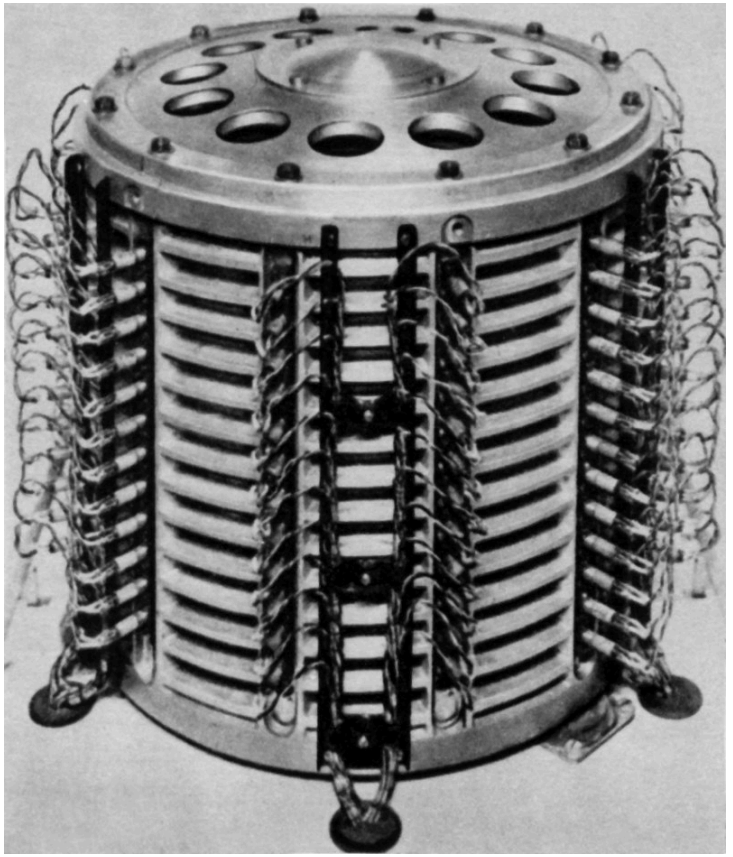
Online Resources for Nucleotide Data

Why do we need databases?

- To archive and preserve information
- To put all the things in one place (facilitate discovery)
- To enforce and maintain format standards
- To allow reuse of data (its expensive, use it more than once!)
- To prevent fraud in research
- To have reproducibility of research
- To store metadata



Metadata

- Metadata is data about data
- Where did the data come from?
  - Organism or substrate, experimental conditions, location, time and date, tissue
- How was the data collected?
  - Field methods, lab methods, instruments, calibration
- How has the data been processed?
  - Normalization, removal of “bad” data, any processing at all
- User rights and management for the data
  - Is this open for additional publication or is it embargoed?
  - Does it carry a license?

http://twitpic.com/6ry6ar

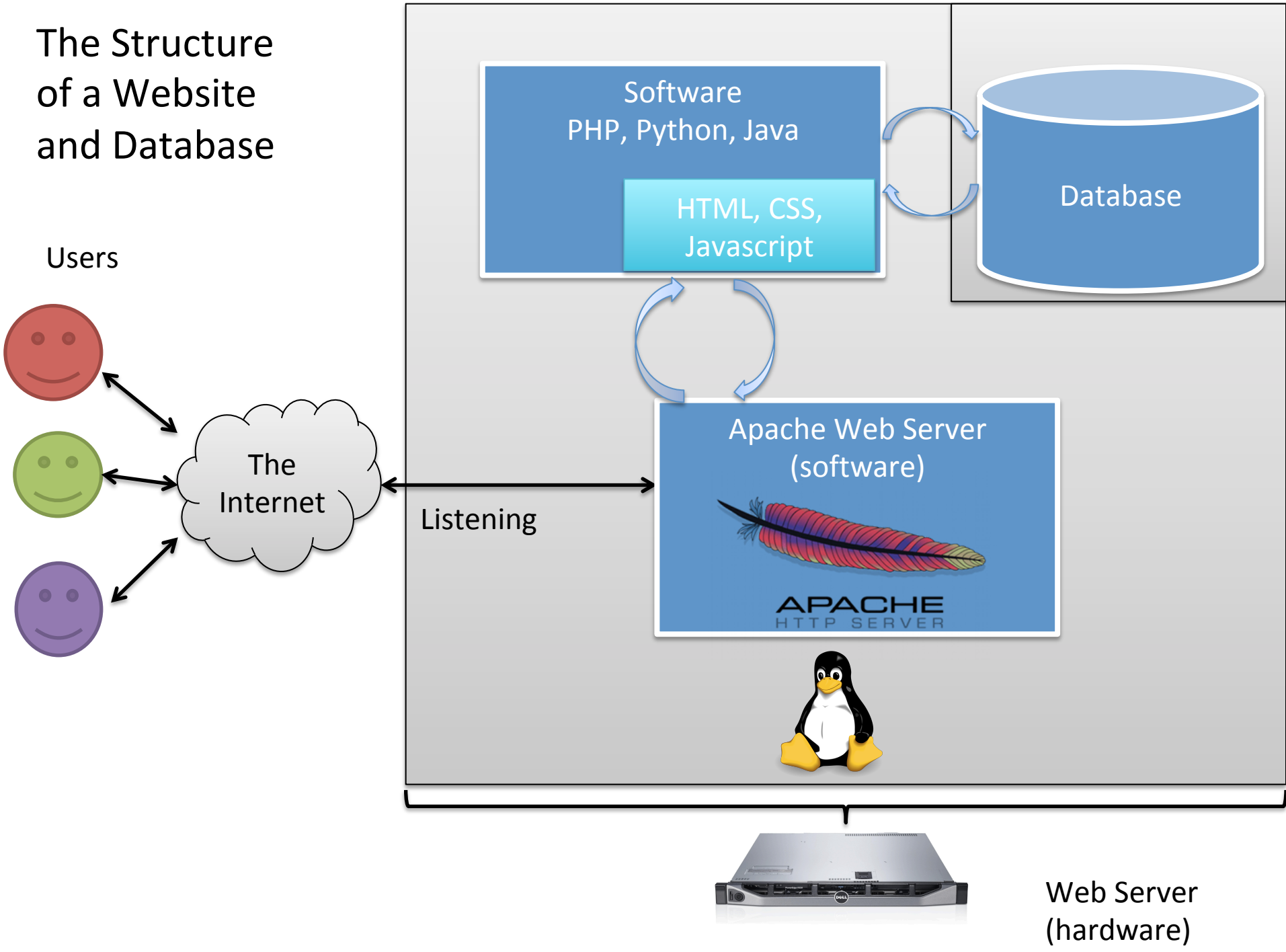
A Few Types of Databases

I. International, Primary Repositories
II. Protein DB resources
III. Community DBs

These are quite possibly totally unrelated to your data of interest. Publications and internet searches will help you identify the right database for you.

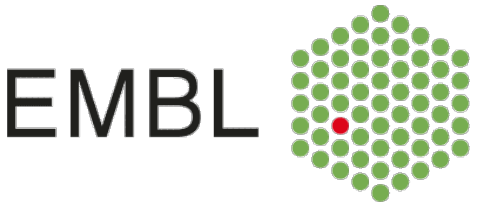
Sometimes there just isn't a home. Non-human metabolomics data?

The Structure of a Website and Database



International Nucleotide Sequence Database (INSD)

- Consists of the following 3 dbs:
  - DDBJ (DNA Data Bank of Japan)
  - EMBL (European Molecular Biology Laboratory)
  - NCBI (National Center for Biotechnology Information)
- repositories for nucleotide sequence data from all organisms
- all three databases accept nucleotide sequence submissions, and then exchange new and updated data on a daily basis
- Primary database = house original sequence data



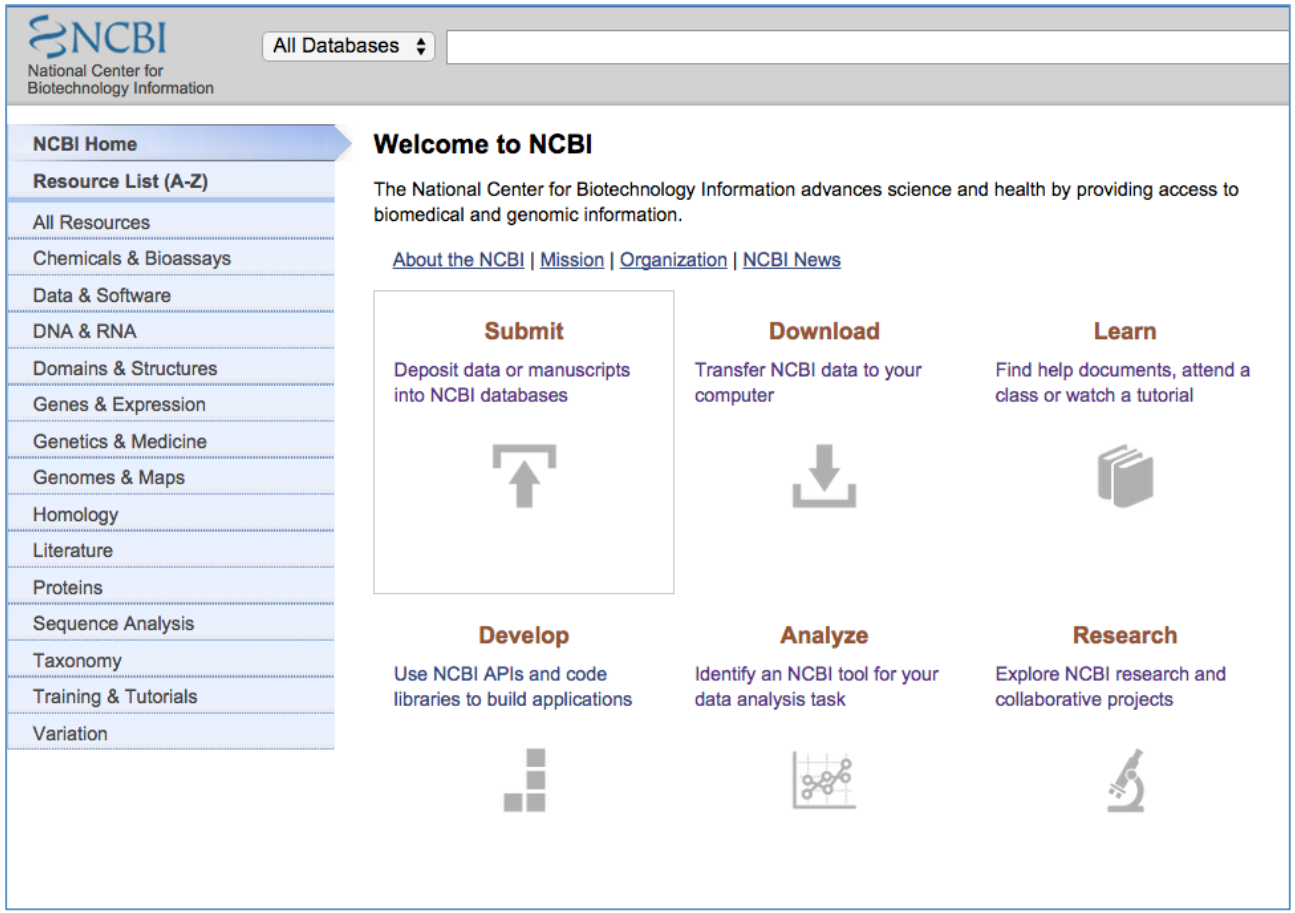
INSD

Data type	DDBJ	EMBL-EBI	NCBI
Next generation reads	Sequence Read Archive	European Nucleotide Archive (ENA)	Sequence Read Archive
Capillary reads	Trace Archive		Trace Archive
Annotated sequences	DDBJ		GenBank
Samples	BioSample		BioSample
Studies	BioProject		BioProject

http://www.insdc.org/

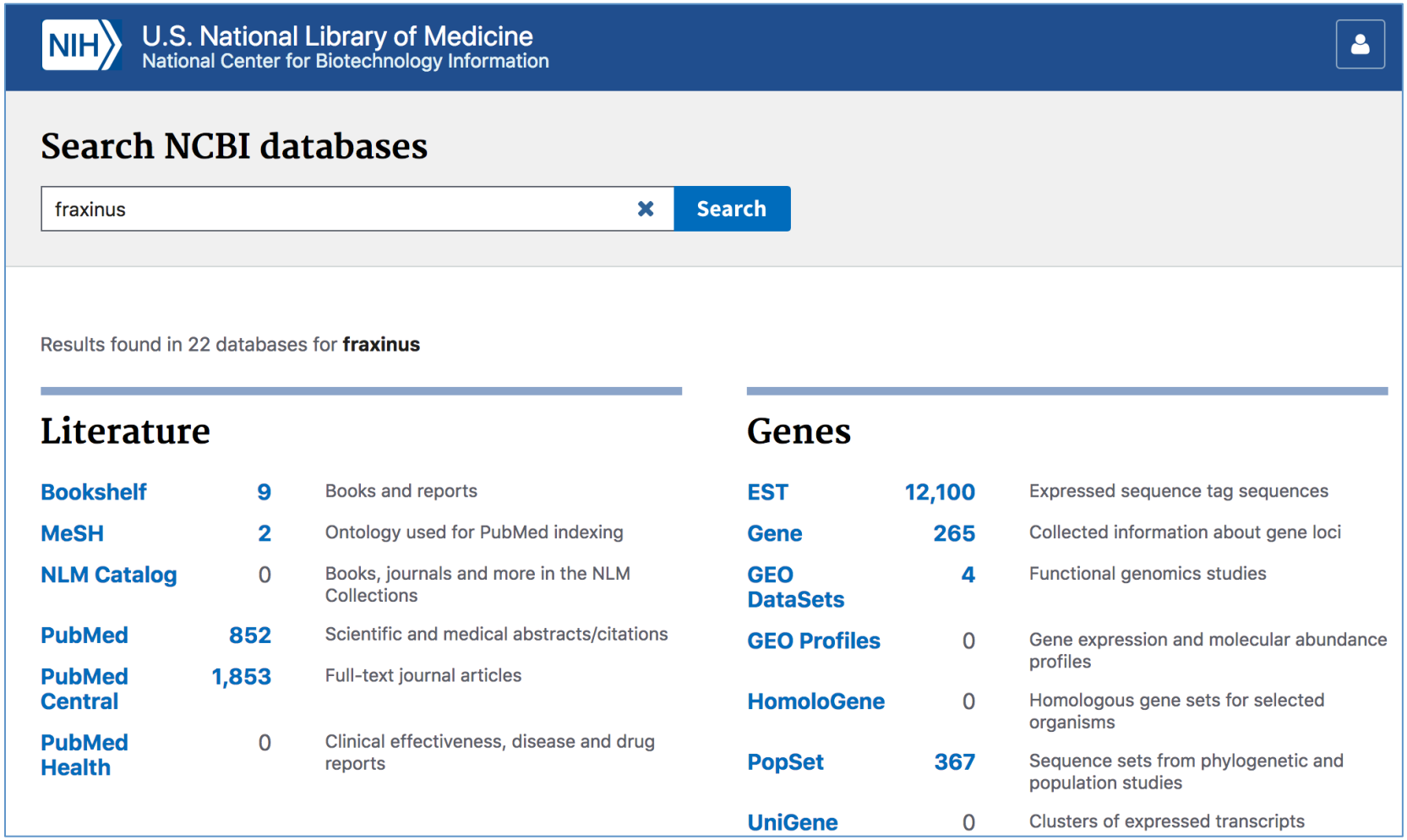
NCBI

- Discover
- Download
- Submit
- Analyze



http://www.ncbi.nlm.nih.gov/

Discover


U.S. National Library of Medicine
National Center for Biotechnology Information
Search NCBI databases
fraxinus
Search
Results found in 22 databases for fraxinus
Literature
Bookshelf 9 Books and reports
MeSH 2 Ontology used for PubMed indexing
NLM Catalog 0 Books, journals and more in the NLM Collections
PubMed 852 Scientific and medical abstracts/citations
PubMed Central 1,853 Full-text journal articles
PubMed Health 0 Clinical effectiveness, disease and drug reports
Genes
EST 12,100 Expressed sequence tag sequences
Gene 265 Collected information about gene loci
GEO DataSets 4 Functional genomics studies
GEO Profiles 0 Gene expression and molecular abundance profiles
HomoloGene 0 Homologous gene sets for selected organisms
PopSet 367 Sequence sets from phylogenetic and population studies
UniGene 0 Clusters of expressed transcripts

Download

http://www.ncbi.nlm.nih.gov/home/download.shtml

Download

The majority of NCBI data are available for downloading, either directly from the NCBI FTP site or by using software tools to download custom datasets.

ADDITIONAL LINKS

How to download custom data sets

Large Data Download Best Practices

SRA Download Reference

FTP

Download data from the NCBI FTP site

Aspera

High-speed downloads provided by Aspera software

Download Tools

Tools and APIs for downloading customized datasets

- Private software owned by IBM
- Free for clients
- Can be hundreds of times faster than http and ftp
- For NCBI, you need to download and install a web browser plug in, Aspera Connect

NCBI

Fast Aspera Download

How to setup Aspera.

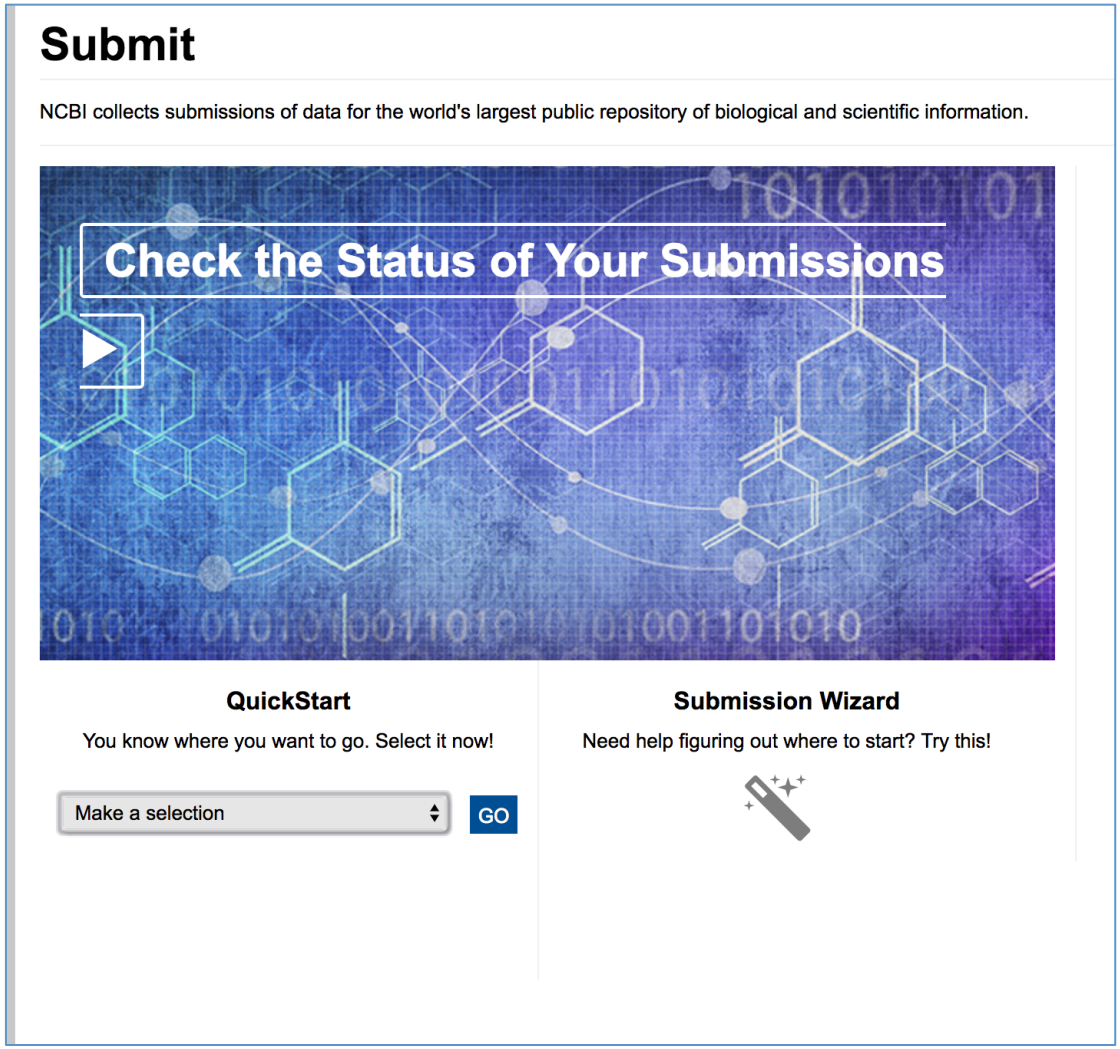
Please ensure you are running a current version of AsperaConnect. It is available at Aspera Connect under the "RESOURCES" tab.
Set your bandwidth rate and continue increasing it until the data transfer rate plateaus. Many sites can transfer data at 200-500Mbps. and nearly all sites can transfer at faster than 10Mbps.
Please refer to Aspera Transfer Guide and Aspera's documentation for more information.

Collapse tree

Name	Total size	Content	Last update
SRR292241	956.32 **Mb**	1 file	2015-06-28 01:33
SRR292241.sra	956.32 **Mb**		2015-06-28 01:33

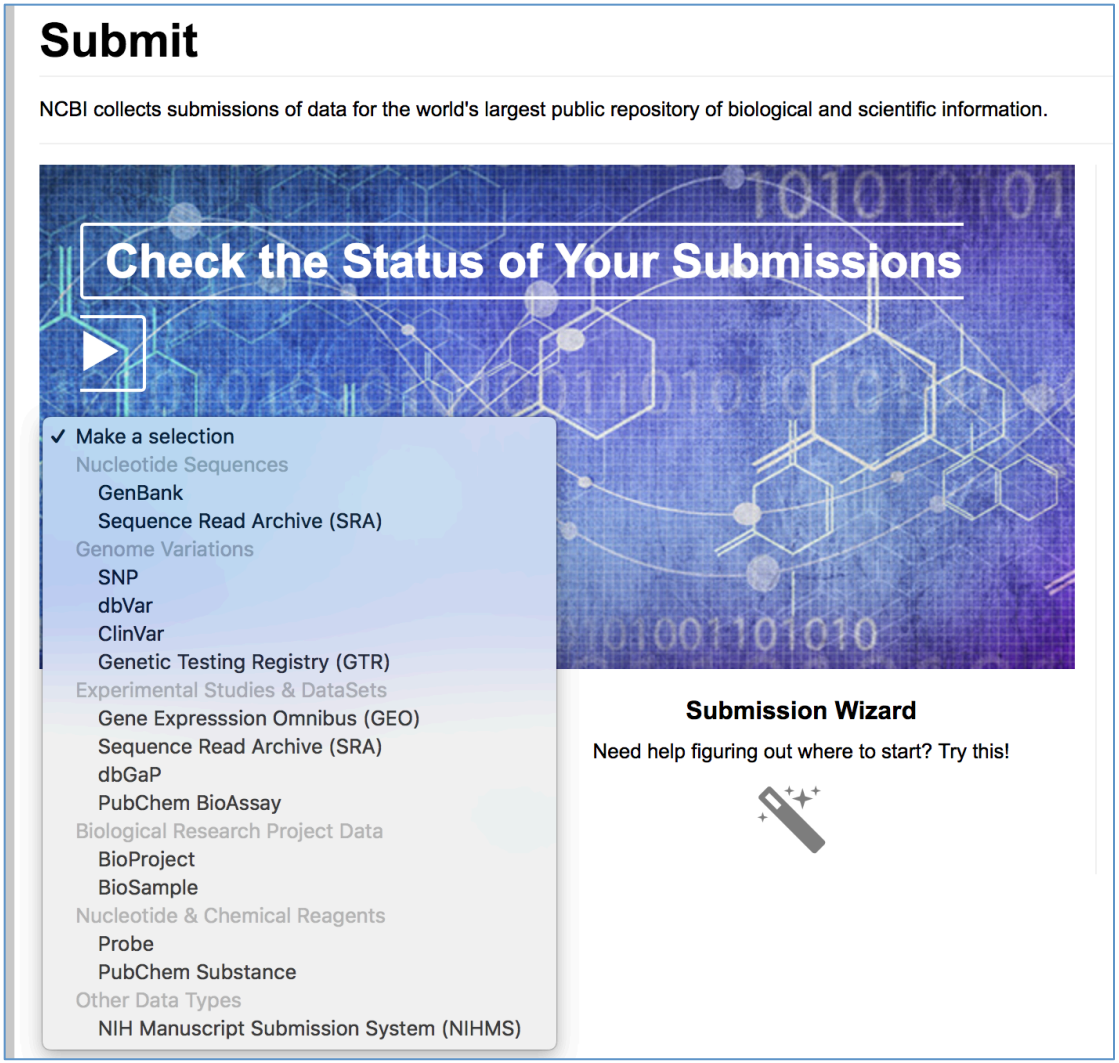
Submission Portal

https://www.ncbi.nlm.nih.gov/home/submit/



Submission Portal

https://www.ncbi.nlm.nih.gov/home/submit/



Sequence Read Archive

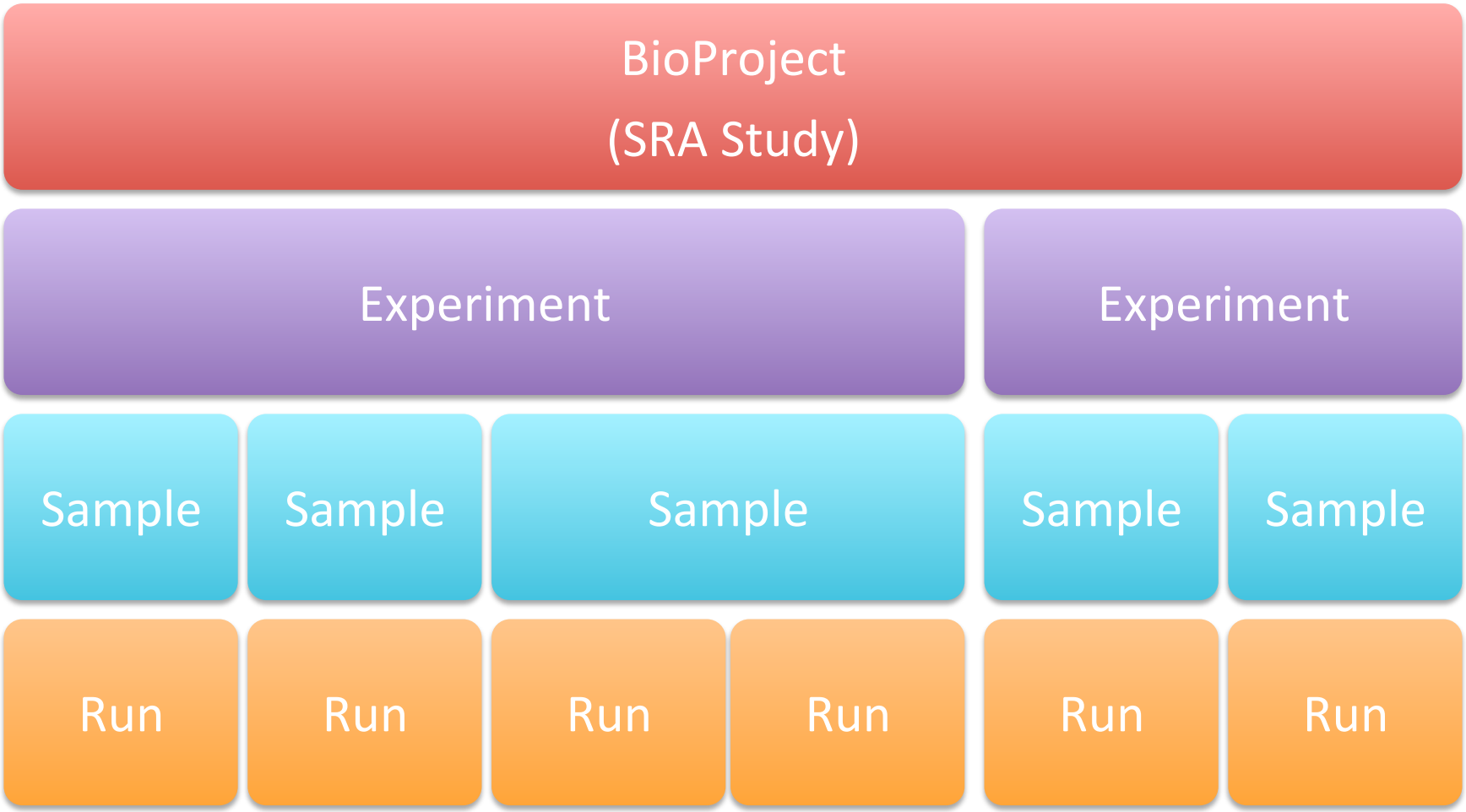
- accepts next generation sequence data
  - Raw sequencing data
  - Alignment information
- http://www.ncbi.nlm.nih.gov/sra

Emphasis on metadata

- **Study (BioProject)** – A study is a set of experiments and has an overall goal.
- **Experiment** – An experiment is a consistent set of laboratory operations on input material with an expected result.
- **Sample** – An experiment targets one or more samples. Results are expressed in terms of individual samples or bundles of samples as defined by the experiment.
- **Run** – Results are called runs. Runs comprise the data gathered for a sample or sample bundle and refer to a defining experiment.

Hierarchical Design

https://www.ncbi.nlm.nih.gov/sra/docs/submitupdate/#sras-study-vs-bioprojects-projec



BioProjects

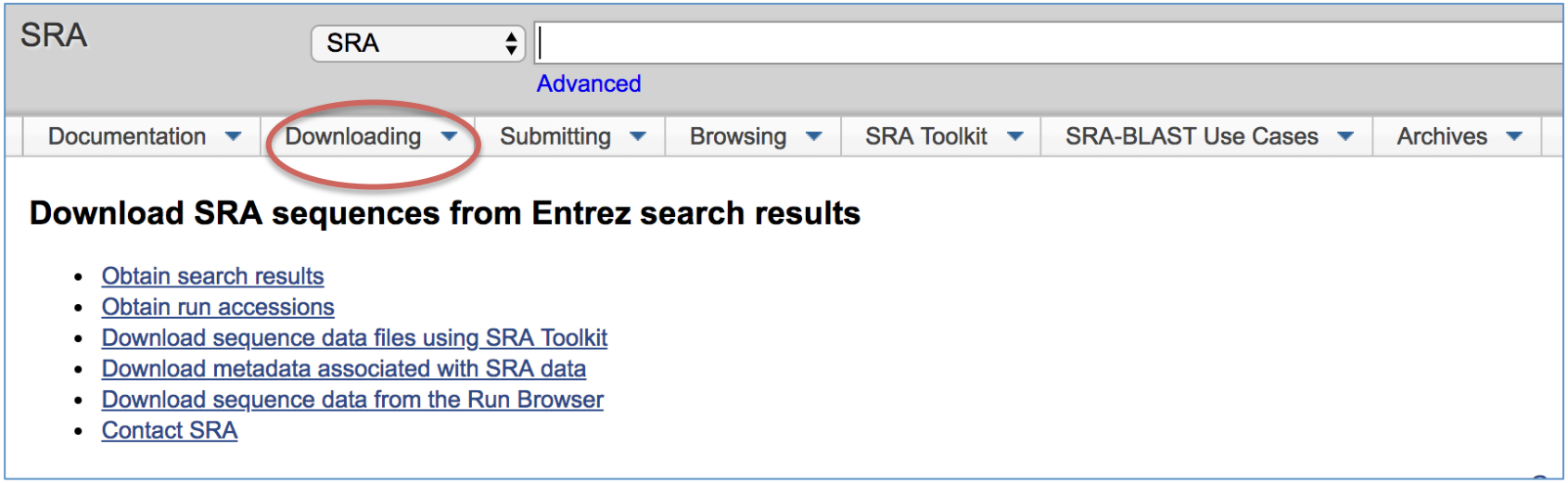
A BioProject is a collection of biological data related to a single initiative, originating from a single organization or from a consortium. A BioProject record provides users a single place to find links to the diverse data types generated for that project.

- Biosamples
- Raw reads
- Genome assembly
- Transcriptome assembly
- Genome annotation
- Markers

- You can create a BioProject page at the very beginning of the project (without data)
- Provide ongoing updates

Sequence Read Archive Format

- Their own format : SRA format
- (if you want an easily clickable link, try ENA)
- there is a web tool for downloading fastq files if you have a list of accessions and want to do this over the web:
- https://www.ncbi.nlm.nih.gov/sra/docs/sradownload/



SRA Toolkit

- CLI tool for downloading and converting to/ from SRA format
- Most important command:

  - **fastq-dump**: Download SRA data from the internet and convert into fastq format

Submitting to the SRA

- Journals will require that you submit all NGS data to SRA or another INSD (and most other ‘omic data forms also need to be submitted somewhere!)
- Collect all data while the experiment is being done
- Know what data you need – they have spreadsheets!
- Start the submission process early (especially if you have a lot of data)

NCBI Data Submission: Earlier is Better!

For submitting any processed data such as a genome sequence: NCBI does a lot of contamination screening, so plan ahead!

1. submit and make sure you pass their QA screens
2. Receive an accession number but keep the data private
3. Do downstream analysis
4. When you are ready to publish, make data public

If you don’t do this, then they may ask you to completely change your data, which will (possibly) invalidate your downstream analysis.

Submitting to the SRA

Before you begin

Gather information

Why did you perform your analysis?

- Project title and abstract
- Aims and objectives
- Organism(s) sequenced
- Optional: Funding sources, publications, etc.

What did you sequence?

- Descriptive sample information
- Tabular format is ideal
- Examples: Organism(s), age(s), gender(s), location data, cell line(s), etc.

How did you sequence your samples?

- Sequencing methods
- Kits used
- Instrument model(s)

What is your data file format?

- Files in acceptable format(s): BAM, FASTQ, etc.
- MD5 checksum for each file
- Minimum of 1 unique dataset per sample

Register metadata

BioProject → **SRA Study**

- A description of the research effort
- "Why" you sequenced your samples

BioSample → **SRA Sample**

- A description of biologically or physically unique specimens
- "What" you sequenced

Provide technical details

SRA Experiment

- A description of a sample-specific sequencing library
- "How" you performed the sequencing
- Multiple Experiments can "point" to a single Sample, but not vice-versa

Transmit data files

SRA Run

- All files linked to a Run are "merged" into a single dataset
- Files are converted to SRA format
- Files submitted by FTP or Aspera once steps 1 and 2 are complete

Castanea mollissima strain:Vanuxem (Chinese chestnut)

Accession: PRJNA266703 ID: 266703

Castanea mollissima strain:Vanuxem Targeted Locus (Loci)

The integrated genetic and physical map for Chinese chestnut was utilized to identify bacterial artificial clones (BACs) located in the three previously identified QTL regions conferring blight resistance. More...

See Genome Information for Castanea mollissima

Related Resources:

- Link to assembly results

NAVIGATE ACROSS

2 additional projects are related by organism.

Project Data Type: Targeted Locus (Loci)

Attributes: Scope: Monoisolate; Material: Genome; Capture: Targeted Locus Loci; Method type: Sequencing

Relevance: Environmental

Project Data:

Resource Name	Number of Links
SEQUENCE DATA	
SRA Experiments	8
OTHER DATASETS	
BioSample	1

▾ SRA Data Details

Parameter	Value
Data volume, Gbases	7
Data volume, Mbytes	7147

Lineage: *Eukaryota*; *Viridiplantae*; *Streptophyta*; *Embryophyta*; *Tracheophyta*; *Spermatophyta*; *Magnoliophyta*; *eudicotyledons*; *Gunneridae*; *Pentapetalae*; *rosids*; *fabids*; *Fagales*; *Fagaceae*; *Castanea*; *Castanea mollissima* [Taxonomy ID: 60419]

Submission:

Registration date: 8-Nov-2014

University of Tennessee Institute of Agriculture

European Nucleotide Archive

- www.ebi.ac.uk/ena
- Mirrors all data in NCBI
- Can submit/download from here
- They use fastq format – no conversion needed!
- Can be slower for large datasets b/c they are far away

Protein Databases

- NCBI RefSeq - A comprehensive, integrated, non-redundant, well-annotated set of reference sequences including genomic, transcript, and protein.
  - 113 million proteins from over 81,000 organisms
  - Last time I taught this in 2016 it was ~52 million proteins

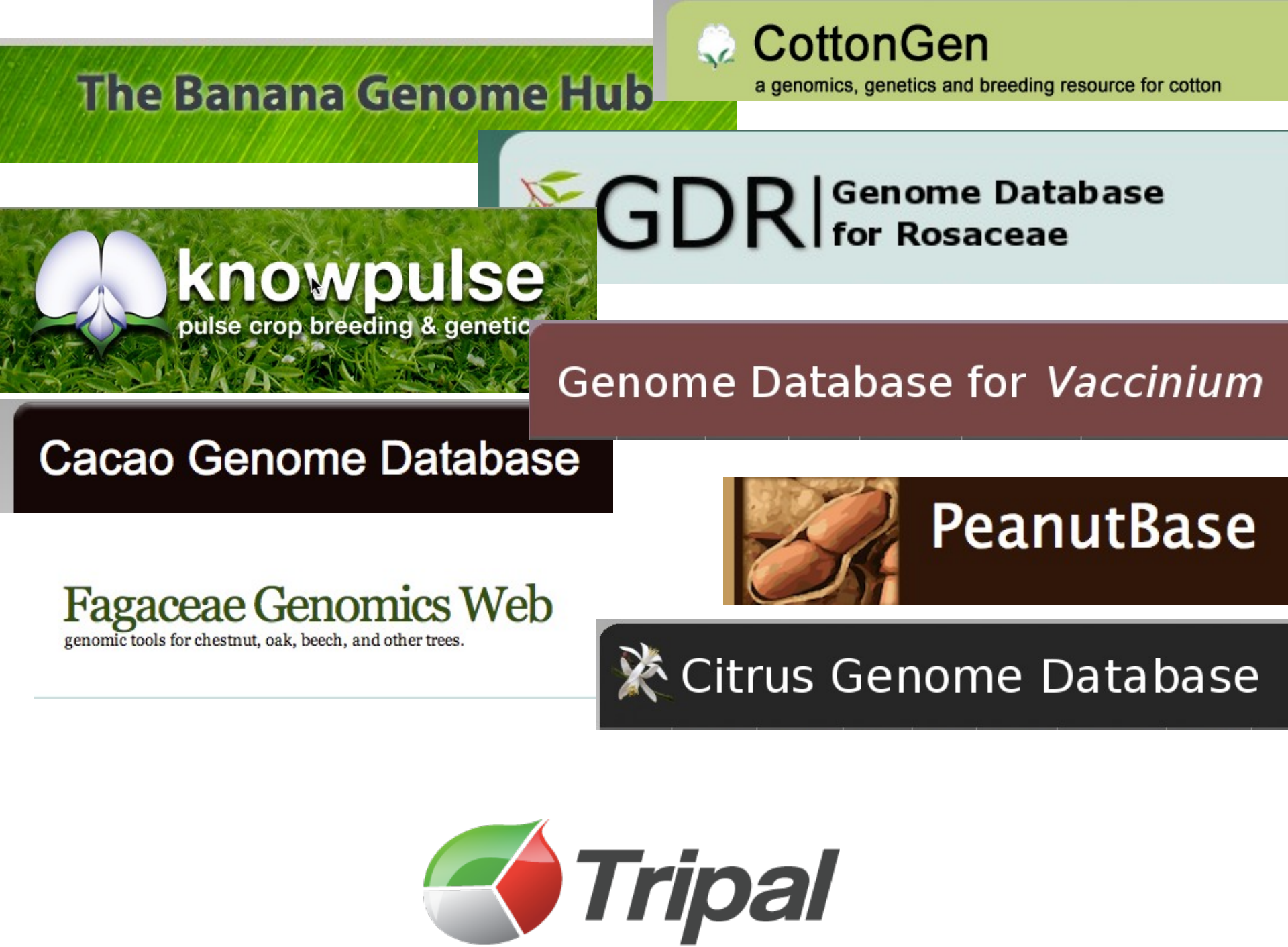
- Uniprot - a comprehensive, high-quality and freely accessible resource of protein sequence and functional information. Two sections:
  - Swiss-Prot – manually annotated and reviewed (~550,000 proteins)
  - TrEMBL – automatically annotated (~120 million proteins)

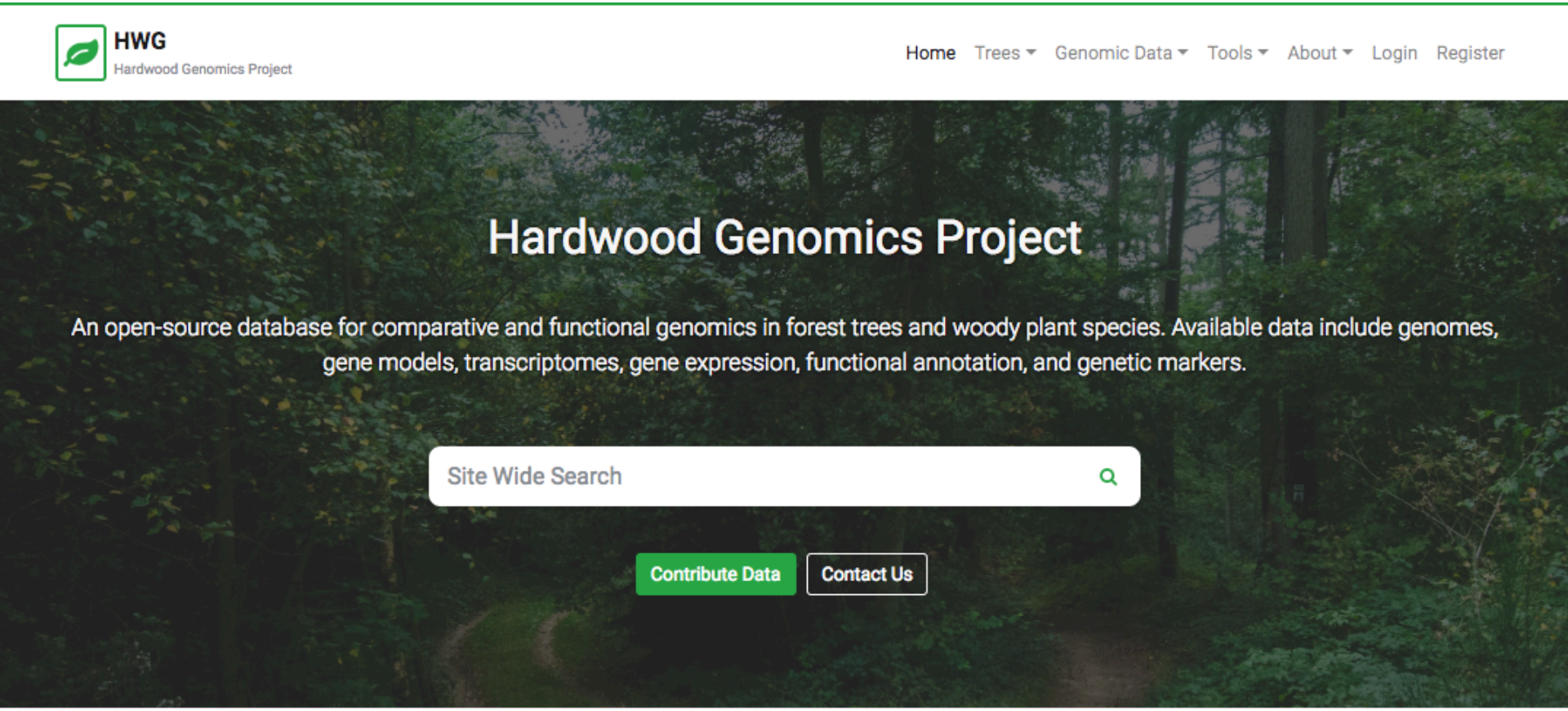
SwissProt

- Manual annotation:
  - Identification of homologs w/ BLAST
  - Structural: Alternative splicing, frameshifts
  - Protein domain id and protein family classification
  - Association with relevant literature
    - Extensive cataloging of information from laboratory experiments
    - Gene Ontology term assignment

Community Databases

- Usually set up to serve one organism or group of organisms
- Sometimes set up to serve a certain type of data
  - Greengenes (16S rRNA)
  - miRBase (miRNAs)
  - MINT (protein-protein interactions)
- Manual curation
- Broader audience, particularly crop breeders
- Combining and interlinking diverse datasets
- Outreach efforts to communities, including training and specific tool development


The Banana Genome Hub
CottonGen
a genomics, genetics and breeding resource for cotton
GDR | Genome Database for Rosaceae
knowpulse
pulse crop breeding & genetic
Genome Database for Vaccinium
Cacao Genome Database
PeanutBase
Fagaceae Genomics Web
genomic tools for chestnut, oak, beech, and other trees.
Citrus Genome Database
Tripal


HWG
Hardwood Genomics Project
Home
Trees
Genomic Data
Tools
About
Login
Register
Hardwood Genomics Project
An open-source database for comparative and functional genomics in forest trees and woody plant species. Available data include genomes, gene models, transcriptomes, gene expression, functional annotation, and genetic markers.
Site Wide Search
Contribute Data
Contact Us

When The Sequencing Data Comes In
#WhatShouldWeCallGradSchool

http://whatshouldwecallgradschool.tumblr.com/post/127656695585/when-the-sequencing-data-comes-in