# Opportune time to study “function” on a large scale

## Now so many variants to characterize

### Functional characterization will be the connection between a individual personal genome & biology

## Recent development of new technologies (CRISPR, large-scale epigenomics, single cell, &c)

# Need for a foundational resource to integrate information on many discovered variants

# What to study?

## The types of function: organismal phenotype to cellular role to biochemical mechanism

### Molecular phenotypes can be studied at scale & systematized . Not as easy for organismal phenotype. Also, their manifestation is closer to the variants

## Assays with a sweet spot

### New technologies, lots of readout with modest investment

### Best models -- is it mouse? -- & model diseases

# Dichotomy of Directions

## Top-down Prioritization: develop standardized catalogs of elements &/or all possible variants & then intersect them with found variants to prioritize

### Shendure challenge talk

## Bottom-up: start from a list of variants and characterize them functionally

## Consensus both have merits

# Dichotomy of Approaches

## Domain level experts & detailed assays will be necessary as a complement to standardized high-throughput expts

### Many important assays can not be scaled

## Different Levels of Validation: V vs v

### "v"alidation : Rough molecular phenotype, generic

### "V"alidation: in the right cell, right condition...

### Importance of cellular context for detailed understanding

## Important to have both & integrate them (using special DBs)

# Then scaling from the genome-scale to population-scale

## Success of eQTL & related projects

## Personal functional genomics, value in longitudinal studies

# More to functional genomics than variant characterization

## Cell type characterization (healthy vs. pre-disease vs. disease state) & epigenomics via large-scale seq.

## Systems-level understanding

## Regev challenge talk: Single-cell transcriptomics & Human Cell Atlas Project