

Using "Big Data" to Discover Cancer Mechanisms

CRCHD Professional Development Workshop

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A program of the National Cancer Institute of the National Institutes of Health

The NCI supports cancer research across the disease spectrum.

Division of Cancer Biology Population-based research Basic research seeks to explores the causes of cancer, understand the fundamental cancer trends, and factors that aspects of nature. It provides the affect the delivery and outcomes foundation for advances against of cancer care in specific cancer. populations. Translational research moves Clinical research tests drugs, basic research findings into the medical devices, or other clinic and clinical research findings into everyday care. In interventions in human volunteers to improve all aspects turn, results from clinical and population-based studies can of patient care. quide basic research.

DCB supports the most basic cancer research at NCI, with an investigator initiated (R01/R21/P01) portfolio of ~2500 awards.

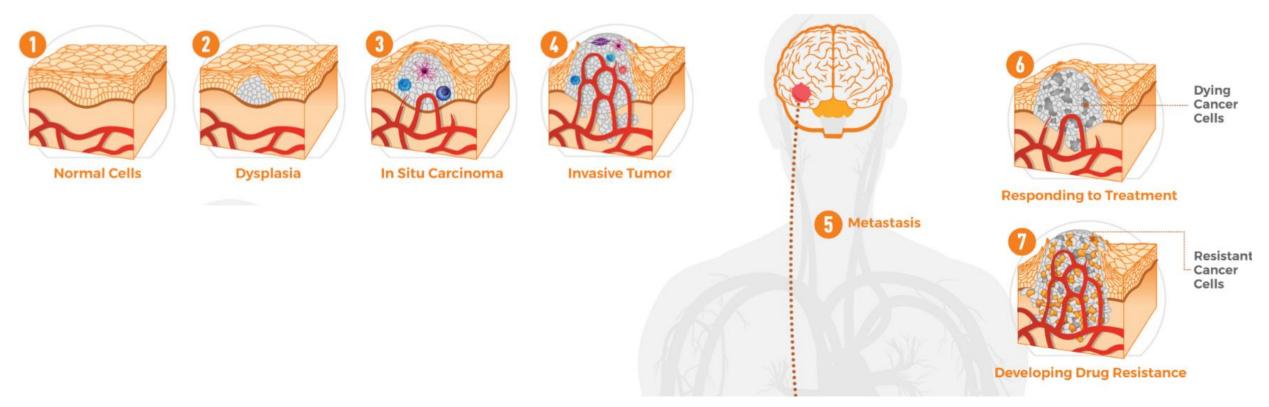


Including a wide range of programs generating "Big Data" and (importantly!) computational approaches

- ✓ The Cancer Genome Atlas (TCGA)
- ✓ Therapeutically Applicable Research To Generate Effective Treatments (<u>TARGET</u>)
- ✓ Clinical Proteomics Tumor Analysis Consortium (<u>CPTAC</u>)
- ✓ The Cancer Imaging Archive (TCIA)
- ✓ Surveillance, Epidemiology, and End Results Program (<u>SEER</u>)
- ✓ Cancer Target Discovery and Development (<u>CTD²</u>)
- ✓ Informatics Technology for Cancer Research (ITCR)
- ✓ Cancer Intervention and Surveillance Modeling Network (CISNET)
- ✓ Physical Science in Oncology Network (<u>PS-ON</u>)
- ✓ The Human Tumor Atlas Network (<u>HTAN</u>)
- ✓ Cancer Systems Biology Consortium (<u>CSBC</u>)

Cancer Moonshot Recommendation I: Generation of Human Tumor Atlases

Create dynamic 3D maps of human tumor evolution to document the genetic lesions and cellular interactions of each tumor as it evolves from a precancerous lesion to advanced cancer.



Adapted from "Cancer and the Human Tumor Atlas Network" NCI's Annual Plan and Budget for Fiscal Year 2020

What is a human tumor atlas?

A comprehensive human tumor atlas is defined as the **multidimensional molecular, cellular, and morphological mapping** of human cancers, **complemented with critical spatial information** (at the molecular, cellular, and/or tissue level) that **facilitate visualization of the structure, composition, and multiscale interactions** within the tumor ecosystem.

Human Tumor Atlas Network (HTAN)

Constructing 3D atlases of the multidimensional cellular, morphological, molecular features of human cancers over time.

- Focus on *high-risk* cancers; including those responsive/non-responsive to immunotherapy; pediatric cancers
- Represent a *diverse patient population*, including minority and underserved patients
- Describe transitions during cancer: premalignant lesions to malignancy, locally invasive to metastatic cancer, and the development of therapeutic resistance
- Enable *predictive modeling* to refine therapeutic choices for patients.

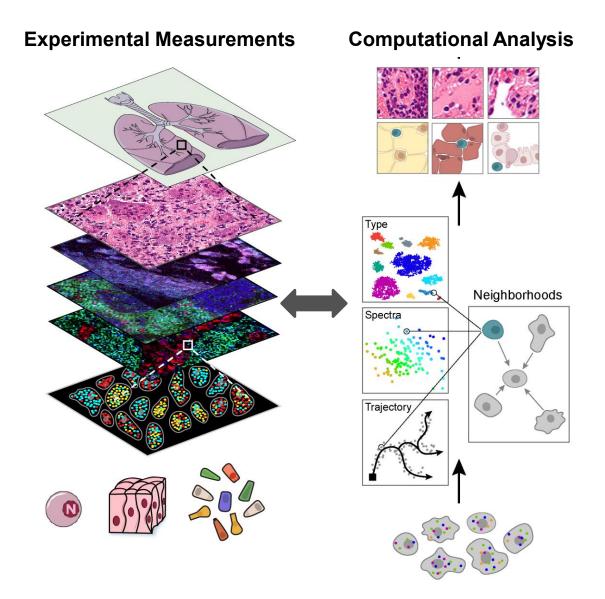


Figure from A. Regev and HTAPP Team

The HTAN in the context of other "Atlas" initiatives:



THE CANCER GENOME ATLAS

National Cancer Institute National Human Genome Research Institute





CLINICAL PROTEOMIC TUMOR ANALYSIS CONSORTIUM









The Human <u>BioMolecular</u> Atlas Platform (<u>HuBMAP</u>)

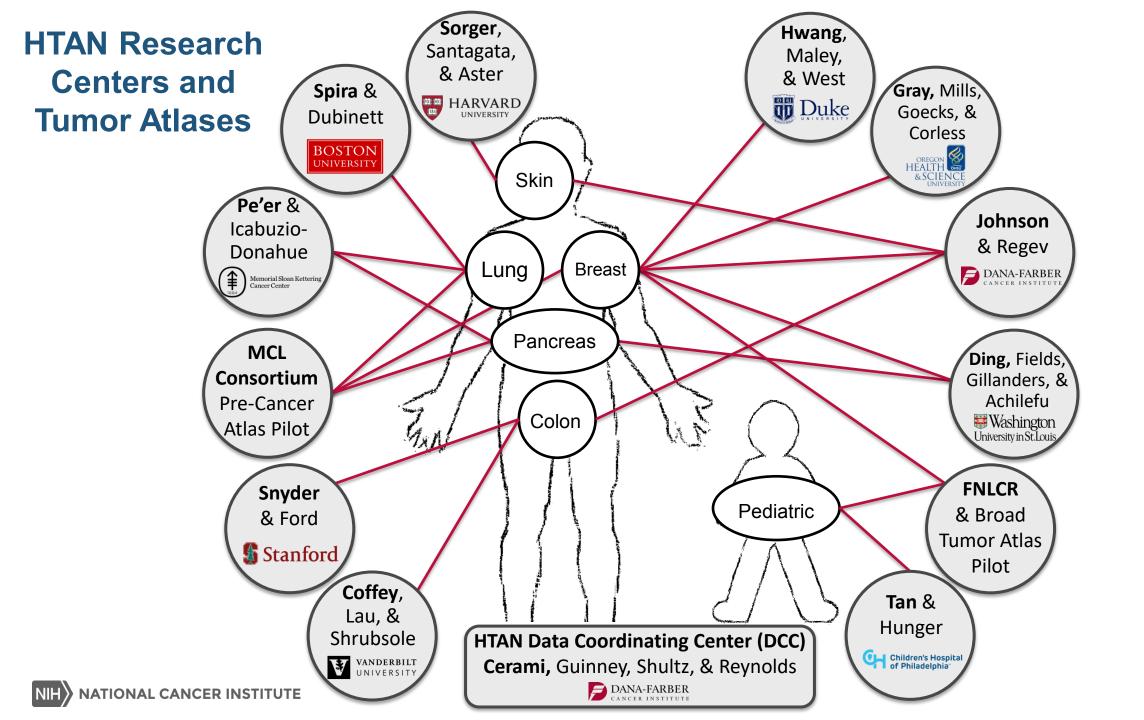
NIH Common Fund Program

Human Tumor Atlas Network

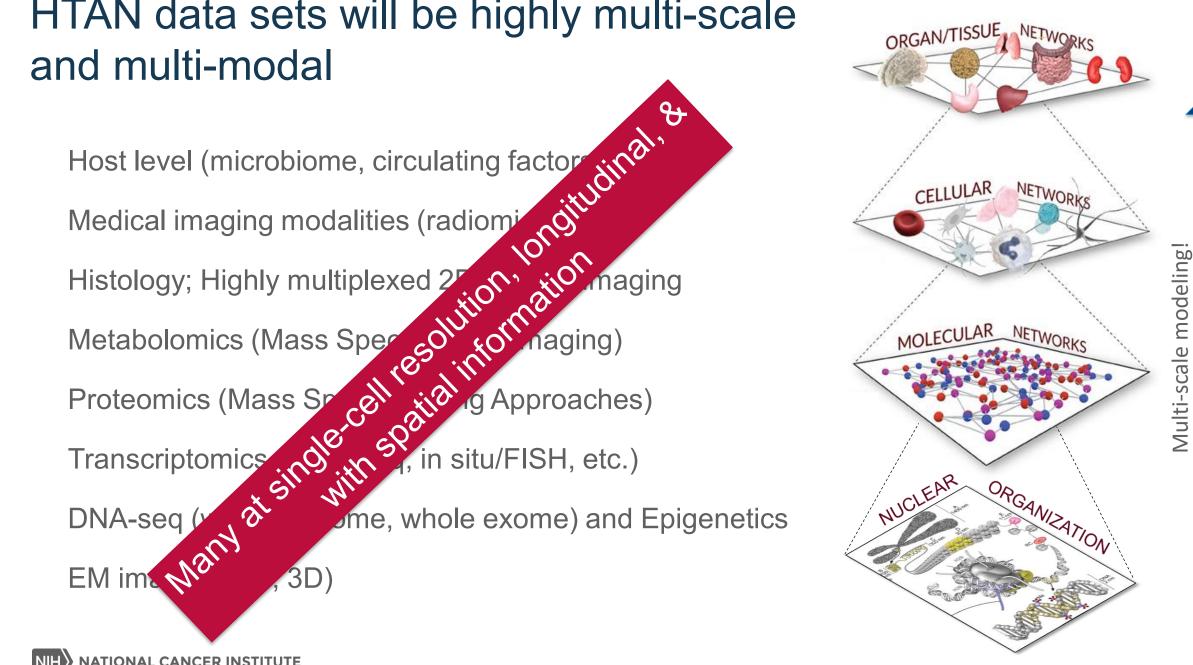
- Emphasis on spatial relationships and interactions
- Prospective/longitudinal sample collection (time)
- Extensive clinical data
- Atlases describing disease transitions



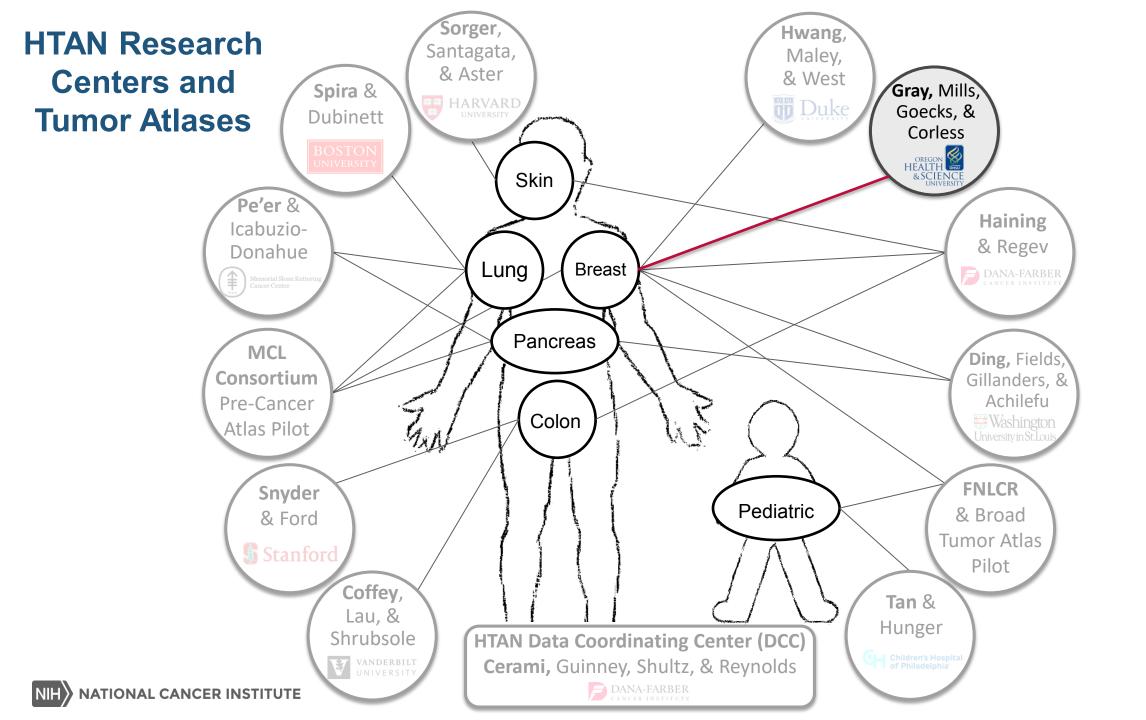




HTAN data sets will be highly multi-scale and multi-modal



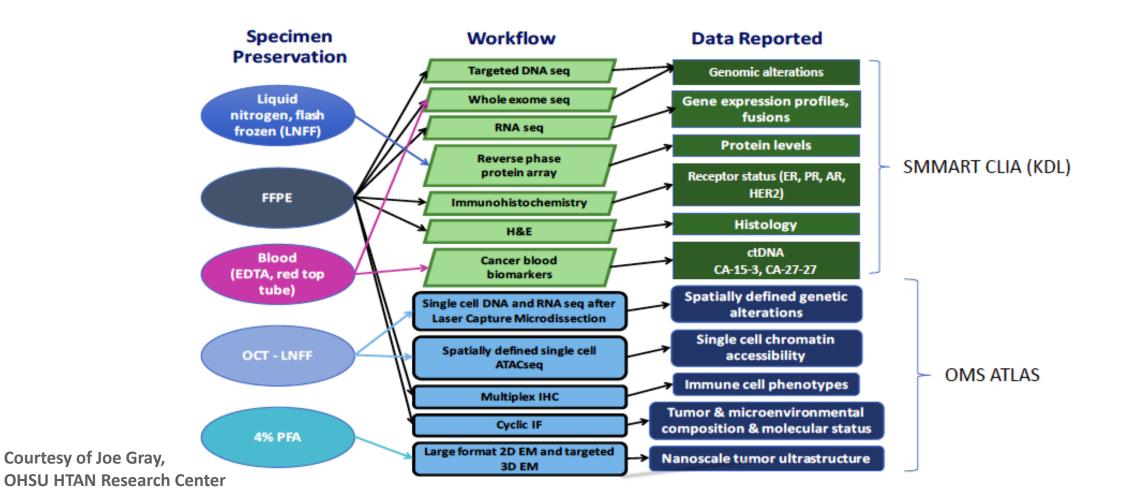
Data Integratior

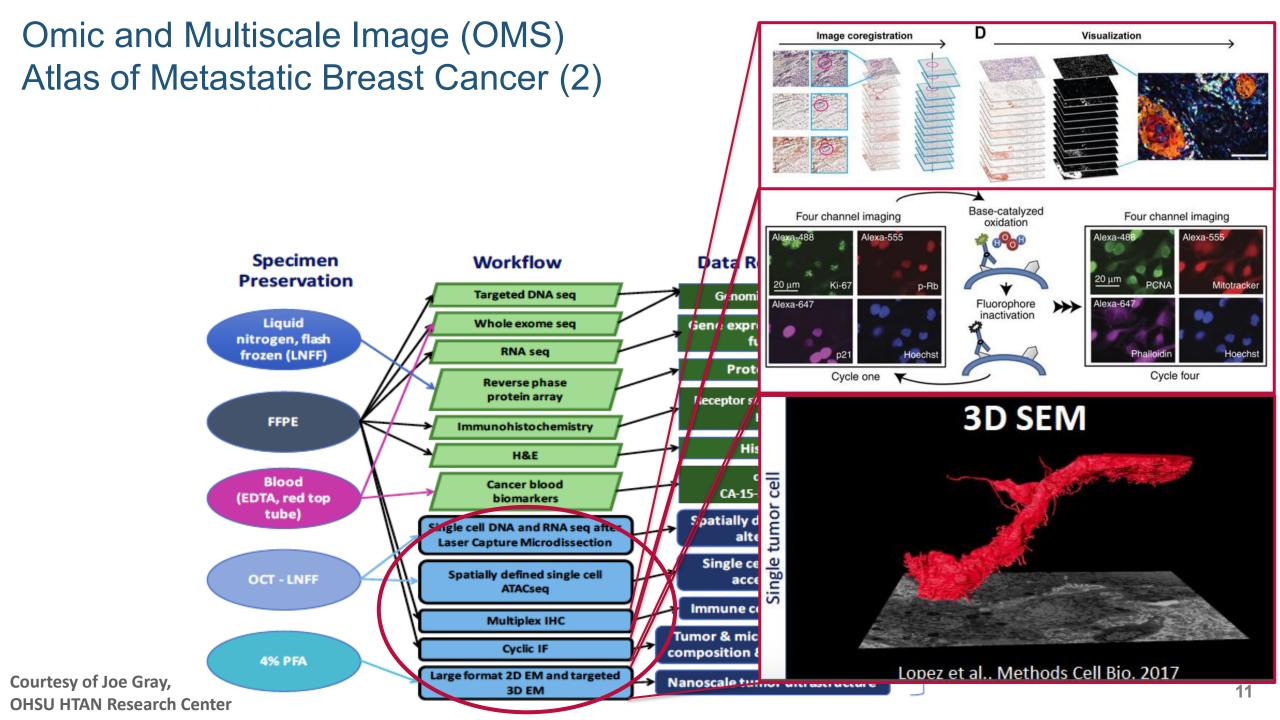


Omic and Multiscale Image (OMS) Atlas of Metastatic Breast Cancer

Overarching goal: Identify therapeutic vulnerabilities and mechanisms of resistance in evolving metastatic breast cancers.

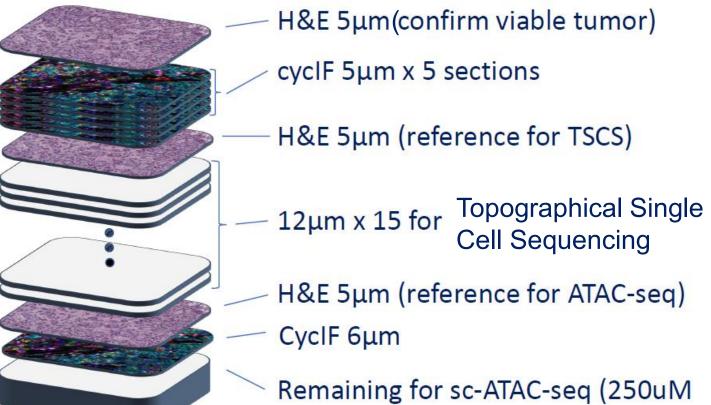
- HRBC treated with CDK4/6 inhibitors + anti-estrogen
- TNBC treated with PARP inhibitor + immune checkpoint inhibitors





Tissue processing to facilitate spatial registration of cycIF, TSCS and sc-ATAC-seq



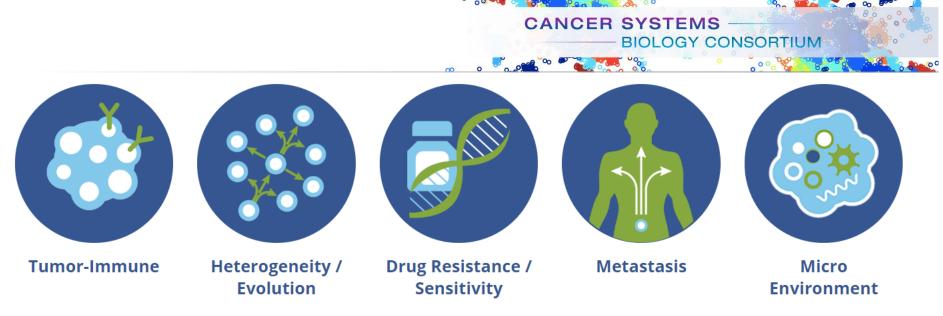


punches throughout biopsy)

Courtesy of Joe Gray, OHSU HTAN Research Center

NCI Cancer Systems Biology Consortium (CSBC)

 In the CSBC we define systems biology as the explicit integration of experimental biology and computational or mathematical modeling to build, test and/or validate hypotheses or ideas

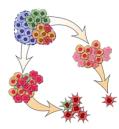


Currently: 13 Research Centers (multi-project) and 13 Research Projects

New U01 Funding Opportunity Announcement: PAR-19-287

H NATIONAL CANCER INSTITUTE

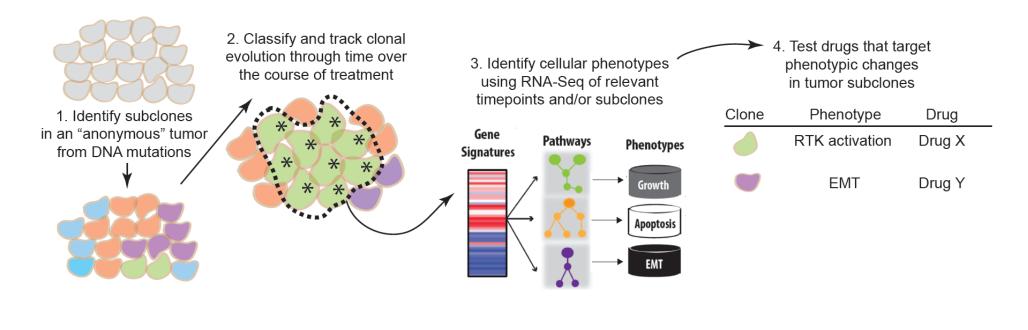
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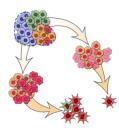
CSBC Center of HoPE (Heterogeneity of Phenotypic Evolution) PI: Andrea Bild



Combating subclonal evolution of resistant cancer phenotypes



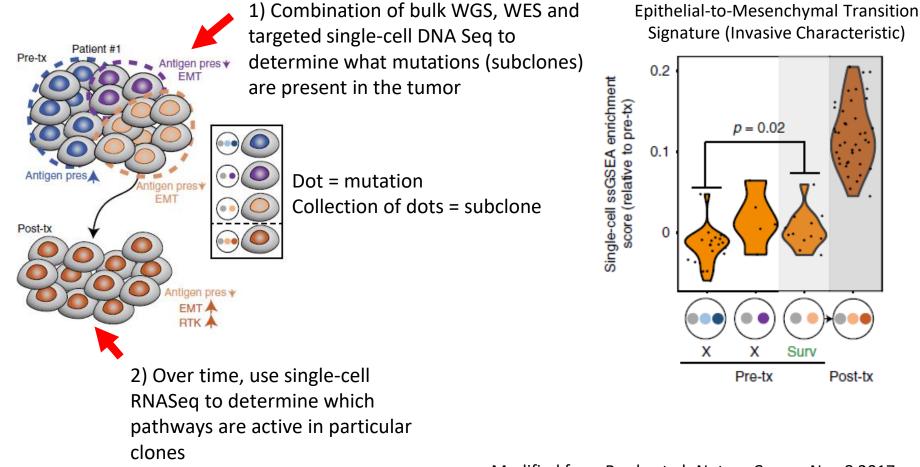
Track tumor evolution to determine appropriate treatment options



CSBC Center of HoPE (Heterogeneity of Phenotypic Evolution) PI: Andrea Bild



Combating subclonal evolution of resistant cancer phenotypes



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Post-tx



Launch: June 3, 2019

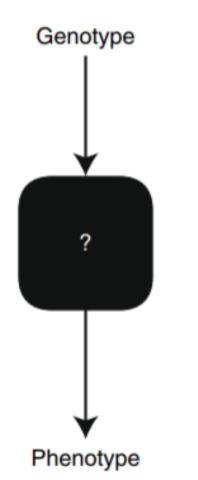
510 pre-registered participants

https://www.synapse.org/tumorDeconvolutionChallenge

Contact: brian.white@sagebase.org



Don't worry. AI/DL/ML will solve it. --might be true in some contexts --but maybe (very likely) not for others



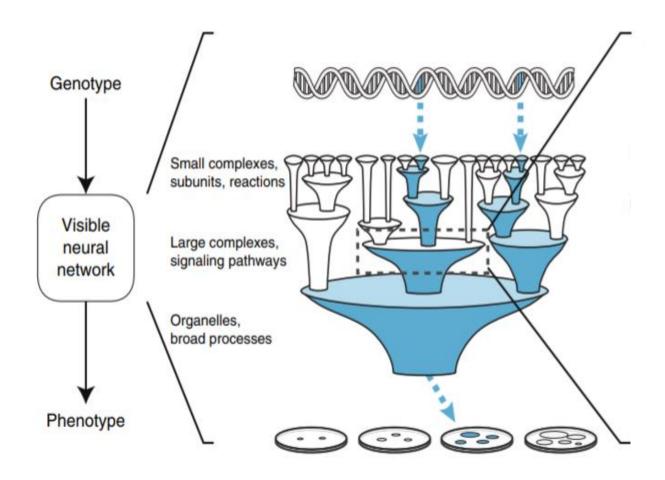
Ideker Lab UCSD Ma et al. *Nature Methods* May 2018 doi:10.1038/nmeth.4627



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The Cancer Cell Map Initiative Pls: Nevan Krogan (UCSF) & Trey Ideker (UCSD)



Ideker Lab UCSD Ma et al. *Nature Methods* May 2018 doi:10.1038/nmeth.4627



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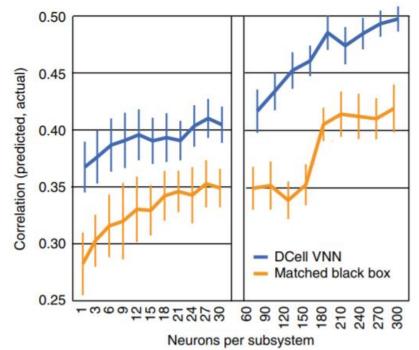


The Cancer Cell Map Initiative Pls: Nevan Krogan (UCSF) & Trey Ideker (UCSD)

information is randomized 0.7 Limit of experimental reproducibility 0.50 0.6 Correlation (predicted, actual) 0.5 -0.45 Correlation (predicted, actual) 0.4 0.40 0.3 -0.35 0.2 -0.1 0.30 0.0 MMMC Ontohype GBA Matched 184 FUIN 0.25 conne DCell Previous predictors Black box VNN of genetic interaction neural networks

Same structure, but ontology

Information is lost if biology is not used to inform the model



Ideker Lab UCSD



Ma et al. Nature Methods May 2018 doi:10.1038/nmeth.4627

Please contact me with questions: <u>shannon.hughes@nih.gov</u>

Follow us on Twitter: @NCISysBio and @NCIHTAN Check out currently funded projects: <u>www.csbconsortium.org</u>

CSBC U01 Funding Announcement: <u>PAR-19-287</u>

Informatics Technologies for Cancer Research (ITCR) Funding Announcements: <u>https://itcr.nci.nih.gov/</u> (R21/U01/U24)

