National Cybersecurity Center of Excellence

NCCoE Virtual Workshop on Cybersecurity of Genomic Data

Wednesday, January 26, 2022, 11:00 AM – 4:30 PM (ET)



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This webinar is being recorded.



AGENDA



Segment	Time
Segment 1: Workshop Overview and Background	11:00 AM - 11:40 AM
Segment 2: Keynotes	11:40 AM – 12:20 PM
Segment 3: Challenges from the Field	12:20 PM – 12:50 PM
Intermission	12:50 PM – 1:30 PM
Segment 4: Challenges Sessions	1:30 PM – 2:25 PM
Break	2:25 PM – 2:35 PM
Segment 4 (Continued): Challenges Sessions	2:35 PM – 3:45 PM
Break	3:45 PM – 3:50 PM
Segment 5: Open Lightning Round	3:50 PM – 4:20 PM
Segment 6: Next Steps	4:20 PM – 4:30 PM

Welcome to the NCCoE Virtual Workshop on Cybersecurity of Genomic Data

Natalia Martin, NIST





Virtual Workshop on the Cybersecurity of Genomic Data

Natalia Martin, Acting Director for National Cybersecurity Center of Excellence (NCCOE), NIST



About the NCCoE





WHO WE ARE



A solution-driven, collaborative hub addressing complex cybersecurity problems



OUR GOALS





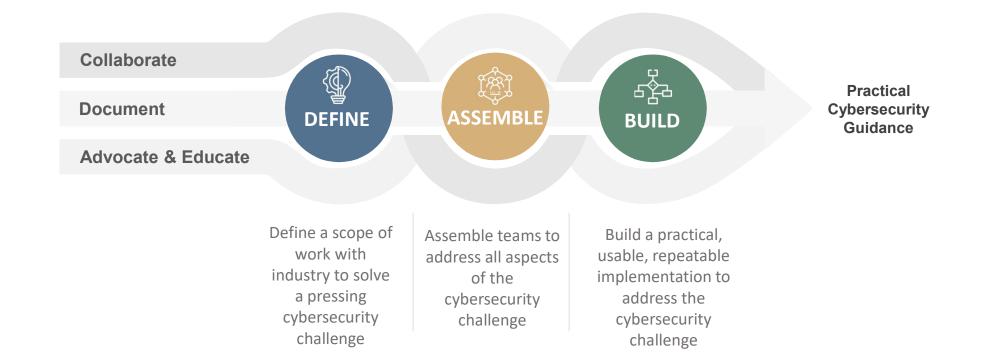
Improve cybersecurity for businesses and commerce

Lower the learning curve for cybersecurity

Spark innovation in secure technology

OUR APPROACH





Virtual Workshop on the Cybersecurity of Genomic Data

Workshop Overview

Ron Pulivarti, NIST





Housekeeping

- We support the health and well being for all.
 - We are supporting virtual collaboration.
 - We have three breaks planned for the day.
- We want audience engagement.
 - Please pose your questions for today's workshop using the Q&A window.
 - Please voice your insights in the Open Lightening Round from 3:50 4:30 PM.
- We intend to share our learnings today.
 - We are recording this session for future post on the NCCoE Website.
 - We will summarize key insights.





NIST Experiences in Genomics, Cybersecurity, and Privacy

Samantha Maragh (NIST) Naomi Lefkovitz (NIST) Ron Pulivarti (NIST)





Human Genomics at NIST

Samantha Maragh Leader, Genome Editing Program



The Human Genome





- The instruction code for humans
- ~6.4 billion letters long
- Present in each cell of a person
- ~ Half inherited from each biological parent
- Code is highly similar between people, but each person has a unique identifiable sequence



Uses of human genomic information



Treatment A

Treatment B

Treatment C

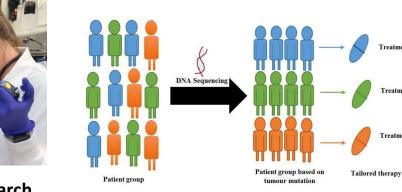




Human Identification



Population Diversity and Ancestry



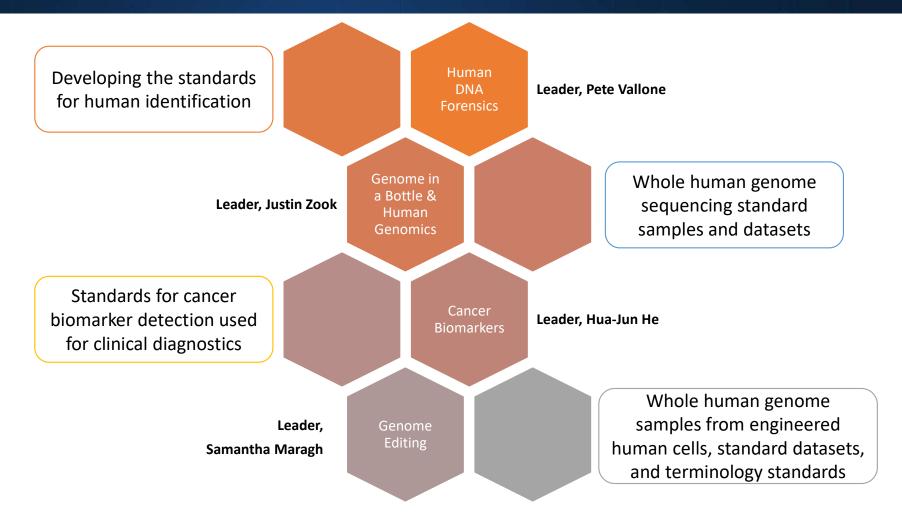
Human Health: Treatment



Human Health: Diagnostics

Scientific Research

NIST expertise with human genomics



NIST

NIST formed the Genome in a Bottle Consortium in 2012 NIST

GIAB has characterized variants in 7 human genomes and released NIST whole genome DNA standards

Pilot Genome National Institute of Standards & Technology NA12878 Report of I nvestigation HG001* Reference Material 8391 Human DNA for Whole-Genome Variant Assessment (Son of Eastern European Ashkenazim Jewish Ancestry) This Reference Material (RM) is intended for validation, optimization, and process evaluation purposes. It consists This Keterence Material (KM) is infeated for valuation, optimization, and process evaluation purposes. It consists of a mide whole futuring genome support of Eastern European Addenzazing break in accuse, yand it can be used and the second genomic DNA extracted from a single large growth of human lymphoblastoid cell line GM24386 from the Coriel institute for Medical Research (Canades, NJ). The vial contains approximately 10 go of genomic DNA, with the peak of the nominal length distribution longer than 45.5 kb, as referenced by Lambda DNA, and the DNA is in TE buffer (10 mM TRIS; 1 mM EDTA, pH 8.0). AJ Trio HG003* HG004* HG002* 8392 Chinese Trio HG007 HG006 HG005*

*NIST RMs developed from large batches of DNA

nature biotechnology

Resource Published: 01 April 2019

An open resource for accurately benchmarking small variant and reference calls

Justin M. Zook ⊠, Jennifer McDaniel, Nathan D. Olson, Justin Wagner, Hemang Parikh, Haynes Heaton, Sean A. Irvine, Len Trigg, Rebecca Truty, Cory Y. McLean, Francisco M. De La Vega, Chunlin Xiao, Stephen Sherry & Marc Salit

nature biotechnology

Resource | Published: 15 June 2020

A robust benchmark for detection of germline large deletions and insertions

Justin M. Zook 🖂, Nancy F. Hansen, [...] Marc Salit

nature biotechnology

Analysis | Published: 11 March 2019

Best practices for benchmarking germline small-variant calls in human genomes

Peter Krusche, Len Trigg, Paul C. Boutros, Christopher E. Mason, Francisco M. De La Vega, Benjamin L. Moore, Mar Gonzalez-Porta, Michael A. Eberle, Zivana Tezak, Samir Lababidi, Rebecca Truty, George Asimenos, Birgit Funke, Mark Fleharty, Brad A. Chapman, Marc Salit, Justin M. Zook ⊡ & the Global Alliance for Genomics and Health Benchmarking Team

PLOS COMPUTATIONAL BIOLOGY

G OPEN ACCESS D PEER-REVIEWE

A crowdsourced set of curated structural variants for the human genome

Lesley M. Chapman, Noah Spies, Patrick Pai, Chun Shen Lim, Andrew Carroll, Giuseppe Narzisi, Christopher M. Watson, Christos Proukakis, Wayne E. Clarke, Naoki Nariai, Eric Dawson, Garan Jones, Daniel Blankenberg, [...]Justin M. Zook 📾



CRISPR technologies and uses

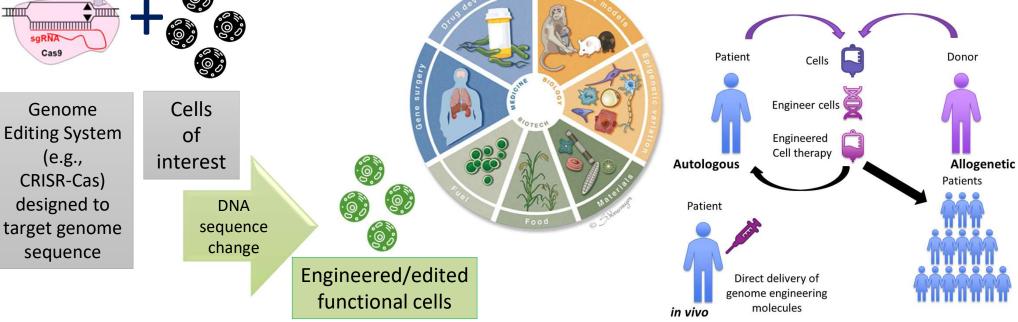
CRISPR-Cas

CRISPR - Clustered Regularly Interspaced Short Palindromic Repeats Cas - CRISPR associated protein

CRISPR-Cas system were identified in nature as bacterial immune systems and have been pivoted to enable modification of the genetic code within cells at designed target positions (genome editing)









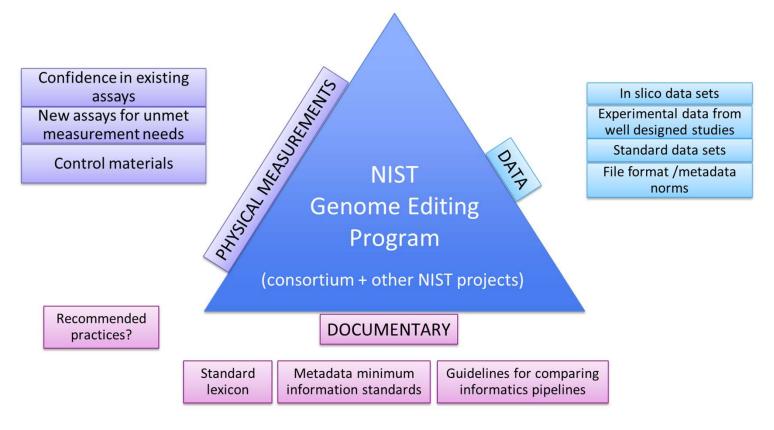


NIST experience with CRISPR technologies



Vision: Support quality in measurements for translating genome edited product to market

Goal: Develop measurement tools standards to <u>increase the confidence</u> of utilizing genome editing technologies in research and commercial products.

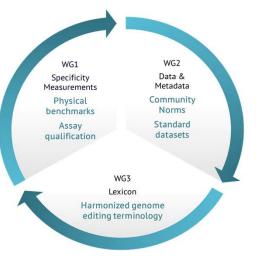


NIST Genome Editing Consortium (launched October 2018)

MISSION

Convene experts across academia, industry, non-profit & government to addresses the measurements and standards needed to increase confidence of utilizing genome editing technologies in research and commercial products

ORGANIZATION



MEMBER BENEFITS

- Access to a neutral forum for addressing precompetitive needs
- Participation in the development of experimental benchmarks, guidelines and terminology
- Access to tools developed by the consortium ahead of public release

MEMBERS

- KromaTiD Lonza Macrogen Mass General Hospital Mission Bio Novartis
- New England Biolabs NIH/NINDS NIH SCGE
- Precision Biosciences .
- Scientific Twinstrand **Bioscineces** UCSC WhiteLab Genomics

Sangamo Therapeutics

St. Jude Children's

Research Hospital

SeQure Dx

Synthego

ThermoFisher

NIST coordinates with FDA and Center for Veterinary Medicine (CVM)

bionano



CATALYTI

HI INSCRIPTA

* Former members

contribute \$20,000 annually or in-kind

Agilent

Aldevron

Bio-Rad

Cergentis

DARPA

EMBL-EBI

FDA CBER

Illumina

Inscripta

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Applied StemCell

Bionano Genomics

Caribou Biosciences

Catalytic Data Science

AstraZeneca

Bluebird bio*



Importance of securing human genomics data NIST

- ✓ Data integrity
- ✓ Data reliability



- \checkmark Maintain limited access to individual genomic information
 - ✓ Protect knowledge / intellectual property
 - ✓ Data reusability / prevent loss
 - Prevent against nefarious use or misuse
 - ✓ Privacy

Credit: mcmurryjulie

Contact Us

Contact

Samantha Maragh Leader, Genome Editing Program

Email address

samantha@nist.gov





Privacy at NIST

Naomi Lefkovitz



Relationship Between Cybersecurity and Privacy Risk



Cybersecurity Risks

associated with cybersecurity incidents arising from loss of confidentiality, integrity, or availability cyber securityrelated privacy events

Privacy Risks

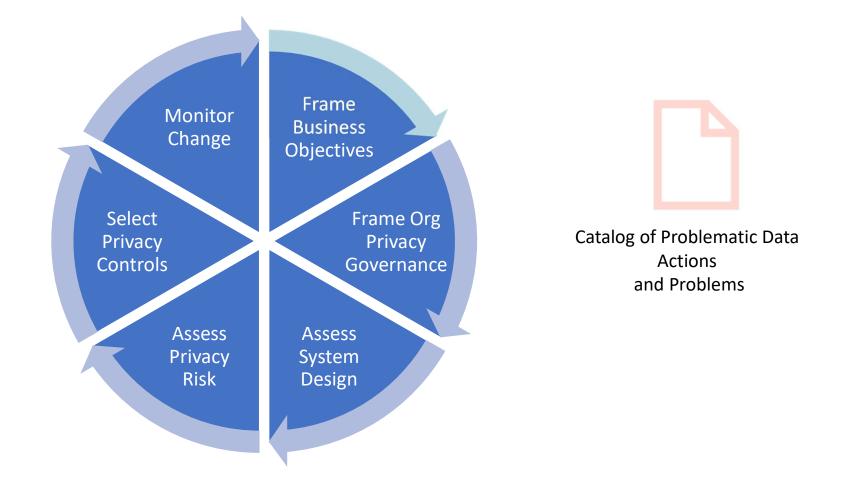
associated with privacy events arising from data processing **Data:** A representation of information, including digital and non-digital formats

Privacy Event: The occurrence or potential occurrence of problematic data actions

Data Processing: The collective set of data actions (i.e., the complete data life cycle, including, but not limited to collection, retention, logging, generation, transformation, use, disclosure, sharing, transmission, and disposal)

Privacy Risk: The likelihood that individuals will experience problems resulting from data processing, and the impact should they occur

NIST Privacy Risk Assessment Methodology (PRAM)



NIST Privacy Engineering Objectives



Predictability: enabling reliable assumptions by individuals, owners, and operators about data and their processing by a system, product, or service.

Manageability: providing the capability for granular administration of data, including alteration, deletion, and selective disclosure.

Disassociability: enabling the processing of data or events without association to individuals or devices beyond the operational requirements of the system.

NIST Privacy Framework Core



Functions	Categories	Subcategories
Identify-P		
Govern-P		
Control-P		
Communicate-P		
Protect-P		

Resources





Websites

https://www.nist.gov/privacyframework



Mailing List

List.nist.gov/privacyframework



Contact Us

PrivacyFramework@nist.gov

National Institute of Standards and Technology - Cybersecurity

Ron Pulivarti, Senior Cybersecurity Engineer for the Healthcare Sector at the National Cybersecurity Center of Excellence (NCCoE), which is part of NIST



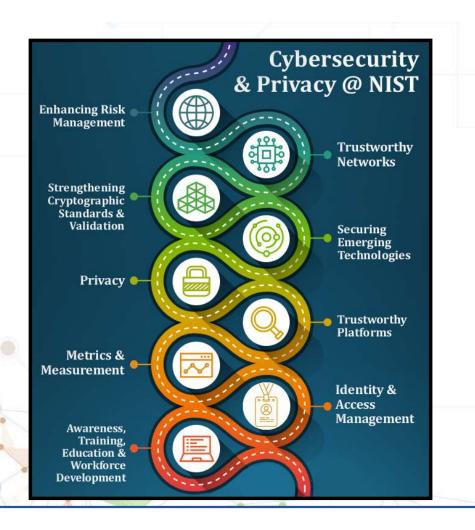
National Institute of Standards and Technology U.S. Department of Commerce

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Celebrating 50 years of Cybersecurity at NIST

NIST National I Standards U.S. Depart





NINE PRIORITY AREAS:

Enhancing Risk Management Trustworthy Networks Strengthening Cryptographic Standards & Validation Securing Emerging Technologies Privacy Trustworthy Platforms Metrics & Measurement Identity & Access Management Awareness, Training, Education & Workforce Development

NIST National In: Standards of U.S. Departme

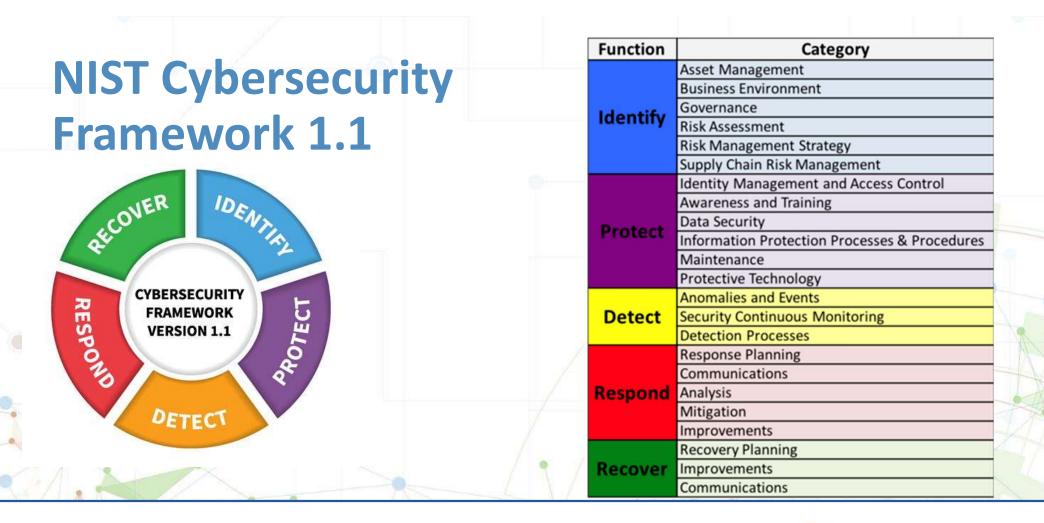




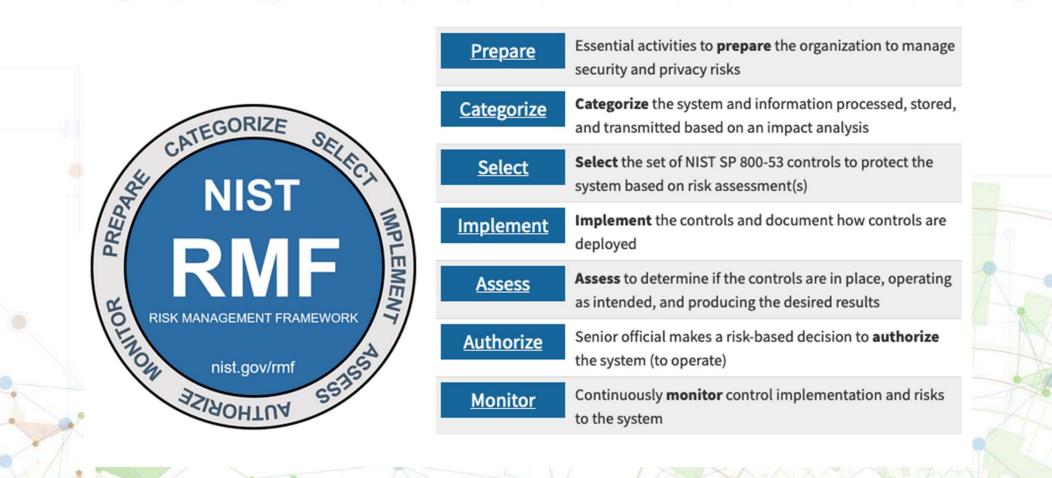


NIST





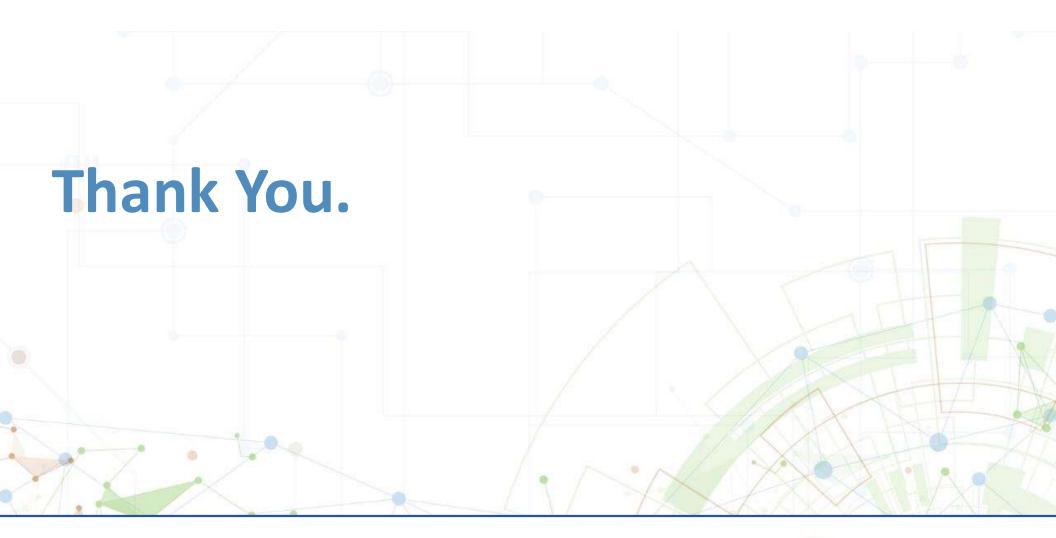














NIST Experiences in Genomics, Cybersecurity, and Privacy

Moderated Questions and Answers

