Devel.* 1994;8: 1087-105. PMID: 7926789
b. Ross-Macdonald P, Coelho PSR, Roemer T, Agarwal S, Kumar A, Jansen R, Cheung K-H, Sheehan A, Symoniatis D, Umansky L, Heitman M, Nelson FK, Iwasaki H, Hager K, Gerstein M, Miller P, Roeder GS, **Snyder M**. Large-scale analysis of the yeast genome by transposon tagging and gene disruption. *Nature*. 1999;402: 413-418 (Featured in News and Views) PMID: 10586881
c. Zhu H, Bilgin M, Bangham R, Hall D, Casamayor A, Bertone P, Lan N, Jansen R, Bidlingmaier S, Houfek T, Mitchell T, Miller P, Dean DA, Gerstein M, **Snyder M**. Global analysis of protein activities using proteome chips. *Science*. 2001;293: 2101-2105. (Featured in many journals, websites and newspapers.) PMID: 11474067
d. Zhu H, Klemic JF, Chang S, Bertone P, Klemic KG, Smith D, Gerstein M, Reed MA, **Snyder M**. Analysis of yeast protein kinases using protein chips. *Nat Genet.* 2000;26: 283-289. PMID: 11062466

3. Wearables and microsampling for monitoring human health: We have pioneered the use of wearables for monitoring human health and early disease detection. This includes early infectious disease detection (Lyme respiratory viral infection) and these approaches are being actively pursed by scientists and health care systems. We have also pioneered the use of continuous glucose monitors (CGM) for glucose dysregulation detection and monitoring in normal individuals and those with prediabetes.

a. Li X, Dunn J, Salins D, Zhou G, Zhou W, Schüssler-Fiorenza Rose SM, Perelman D, Colbert E, Runge R, Rego S, Sonecha R, Datta S, McLaughlin T, **Snyder MP**. Digital Health: Tracking Physiomes and Activity Using Wearable Biosensors Reveals Useful Health-Related Information. *PLoS Biol*. 2017 Jan 12;15(1):e2001402. eCollection 2017 Jan. PMCID: PMC5230763
b. Hall H, Perelman D, Breschi A, Limcaoco P, Kellogg R, McLaughlin T, Snyder M. Glucotypes reveal new patterns of glucose dysregulation. *PLoS Biol*. 2018 Jul 24;16(7):e2005143. doi: 10.1371/journal.pbio.2005143. eCollection 2018 Jul. PMID: 30040822
c. Mishra T, Wang M, Metwally AA, Bogu GK, Brooks AW, Bahmani A, Alavi A, Celli A, Higgs E, Dagan-Rosenfeld O, Fay B, Kirkpatrick S, Kellogg R, Gibson M, Wang T, Hunting EM, Mamic P, Ganz AB, Rolnik B, Li X, **Snyder MP**. Pre-symptomatic detection of COVID-19 from smartwatch data. Nat Biomed Eng. 2020 Dec;4(12):1208-1220. doi: 10.1038/s41551-020-00640-6. Epub 2020 Nov 18.PMID: 33208926
d. Shen, X., Kellogg, R., Panyard, D.J. *et al.* Multi-omics microsampling for the profiling of lifestyle-associated changes in health. *Nat. Biomed. Eng* (2023). https://doi-org.stanford.idm.oclc.org/10.1038/s41551-022-00999-8

4. Genome and transcriptome characterization technologies: We have developed many technologies for genome and transcriptome characterization. a) Together with Patrick Brown we invented ChIP-chip. Originally we established this for yeast and our group then developed it for mammalian cells, when many leading figures in the field felt this would not be possible. During the course of this work we built the first tiling arrays for a human chromosome and the first high resolution whole genome tiling array. We later adapted this method with new high throughput sequencing technologies (ie ChIP-Seq). b) We also developed paired end sequencing using high-throughput sequence technologies enabling the large scale analysis of structural variation at high resolution for the first time. We demonstrated that most structural variation events were due to nonhomologous recombination, in contrast to what was previously thought. c) We were the first to sequence a genome using next generation technology, at a time when most leading laboratories thought the technology was too error-prone for this to be

possible; we sequenced the genome of the pathogen, *Acinetobacter baumani*, with NGS. D) We invented RNA-sequencing.

a. Smith MG, Gianoulis TA, Pukatzki S, Mekalanos J, Ornston LN, Gerstein M, **Snyder M**. New insights into *Acinetobacter baumannii* pathogenesis revealed by high-density pyrosequencing and transposon mutagenesis. *Genes Dev.* 2007;21: 601-14. PMCID: PMC1820901
b. Korbel JO, Urban AE, Affourtit JP, Godwin B, Grubert F, Simons JF, Kim PM, Palejev D, Carriero NJ, Du L, Taillon BE, Chen Z, Tanzer A, Saunders AC, Chi J, Yang F, Carter NP, Hurles ME, Weissman SM, Harkins TT, Gerstein MB, Egholm M, Snyder M. Paired-end mapping reveals extensive structural variation in the human genome. Science. 2007 Oct 19;318(5849):420-6. Sep 27.PMID: 17901297
c. Nagalakshmi U, Wang Z, Waern K, Shou C, Raha D, Gerstein M, **Snyder M**. The transcriptional landscape of the yeast genome defined by RNA sequencing. *Science*. 2008 Jun 6;320(5881):1344-9. PMCID: PMC2951732
d. Wang Z, Gerstein M, Snyder M. RNA-Seq: a revolutionary tool for transcriptomics. *Nat Rev Genet*. 2009 Jan;10(1):57-63. Review. PMCID: PMC2949280

5. Regulatory Networks and Human Variation: We built many of the first large scale regulatory networks in eucaryotes for TF binding, phosphorylation, etc. Importantly, our laboratory was the first to demonstrate that transcription factor binding varies extensively among closely related species and individuals, indicating that the major difference between closely related organisms and individuals occurs at the level of gene regulation rather than protein coding genes. This was a large surprise at the time as most groups were sequencing different species to try to find regulatory regions using sequence conservation—an approach that has limited success, and in fact is usually wrong. We have extended the work to demonstrate that protein and translation efficiency varies extensively as well. Finally, we have built and analyzed dynamic networks in individuals who have undergone exercise, weight gain and loss and recently fiber intake.

a. Kasowski M, Grubert F, Heffelfinger C, Hariharan M, Asabere A, Waszak SM, … Gerstein MB, Korbel JO, **Snyder M**. Variation in transcription factor binding among humans. *Science*. 2010. 328(5975): 232-5. PMCID: PMC2938768
b. Kasowski M, Kyriazopoulou-Panagiotopoulou S, Grubert F, Zaugg JB, Kundaje A, Liu Y, Boyle AP, Zhang QC, Zakharia F, Spacek DV, Li J, Xie D, Olarerin-George A, Steinmetz LM, Hogenesch JB, Kellis M, Batzoglou S, **Snyder M**. Extensive variation in chromatin states across humans. *Science*. 2013; 342(6159):750-2. PMCID: PMC4075767
c. Gerstein MB, Kundaje A, Hariharan M, Landt SG, Yan KK, Cheng C, Mu XJ, Khurana E, Rozowsky J, … Farnham PJ, Myers RM, Weissman SM, **Snyder M**. Architecture of the human regulatory network derived from ENCODE data. *Nature*. 2012. 489(7414): 91-100. PMCID: PMC4154057
d. Lancaster SM, Lee-McMullen, B, Abbott CW, Quijada JV, Hornburg, D, Park H, Perelman D, Peterson DJ, Tang M, Robinson, A, Ahadi S, Contrepois K, Hung K, Ashland A, McLaughlin T, Boonyanit A, Horning A, Justin L Sonnenburg JL, **Snyder MP**. Global, distinctive, and personal changes in molecular and microbial profiles by specific fibers in humans. Cell Host Microbe. 2022 30:848-862.e7. PMID: 35483363 PMCID: PMC9187607

h-index (Google Scholar) 182; Citations >200K

Lab Website: https://med.stanford.edu/content/sm/snyderlab.html.html

Complete List of Published Work in MyBibliography (over 850 publications total):

http://www.ncbi.nlm.nih.gov/sites/myncbi/michael.snyder.1/collections/48425103/public/