LOCATION: International
CHAMPIONS: Melissa Haendel, Monica Munoz-Torres, Peter Robinson, Tudor Groza
A bit different than most driver projects in that we are about **DATA HARMONIZATION** rather than about producing data (most similar to VICC)

Monarch provides: standards & ontologies, best practices, and semantic tools
- **Human Phenotype Ontology**; contributions to other GA4GH recommended standards e.g., NCI Thesaurus, LOINC, ...
- Disease-to-phenotype data models and annotations
- Phenotype profile matching and variant prioritization algorithms
- Exomiser variant analysis tool, used especially for **rare and Mendelian disease** diagnostics
- SEPIO ontology and modeling framework for evidence and provenance information

Main products we’ve contributed to within GA4GH to date:
- **Phenopackets** (Haendel co-leads Clinical & Phenotypic Data Capture WS)
- Variant Annotation standard (Brush co-leads in Genome Knowledge Standards WS)
- VICC manuscript and variant alignment
- DUO ontology, data licensing

What we’d like from GA4GH at THIS MEETING:
- Finalize integration between Variant Annotation and Phenopackets and release Phenopackets 1.0!!!
- Better understanding of **semantic data representation and integration needs** from driver projects
- Coordinate & advance **data & knowledge licensing** standards w/ Regulatory and Ethics ([ReusableDataProject](https://ga4gh.org))