

HAYDEN METSKY

Broad Institute of MIT & Harvard

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Research Interests

I am interested in developing and applying computational techniques that improve medicine and public health. My focus is on building computational approaches—working in tandem with cutting-edge biotechnologies—that enhance how we detect, understand, and respond to infectious diseases.

During my PhD, I led a team that sequenced Zika virus genomes and analyzed Zika's rapid spread across the Americas. The findings demonstrated a dire need for more effective viral surveillance tools. I have since built efficient methods, which harness large-scale genomic data and predictive models, for designing assays that sensitively and comprehensively detect and characterize pathogens.

Education

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| 2014–2020 | Massachusetts Institute of Technology
PhD in Computer Science |
| 2013–2014 | Massachusetts Institute of Technology
MEng in Electrical Engineering & Computer Science |
| 2009–2013 | Massachusetts Institute of Technology
SB in Computer Science and in Physics |

Research and Industry Experience

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| 2020–present | Broad Institute of MIT and Harvard, Sabeti lab
Postdoctoral researcher |
| 2015–2019 | Broad Institute of MIT and Harvard, Sabeti lab
Graduate researcher |
| 2012–2014 | MIT Computer Science and Artificial Intelligence Lab, Kellis lab
Undergraduate and graduate researcher |
| 2011 | Google
Software engineering intern |
| 2010–2011 | Broad Institute of MIT and Harvard, Regev lab
Undergraduate researcher |

Publications and Preprints

Designing viral diagnostics with model-based optimization.

HC Metsky, NL Welch, NJ Haradhvala, L Rumker, YB Zhang, PP Pillai, DK Yang, CM Ackerman, J Weller, PC Blainey, C Myhrvold*, M Mitzenmacher*, PC Sabeti*.

bioRxiv. Apr. 2021. doi:10.1101/2020.11.28.401877.

Deployable CRISPR-Cas13a diagnostic tools to detect and report Ebola and Lassa virus cases in real-time.

KG Barnes*, AE Lachenauer*, A Nitido, S Siddiqui, R Gross, B Beitzel, KJ Siddle, CA Freije, B Dighero-Kemp, SB Mehta, A Carter, J Uwanibe, F Ajogbasile, T Olumade, I Odia, JD Sandi, M Momoh, **HC Metsky**, CK Boehm, AE Lin, M Kemball, DJ Park, L Branco, M Boisen, B Sullivan, MF Amare, AB Tiamiyu, ZF Parker, M Iroezindu, DS Grant, K Modjarrad, C Myhrvold, RF Garry, G Palacios, LE Hensley, SF Schaffner, CT Happi, A Colubri, PC Sabeti.

Nature Communications. Aug. 2020. v. 11, p. 4131. doi:10.1038/s41467-020-17994-9.

Massively multiplexed nucleic acid detection with Cas13.

CM Ackerman*, C Myhrvold*, SG Thakku, CA Freije, **HC Metsky**, DK Yang, SH Ye, CK Boehm, TSF Kosoko-Thoroddsen, J Kehe, TG Nguyen, A Carter, A Kulesa, JR Barnes, VG Dugan, DT Hung, PC Blainey*, PC Sabeti*.

Nature. June 2020. v. 582, p. 277–282. doi:10.1038/s41586-020-2279-8.

CRISPR-based surveillance for COVID-19 using genomically-comprehensive machine learning design.

HC Metsky, CA Freije, TSF Kosoko-Thoroddsen, PC Sabeti, C Myhrvold.

bioRxiv. Mar. 2020. doi:10.1101/2020.02.26.967026.

Combining genomics and epidemiology to track mumps virus transmission in the United States.

S Wohl*, **HC Metsky***, SF Schaffner*, A Piantadosi, M Burns, JA Lewnard, B Chak, LA Krasilnikova, KJ Siddle, CB Matranga, B Bankamp, S Hennigan, B Sabina, EH Byrne, RJ McNall, RR Shah, J Qu, DJ Park, S Gharib, S Fitzgerald, P Barriera, S Fleming, S Lett, PA Rota*, LC Madoff*, BL MacInnis*, NL Yozwiak*, S Smole*, YH Grad*, PC Sabeti*.

PLOS Biology. Feb. 2020. v. 18. doi:10.1371/journal.pbio.3000611.

Programmable inhibition and detection of RNA viruses using Cas13.

CA Freije*, C Myhrvold*, CK Boehm, AE Lin, NL Welch, A Carter, **HC Metsky**, CY Luo, OO Abudayyeh, JS Gootenberg, NL Yozwiak, F Zhang, PC Sabeti.

Molecular Cell. Dec. 2019. v. 76, p. 826–837. doi:10.1016/j.molcel.2019.09.013.

Capturing sequence diversity in metagenomes with comprehensive and scalable probe design.

HC Metsky*, KJ Siddle*, A Gladden-Young, J Qu, DK Yang, P Brehio, A Goldfarb, A Piantadosi, S Wohl, A Carter, AE Lin, KG Barnes, DC Tully, B Corleis, S Hennigan, G Barbosa-Lima, YR Vieira, LM Paul, AL Tan, KF Garcia, LA Parham, I Odia, P Eromon, OA Folarin, A Goba, Viral Hemorrhagic Fever Consortium, E Simon-Lorière, L Hensley, A Balmaseda, E Harris, DS Kwon, TM Allen, JA Runstadler, S Smole, FA Bozza, TML Souza, S Isern, SF Michael, I Lorenzana, L Gehrke, I Bosch, G Ebel, DS Grant, CT Happi, DJ Park, A Gnirke, PC Sabeti*, CB Matranga*.

Nature Biotechnology. Feb. 2019. v. 37, p. 160–168. doi:10.1038/s41587-018-0006-x.

Field-deployable viral diagnostics using CRISPR-Cas13.

C Myhrvold*, CA Freije*, JS Gootenberg, OO Abudayyeh, **HC Metsky**, AF Durbin, MJ Kellner, AL Tan, LM Paul, LA Parham, KF Garcia, KG Barnes, B Chak, A Mondini, ML Nogueira, S Isern, SF Michael, I Lorenzana, NL Yozwiak, BL MacInnis, I Bosch, L Gehrke, F Zhang, PC Sabeti.

Science. Apr. 2018. v. 360, p. 444–448. doi:10.1126/science.aas8836.

Rapid detection of Powassan virus in a patient with encephalitis by metagenomic sequencing.

A Piantadosi, S Kanjilal, V Ganesh, A Khanna, EP Hyle, J Rosand, T Bold, **HC Metsky**, J Lemieux, MJ Leone, L Freimark, CB Matranga, G Adams, G McGrath, S Zamirpour, S Telford, 3rd, E Rosenberg, T Cho, MP Frosch, MB Goldberg, SS Mukerji, PC Sabeti.

Clinical Infectious Diseases. Feb. 2018. v. 66, p. 789–792. doi:10.1093/cid/cix792.

Zika virus evolution and spread in the Americas.

HC Metsky*, CB Matranga*, S Wohl*, SF Schaffner*, CA Freije, SM Winnicki, K West, J Qu, ML Baniecki, A Gladden-Young, AE Lin, CH Tomkins-Tinch, SH Ye, DJ Park, CY Luo, KG Barnes, RR Shah, B Chak, G Barbosa-Lima, E Delatorre, YR Vieira, LM Paul, AL Tan, CM Barcellona, MC Porcelli, C Vasquez, AC Cannons, MR Cone, KN Hogan, EW Kopp, JJ Anzinger, KF Garcia, LA Parham, RMG Ramírez, MCM Montoya, DP Rojas, CM Brown, S Hennigan, B Sabina, S Scotland, K Gangavarapu, ND Grubaugh, G Oliveira, R Robles-Sikisaka, A Rambaut, L Gehrke, S Smole, ME Halloran, L Villar, S Mattar, I Lorenzana, J Cerbino-Neto, C Valim, W Degraeve, PT Bozza, A Gnirke, KG Andersen*, S Isern*, SF Michael*, FA Bozza*, TML Souza*, I Bosch*, NL Yozwiak*, BL MacInnis*, PC Sabeti*.

Nature. June 2017. v. 546, p. 411–415. doi:10.1038/nature22402.

* co-first/last

Software

ADAPT — <https://github.com/broadinstitute/adapt>

CATCH — <https://github.com/broadinstitute/catch>

Conference and Seminar Presentations

Viral diagnostic design with model-based optimization

- *Models, Inference, & Algorithms Initiative*, Broad Institute. Talk, Feb. 2021.

Capturing sequence diversity in metagenomes with comprehensive and scalable probe design

- *MIT-Harvard Microbiome Symposium*, MIT. Poster, Mar. 2019.
- *Virus Genomics and Evolution Conference*, Wellcome Genome Campus, Cambridge, UK. Poster, June 2018.

Genomics-guided pathogen surveillance and outbreak response

- *Bio-IT World Conference & Expo*, Boston, MA. Talk, May 2018.

Sequencing Zika virus and tracing its evolution and spread in the Americas

- *Bauer Forum*, Harvard University. Talk, June 2017 (with others).
- *Infectious Disease & Microbiome Program*, Broad Institute. Talk, June 2017 (with others).
- *BroadWay*, Broad Institute. Talk, Nov. 2016 (with others).

Capture methods for identification and whole-genome sequencing of viral pathogens

- *NHGRI Research Training and Career Development Meeting*, Bethesda, MD. Poster, Apr. 2016.

Teaching Experience

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| Spring 2014 | Teaching Assistant for MIT 6.046: <i>Design and Analysis of Algorithms</i>
Taught sections to ~70 students and held office hours. Student rating: 6.8/7. |
| Fall 2013 | Teaching Assistant for MIT 6.046: <i>Design and Analysis of Algorithms</i>
Taught sections to ~50 students and held office hours. Student rating: 6.4/7. |
| Spring 2013 | Teaching Assistant for MIT 6.005: <i>Software Construction</i>
Taught sections to ~40 students and held office hours. Student rating: 6.1/7. |
| Spring 2012 | Lab Assistant for MIT 6.01: <i>Introduction to EE and CS</i> |

Peer Review

Peer reviewed articles for journals including *Nature Biotechnology*, *Nature Medicine*, *Cell Reports*, and *Scientific Reports*.

Honors and Awards

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| 2020 | Dimitris N. Chorafas Prize
Awarded by Dimitris N. Chorafas Foundation to “the best doctoral student(s) in the hard sciences in each partner university.” |
| 2014 | Frederick C. Hennie III Award for Outstanding Teaching
Awarded by MIT EECS Department to recognize excellence in teaching. |
| 2013 | Anna Pogoyants UROP Award
Awarded by MIT EECS Department to an undergraduate for an “outstanding undergraduate research project” in computer science. |
| 2009 | Finalist in Intel Science Talent Search |
| 2008 | Sixth place in Siemens Competition in Math, Science, and Technology |