BI694
Bioinformatics & Phylogenetics

Winter Semester 2017

WEEK 5

Sequence Databases

Connecting to Remote Machines

Overview

- BLAST: **B**asic **L**ocal **A**lignment **T**ool
  - Local alignment!
  - Used to compare sequences to database
  - Described by Altschul et al. 1990

National Center for Biotechnology Information

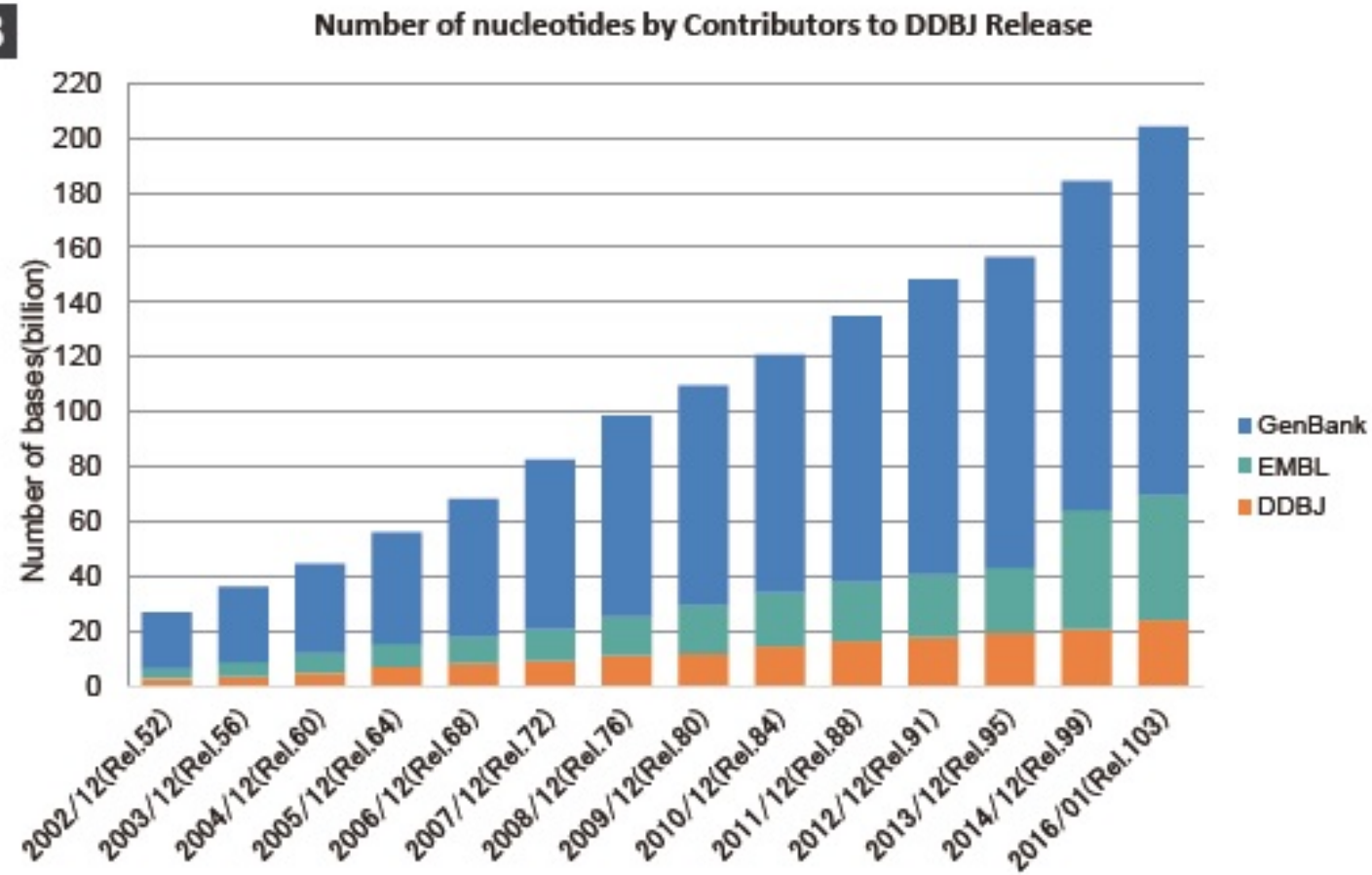
European Molecular Biology Laboratory

DNA Data Bank of Japan

A


DDBJ
DNA Data Bank of Japan
DDBJ Sequence Read Archive
DDBJ Trace Archive
BioProject
INSDC
IAC
ICM
NCBI
GenBank
Sequence Read Archive
Trace Archive
BioProject
EMBL-EBI
EMBL-Bank
Sequence Read Archive
Trace Archive
BioProject

B


Number of nucleotides by Contributors to DDBJ Release
Number of bases(billion)
0
20
40
60
80
100
120
140
160
180
200
220
2002/12(Rel.52)
2003/12(Rel.56)
2004/12(Rel.60)
2005/12(Rel.64)
2006/12(Rel.68)
2007/12(Rel.72)
2008/12(Rel.76)
2009/12(Rel.80)
2010/12(Rel.84)
2011/12(Rel.88)
2012/12(Rel.91)
2013/12(Rel.95)
2014/12(Rel.99)
2016/01(Rel.103)
GenBank
EMBL
DDBJ

UniProt

UniProtKB | Advanced | Search

BLAST | Align | Retrieve/ID mapping | Peptide search | Help | Contact

The mission of UniProt is to provide the scientific community with a comprehensive, high-quality and freely accessible resource of protein sequence and functional information.

UniProtKB

UniProt Knowledgebase

Swiss-Prot (555,426)

Manually annotated and reviewed.

TrEMBL (89,396,316)

Automatically annotated and not reviewed.

UniRef

Sequence clusters

UniParc

Sequence archive

Proteomes

Supporting data

Literature citations

Taxonomy

Subcellular locations

Cross-ref. databases

Diseases

Keywords

News

Forthcoming changes

Planned changes for UniProt

UniProt release 2017_08

Curation of human immunoglobulin genes: a fruitful collaboration between UniProtKB/Swiss-Prot and IMGT | Cross-references to ELM

UniProt release 2017_07

A pseudogene turns into an active DNA methyltransferase dedicated to male fertility

News archive

Getting started

YouTube

Text search

Our basic text search allows you to search all the resources available

BLAST

Find regions of similarity between your sequences

UniProt data

Download latest release

Get the UniProt data

Statistics

View Swiss-Prot and TrEMBL statistics

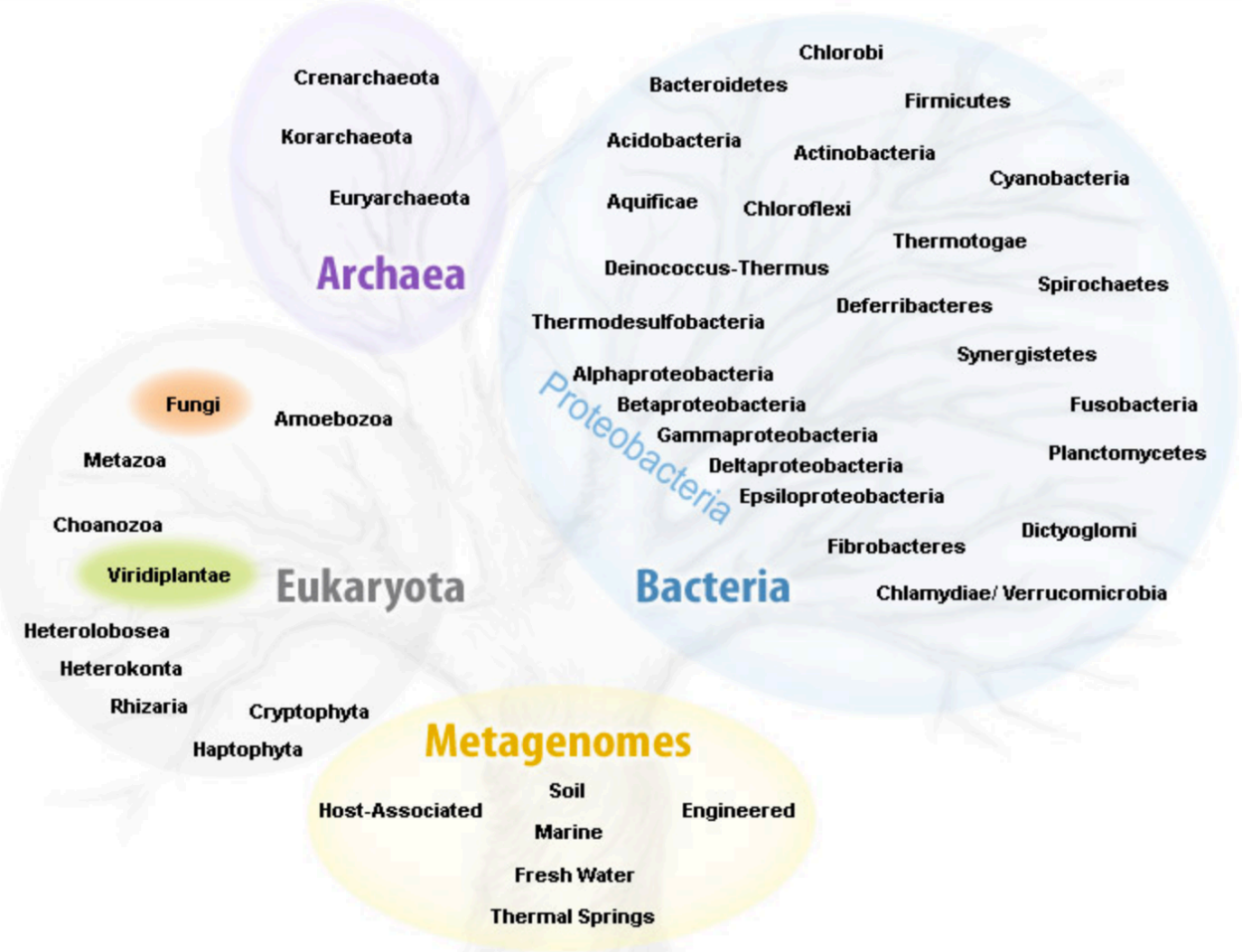
How to cite us

Protein spotlight

A Taste Of Light

August 2017

Light gave life a chance to be. Without it, our planet would not be inhabited by so many living beings of all shapes and sizes. Over time, animals, plants and all sorts of microorganisms have emerged and evolved using this source of photons in different ways. Like hosts of other

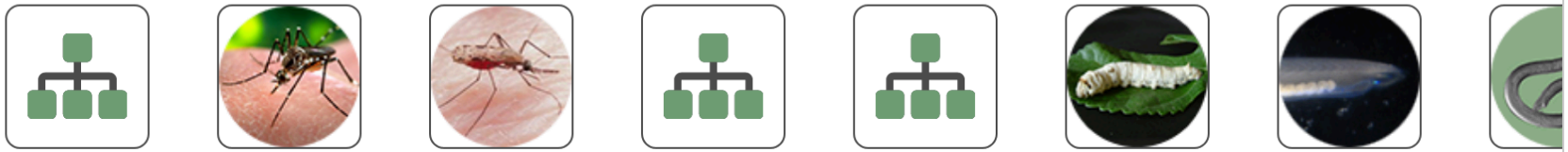


"Tree of Life" drawing by Leila Hornick, copyright 2005

TREE OF LIFE: To use the tree navigation: click a branch name and select the name of the organism of your interest.

Metazome quick search (advanced)

Flagships | All genomes and families | Early Release Genomes



Search in: Click an image or type species/node name

for: Enter keywords or sequence

GO

Help with Metazome

Documentation

- *View a tree representation of the species in Metazome v3.2*
- *View a Quick Start Guide to using Metazome*
- *Check out the FAQs*

About Metazome *3.2*

The Metazome project organizes the proteomes of twenty-four metazoans into gene families defined at nine ancestral nodes on the metazoan evolutionary tree. Families of orthologus and paralogous genes that represent the modern descendents of ancestral gene sets are constructed at key phylogenetic nodes. These families allow easy access to clade-specifi orthology/paralogy relationships as well as clade-specific genes and gene expansions. Where possible, each gene has been annotated with PFAM, KOG, KEGG, and PANTHER assignments, and publicly available annotations from RefSeq, UniProt, EnsEMBL, and JGI are hyperlinked and searchable.

News (details...)

(2016-04-11)
Metazome codebase migrated...

System Status (2017-09-12 04:50)

- ✔ Search
- ✔ BLAST
- ✔ Database
- ✔ BLAT
- ✔ MzMine

Phytozome quick search (advanced)

Flagships | All genomes and families | Early Release Genomes


All released species


Amaranthus hypochondriacus v1.0


Amborella trichopoda v1.0


Ananas comosus v3


Angiosperm


Aquilegia coerulea v3.1


Arabidopsis halleri v1.1


Arabidop v2

Search in | Click an image or type species/node name | for | Enter keywords or sequence | GO

Help with Phytozome

Documentation

- *View a tree representation of the species in Phytozome v12.1*
- *View a Quick Start Guide to using Phytozome*
- *Check out the FAQs*

About Phytozome *12.1.2*

Phytozome, the Plant Comparative Genomics portal of the Department of Energy's Joint Genome Institute, provides JGI users and the broader plant science community a hub for accessing, visualizing and analyzing JGI-sequenced plant genomes, as well as selected genomes and datasets that have been sequenced elsewhere. As of release v12.1, Phytozome hosts 77 assembled and annotation genomes, from 74 viridiplantae species. Forty-three of these genomes have been sequenced, assembled and annotated with JGI Plant Science program resources By integrating this large collecdtion of plant genomes into a single resource and performing comprehensive and uniform annotation and analyses, Phytozome facilitates accurate and insightful comparative genomics studies.

All gene sets in Phytozome have been annotated with KOG, KEGG, ENZYME, Pathway and the InterPro family of protein analysis tools. Inparanoid pairwise orthology and paralogy groups have

News (details...)

(2017-09-07) **Chickpea and *Bsylaticum* added**
(2017-07-31) **4 new genomes released**
(2017-05-09) ***Chromochloris* genome released**

System Status (2017-09-12 04:55)

- ✔ Search
- ✔ BLAST
- ✔ Database
- ✔ BLAT
- ✔ PhytoMine

Pfam 31.0 (March 2017, 16712 entries)

The Pfam database is a large collection of protein families, each represented by **multiple sequence alignments** and **hidden Markov models (HMMs)**. **More...**

QUICK LINKS	YOU CAN FIND DATA IN PFAM IN VARIOUS WAYS...
SEQUENCE SEARCH	Analyze your protein sequence for Pfam matches
VIEW A PFAM ENTRY	View Pfam annotation and alignments
VIEW A CLAN	See groups of related entries
VIEW A SEQUENCE	Look at the domain organisation of a protein sequence
VIEW A STRUCTURE	Find the domains on a PDB structure
KEYWORD SEARCH	Query Pfam by keywords
JUMP TO	enter any accession or ID Go Example

Enter any type of accession or ID to jump to the page for a Pfam entry or clan, UniProt sequence, PDB structure, etc.

Or view the help pages for more information

Recent Pfam blog posts

☒Hide this

Pfam 31.0 is released (posted 8 March 2017)

Pfam 31.0 contains a total of 16712 families and 604 clans. Since the last release, we have built 415 new families, killed 9 families and created 11 new clans. We have also been working on expanding our clan classification; in Pfam 31.0, over 36% of Pfam entries are placed within a clan. The new "stuff" [...]

Pfam train online (posted 8 December 2016)

We now have an online Quick Tour that provides a brief introduction to the Pfam protein families

InterProScan sequence search

This form allows you to scan your sequence for matches against the InterPro protein signature databases, using InterProScan tool.
Enter or paste a protein sequence in FASTA format (complete or not - e.g. PMPIGSKERPTFFEIFKTRCNKADLGPISLN), with a maximum length of 40,000 amino acid long.
Please note that you can only scan one sequence at a time.

Analyse your protein sequence

InterProsScan

InterProScan is a sequence analysis application (nucleotide and protein sequences) that combines different protein signature recognition methods into one resource.
More about InterProScan.

Need more help?

SEQanswers

the next generation sequencing community

SEQanswers Home

User Name | Remember Me?

Password | Log in

Register | FAQ | Community | Calendar | Today's Posts | Search

You are currently viewing the SEQanswers forums as a guest, which limits your access. Click here to register now, and join the discussion

» Site Navigation

- About SEQanswers
- Next Gen Summaries
- Forums
- Wiki
- Instrument Map

» Log in

User Name:

Password:

Remember Me?

Log in

Not a member yet?
Register Now!

» Online Users: 323

3 members and 320 guests

» New Posts

Title, Username, & Date	Last Post	Replies	Views	Forum
Searching for microRNAs Bhumika Arora	Today 02:19 AM by Bhumika Arora	0	37	Bioinformatics
Hisat2 multithreading not working. tirohia	Yesterday 11:10 PM by dpryan	5	194	RNA Sequencing
Introduction marthastevens47	Yesterday 10:05 PM by marthastevens47	0	26	Introductions
IndexOutOfBoundsExce... ArtVandelay	Yesterday 04:54 PM by ArtVandelay	0	64	Bioinformatics
Yes .. BBMap can do that! GenoMax	Yesterday 02:35 PM by TomHarrop	163	33,462	Bioinformatics
what percentage range is normal for undetermined reads in a lane? zeam	Yesterday 01:30 PM by nucacidhunter	1	67	Illumina/Solexa

New Ion Torrent Machines...media roundup

Sep 01, 2015 - 10:15 AM - by ECO

Ion just lifted the embargo so all the bloggers are furiously tapping out their preview details and opinions of Thermo's new sequencers...

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» Recent Job Postings

Bioinformatician/sta...
08-02-2017 05:30 AM
by Bukowski

votes	answers	views	
0	0	2	1 (800) 927 2480 QuickBooks POS Support Number QuickBooks Technical Issue Support Number
0	0	4	1 (800) 927 2480 QuickBooks POS Error Support Number QuickBooks Desktop Error Support Number
0	0	25	Generate a reference-ordered data (ROD) file from FASTA
0	0	29	Rn28s1 28S ribosomal RNA [Mus musculus] annotation in GTF file
0	0	37	Motifs & domains comparisons between proteins
0	0	31	Mendelian randomization analysis..... OR and Beta value
0	2	140	fastQC for Oxford Nanopore reads
		16	How to interpret DEXseq results in therms of significance

rna-seq — written just now by ajayrudelee • 0

quickbooks pos error support number — written 3 minutes ago by ajayrudelee • 0

snp — written 38 minutes ago by omer.asr • 0

genome gene rna-seq sequencing — written 42 minutes ago by efratk • 0

protein alignment comparison motifs and domains — written 1 hour ago by lessismore • 170

or mendelain randomization beta — written 55 minutes ago by Aamiralizai • 0

assembly sequencing — written 4 days ago by efratk • 0

Recent Votes

- Trinity : How To Co-Assemble Different Samples (Tumor And Healthy)
- C: Convert sequence file to fasta format using python
- C: BRCA1 and BRCA2 database's for NGS diagnostics purposes
- C: BRCA1 and BRCA2 database's for NGS diagnostics purposes
- A: BRCA1 and BRCA2 database's for NGS diagnostics purposes
- C: Blastn: Blast short reads against genomes and retain only good hits
- A: AWK: if value falls within a range, print sum of values

Recent Locations • All »

- United Kingdom, just now
- Trento, IT, 2 minutes ago
- Belgium, 5 minutes ago

Recent Awards • All »

- Commentator to Titus • 400
- Scholar to Pierre Lindenbaum ♦ 97k
- Teacher to Kevin Blighe • 340
- Scholar to Alex Reynolds ♦ 20k
- Teacher to Alex Reynolds ♦ 20k
- Scholar to Kevin Blighe • 340

National Center for Biotechnology Information

GenBank

Several databases available; the nucleotide (**nt**) and protein (**nr**) sequence collection probably most widely used.

RefSeq provides a curated set of gene/protein sequences from selected genomes.

What else is available? ESTs, SRA, TSA, genomes…

National Center for Biotechnology Information

GenBank

Downloading data:

ftp://ftp.ncbi.nih.gov/blast/db/

update_blastdb.pl --passive --decompress nr

National Center for Biotechnology Information

GenBank

Downloading data:

ftp://ftp.ncbi.nih.gov/blast/db/

update_blastdb.pl --passive --decompress nr

National Center for Biotechnology Information

GenBank

Getting custom data – the GenBank query builder

National Center for Biotechnology Information

GenBank

Let’s do some sequence searches on our VMs locally and against the remote database

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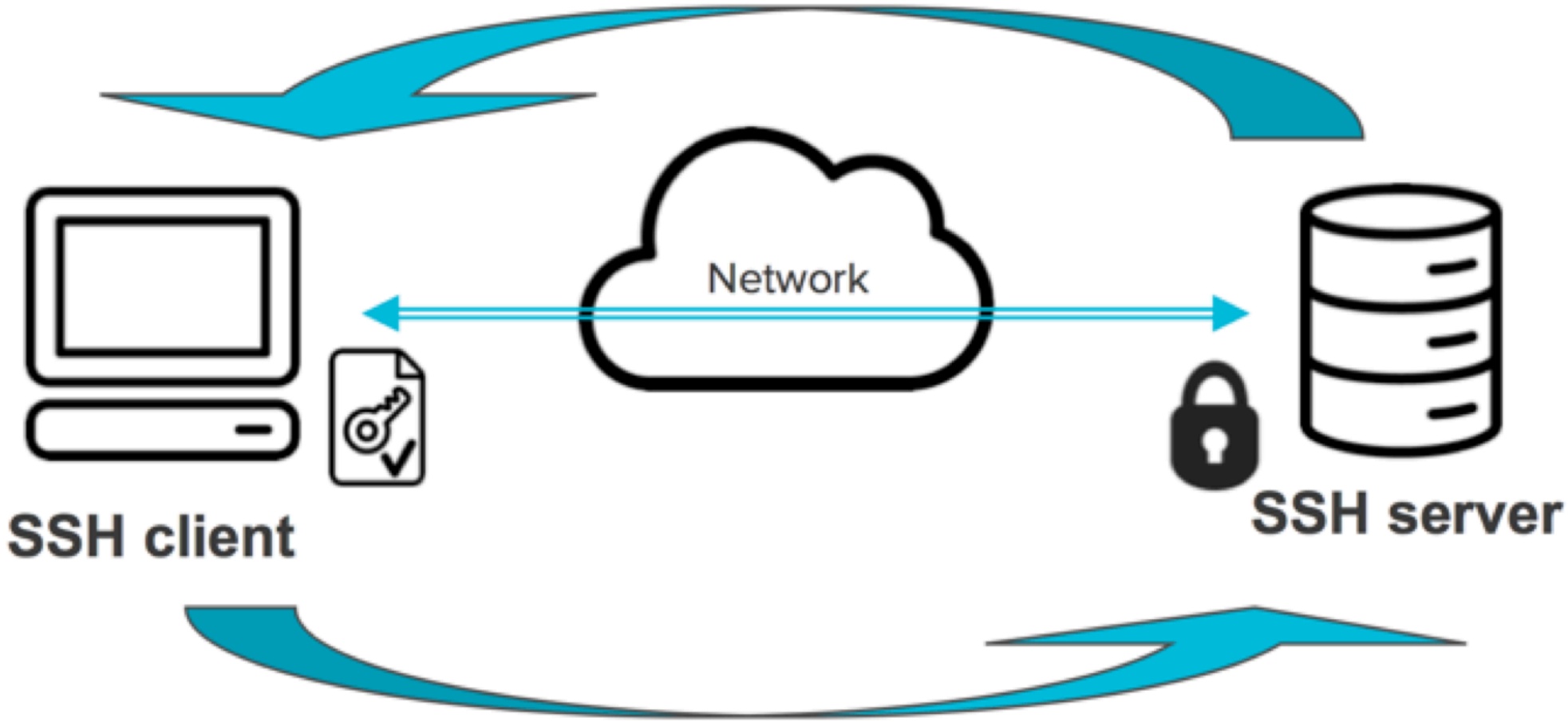
GenBank

What about jobs that take a long time?

We can run these remotely on an analysis server!


SSH...
OpenSSH
KEEPING YOUR COMMUNIQUÉS SECRET
TOP SECRET

1) Server authentication:
Server proves its identity to the client



2) User authentication:
Client proves user's identity to the server

ssh username@168.123.185.xxx

Change your password!

scp – securely copy files over the network

Check the system using htop

Where are we at?