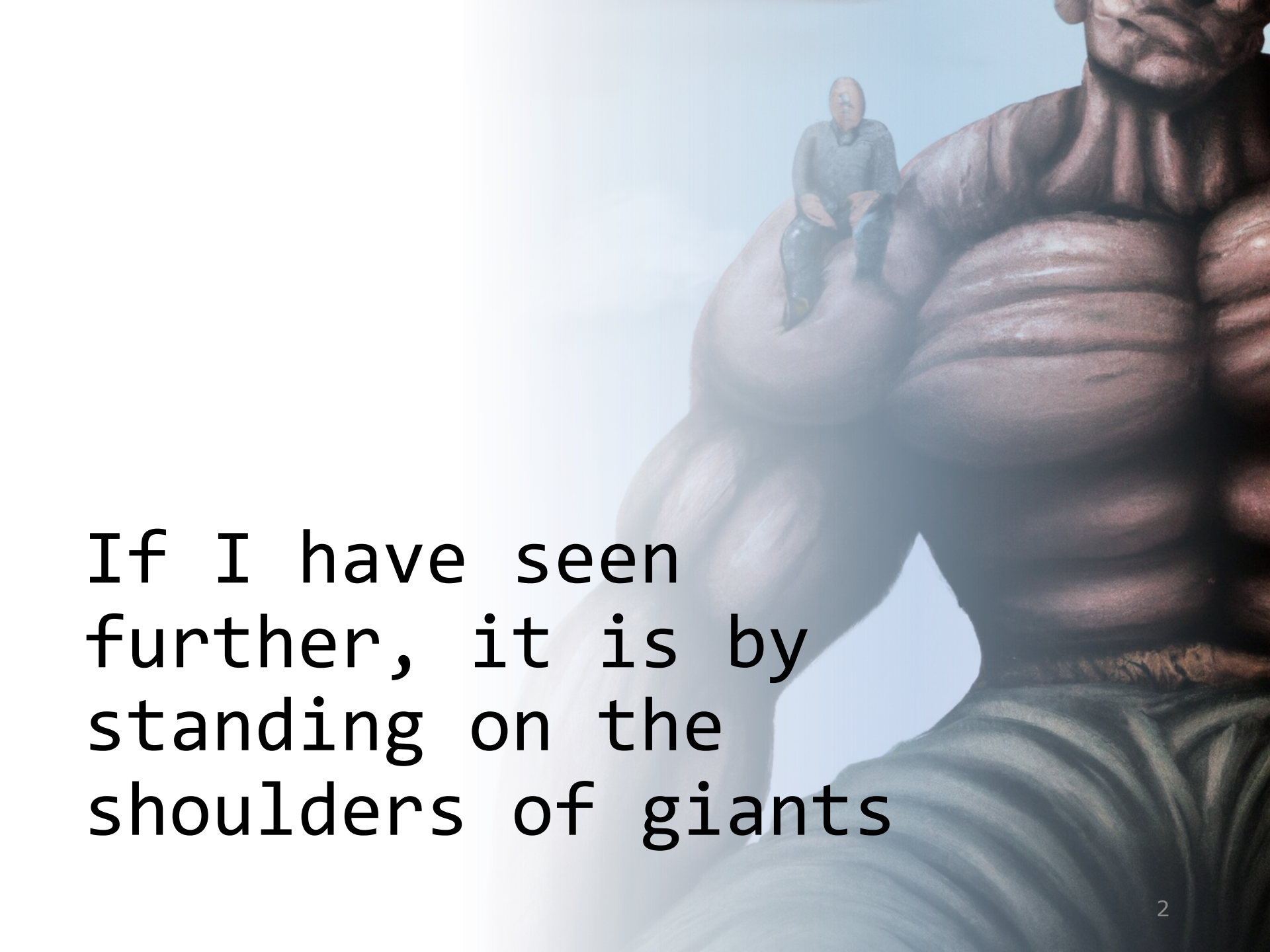


# Introduction to raw sequence databases

Geert van Geest  
Interfaculty Bioinformatics Unit, UniBe  
Training group, SIB

A detailed oil painting of a giant's muscular back and shoulder. The giant's skin is a reddish-brown color, and his muscles are highly defined and layered. A small, dark-skinned figure with a beard and a grey tunic stands on the giant's right shoulder, looking out over a hazy, blue landscape. The figure is holding a long staff or pole.

If I have seen  
further, it is by  
standing on the  
shoulders of giants

# Current giant-shoulder-standing





# Biological databases

- Immense impact on current biological research
- Databases in:
  - Nucleic acids
  - Protein (folding)
  - Metabolomics
  - Taxonomy
  - Imaging
  - Cell lines
  - Molecule/protein/cell interactions
  - ...

# Question

# Biological sequence databases

- **Proteins:** UniProtKB/Swiss-Prot, InterPro
- **Genomes + annotations:** Ensembl, ENA, GenBank/RefSeq, UCSC, ENCODE
- **Raw sequencing data:** [INSDC](#)  
Sequence read archives of ENA, NCBI and DDBJ

# What is a biological database?

- Organizes and standardizes biological information
- (Curated) addition and modification
- Quick searches
- Access by the community through APIs

# FAIR principles

- **F**indable, **A**ccessible, **I**nteroperable, **R**eusable
- To ensure transparency, reproducibility, and reusability
- Enables reuse by:
  - People – same data, other questions
  - Machines - database connections, meta-analyses etc.
- Storage in biological databases typically makes data FAIR



# INSDC

International Nucleotide Sequence Database Collaboration

<b>Data type</b>	<b>DDBJ</b>	<b>EMBL-EBI</b>	<b>NCBI</b>
Next Generation reads	<a href="#">Sequence Read Archive</a>	<a href="#">European Nucleotide Archive</a>	<a href="#">Sequence Read Archive</a>
Assembled Sequences	<a href="#">DDBJ</a>		<a href="#">GenBank</a>
Samples	<a href="#">BioSample</a>		<a href="#">BioSample</a>
Studies	<a href="#">BioProject</a>		<a href="#">BioProject</a>



# Other raw sequencing data portals

- Genome Sequence Archive (Chinese)
- Human controlled access:
  - European Genome Phenome Archive (EGA)
  - JGA – Japan
  - dbGaP – US
- Expression data: ArrayExpress, GEO
- Metagenomics: MGnify

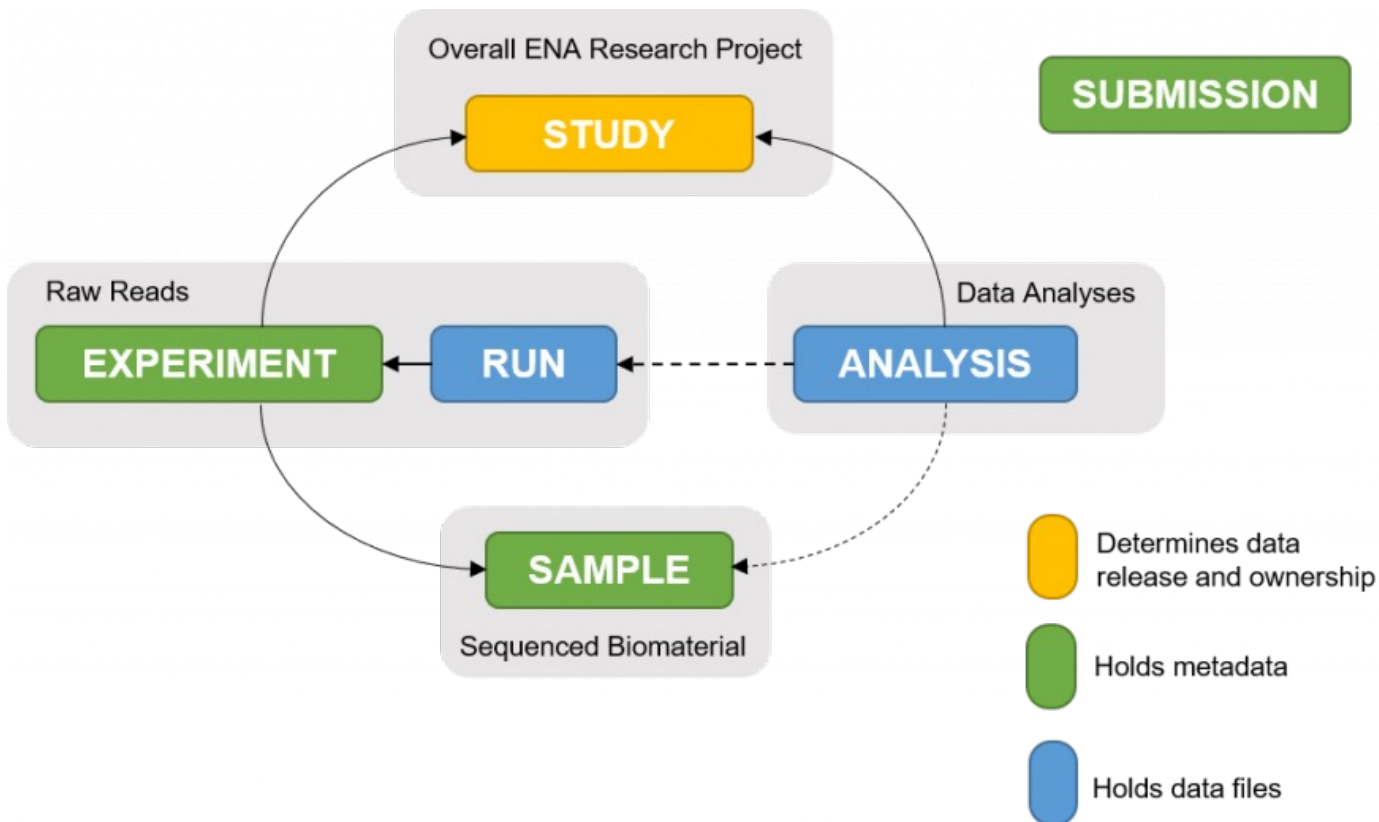
# Other portals

- Use the data submission wizard:  
<https://www.ebi.ac.uk/submission/>

# Databases are interconnected

- INSDC databases are interconnected
- Ensembl uses ENA, RefSeq and UniProtKB for its annotations
- ArrayExpress and GEO submit to their respective SRA
- RefSeq is based on INSDC
- dbGaP and EGA are interconnected
- ...

# ENA database



# Searching ENA

- Raw reads, sequences, assemblies
- Based on any metadata column, like:
  - Organism
  - Geographic origin
  - Sequencing method
  - ..





# Downloading sequence data

- Through the browser
- File Transfer Protocol (FTP):
  - Command line: wget or curl
  - FileZilla
- SRA tools
- <https://nf-co.re/fetchngs>

nextflow

