

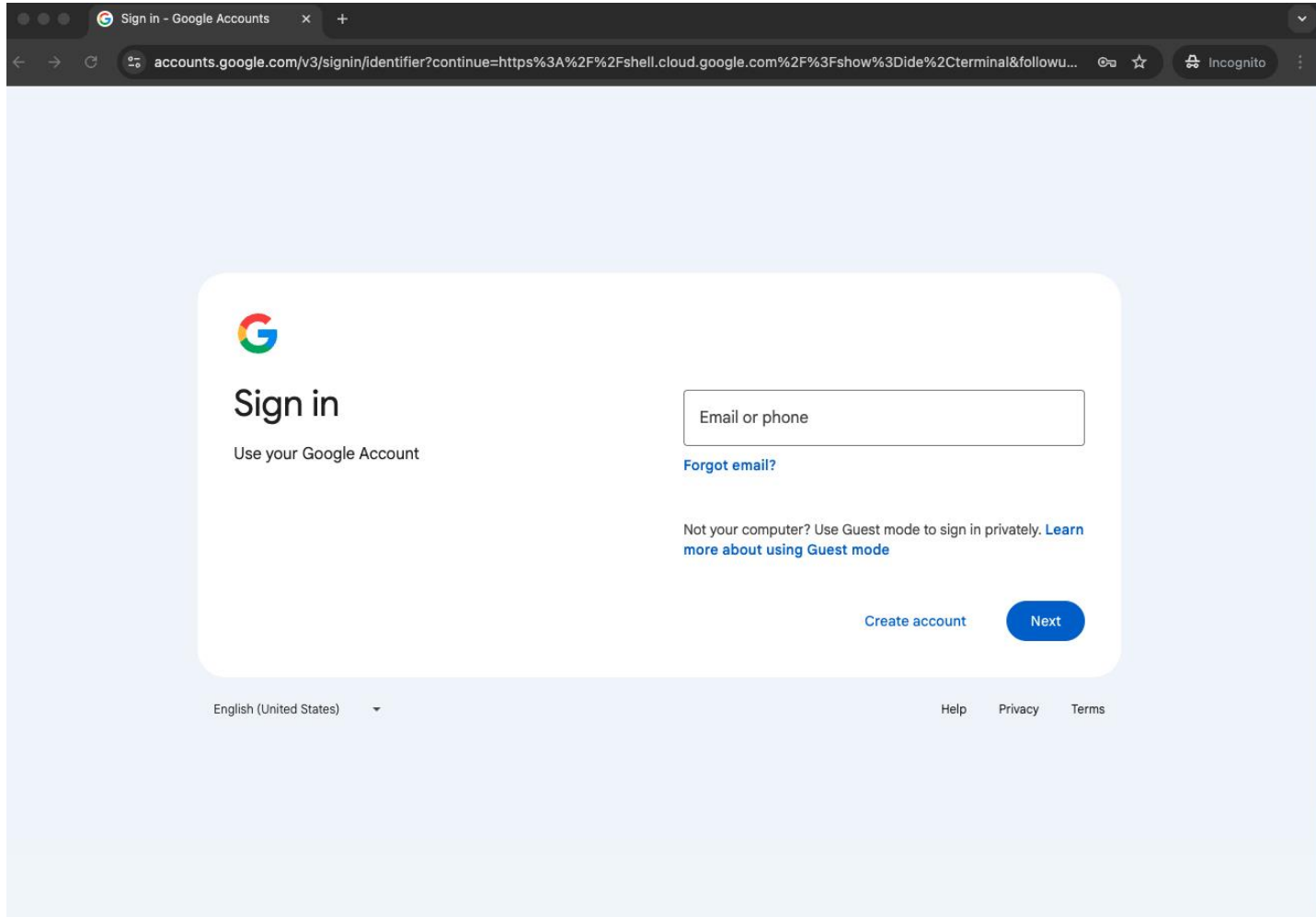
Sommersemester 2025

Vertiefte Bestimmungsübungen an Tieren (MEES003/C3)

Environmental DNA (eDNA) Metabarcoding analysis

Day 0

Go to <https://shell.cloud.google.com/?show=ide%2Cterminal>



Sign in if you have an account

If you don't want to create an account, set up the environment on your PC (see Day 0.md [Optional]).

The following cloud shell will appear:

The screenshot shows a web browser window with the address bar displaying `shell.cloud.google.com/?show=ide%2Cterminal`. The browser is in Incognito mode. The main interface is the Cloud Shell Editor, which includes a sidebar with an Explorer view showing a file tree for a user named SHUMPEI_YAMAKAWA. The tree contains directories like `ncbi-blast-2.16.0+`, `New_directory1`, `R`, `test`, and `test2`, along with a file `README-cloudshell.txt`. The main editor area displays a 'Welcome' message and a 'Get Started with Code OSS for the Web' tutorial. A sidebar on the right features a 'Welcome to Gemini Code Assist' message. At the bottom, a terminal window shows the Cloud Shell welcome message and the prompt `shumpei_yamakawa@cloudshell:~$`.

Cloud Shell

shell.cloud.google.com/?show=ide%2Cterminal

Incognito

Cloud Shell Editor

File Edit Selection View Go Run ...

shumpei_yamakawa

EXPLORER

SHUMPEI_YAMAKAWA

- > ncbi-blast-2.16.0+
- > New_directory1
- > R
- > test
- > test2
- ≡ README-cloudshell.txt

OUTLINE

TIMELINE

Welcome

Get Started with Code OSS for the Web

Customize your editor, learn the basics, and start coding

☐ Just the right amount of UI

The full menu bar is available in the dropdown menu to make room for

Welcome to Gemini Code Assist

Supercharge your workflow with AI-

Layout: U.S.

cloudshell

```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
shumpei_yamakawa@cloudshell:~$
```

The following cloud shell will appear:

Cloud Shell

shell.cloud.google.com/?show=ide%2Cterminal

Cloud Shell Editor

File Edit Selection View Go Run ...

EXPLORER

SHUMPEI_YAMAKAWA

- > ncbi-blast-2.16.0+
- > New_directory1
- > R
- > test
- > test2
- ≡ README-cloudshell.txt

OUTLINE

TIMELINE

Cloud Code - No Project

cloudshell

Enter your command to install the software!

Welcome to Gemini Code Assist

Supercharge your workflow with AI-Layout: U.S.

```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
shumpei_yamakawa@cloudshell:~$
```

Copy and paste the commands from Day0.md.

The screenshot shows a GitHub repository page for `FSUJENA_2025_species_determination`. The file `Day0.md` is selected in the left sidebar. The main content area shows the file's preview, which is highlighted with an orange border. The content includes instructions for installing software, creating a working directory, and running BLAST and SeqKit.

Installing the software

The following software is required for the analysis. Mainly, you can just copy and paste them in your terminal and see if they are working. You need to change the directory path according to your location.

****0. Opening**

1. Creating the working directory and moving to there

```
mkdir test_meta
cd test_meta
```

2. blast

See also <https://www.ncbi.nlm.nih.gov/books/NBK569861/>

```
wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
tar -xvzf ncbi-blast-2.16.0+-x64-linux.tar.gz
cd ncbi-blast-2.16.0+/bin
pwd
#Copy the displayed path!!
echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc
#Paste the path you copied to **YOUR PATH**!!

blastp -h
#If you see the description about Blast Search, then the installation worked.
```

3. seqkit

1. Creating the working directory and moving to there

```
mkdir test_meta  
cd test_meta
```

Type “mkdir test_meta”



A screenshot of a Cloud Shell terminal window. The terminal shows the prompt 'shumpei_yamakawa@cloudshell:~\$' followed by the command 'mkdir test_meta'. The command is highlighted with an orange box, and an orange arrow points to it from the text 'Type “mkdir test_meta”' above. The terminal also displays a welcome message and instructions for setting up the Cloud Platform project.

+ enter



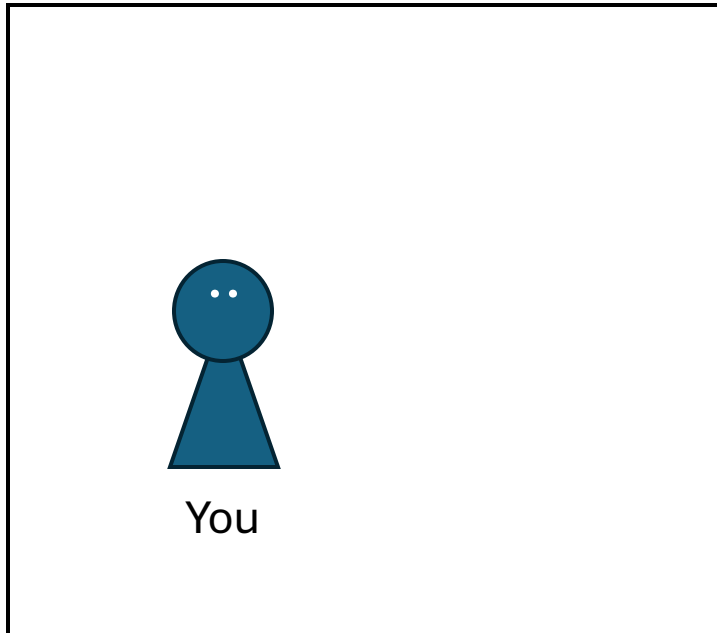
A screenshot of a Cloud Shell terminal window. The terminal shows the prompt 'shumpei_yamakawa@cloudshell:~\$' followed by the command 'mkdir test_meta'. The command has been executed, and the terminal displays the prompt 'shumpei_yamakawa@cloudshell:~\$' again. The terminal also displays a welcome message and instructions for setting up the Cloud Platform project.

Type “cd test_meta” + enter

```
shumpei_yamakawa@cloudshell:~$ cd test_meta/  
shumpei_yamakawa@cloudshell:~/test_meta$
```

What you did...

Home directory

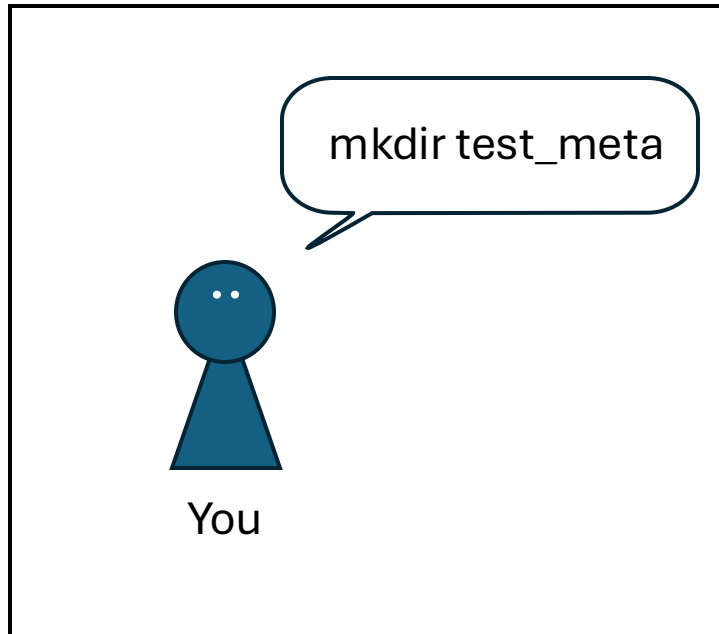


First, you are at “home directory”

(If you want to know the current your location/path, type “pwd”)

What you did...

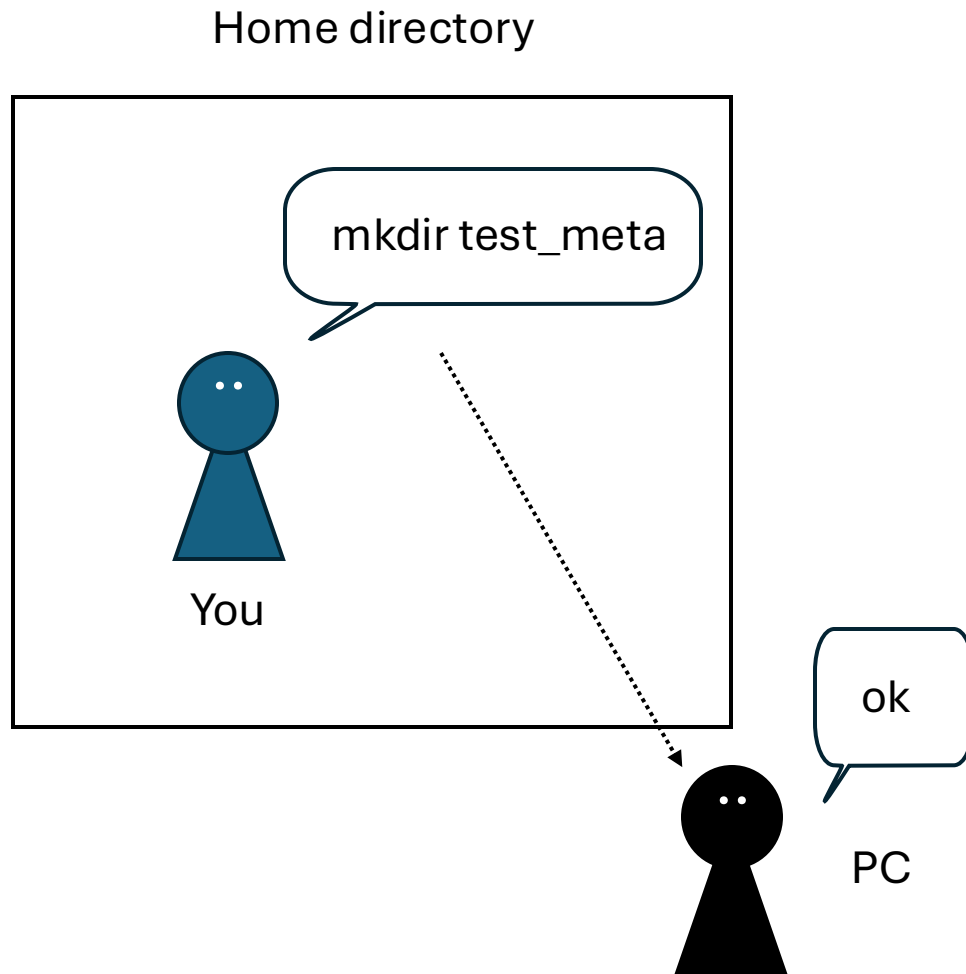
Home directory



Then, you typed “mkdir test_meta”

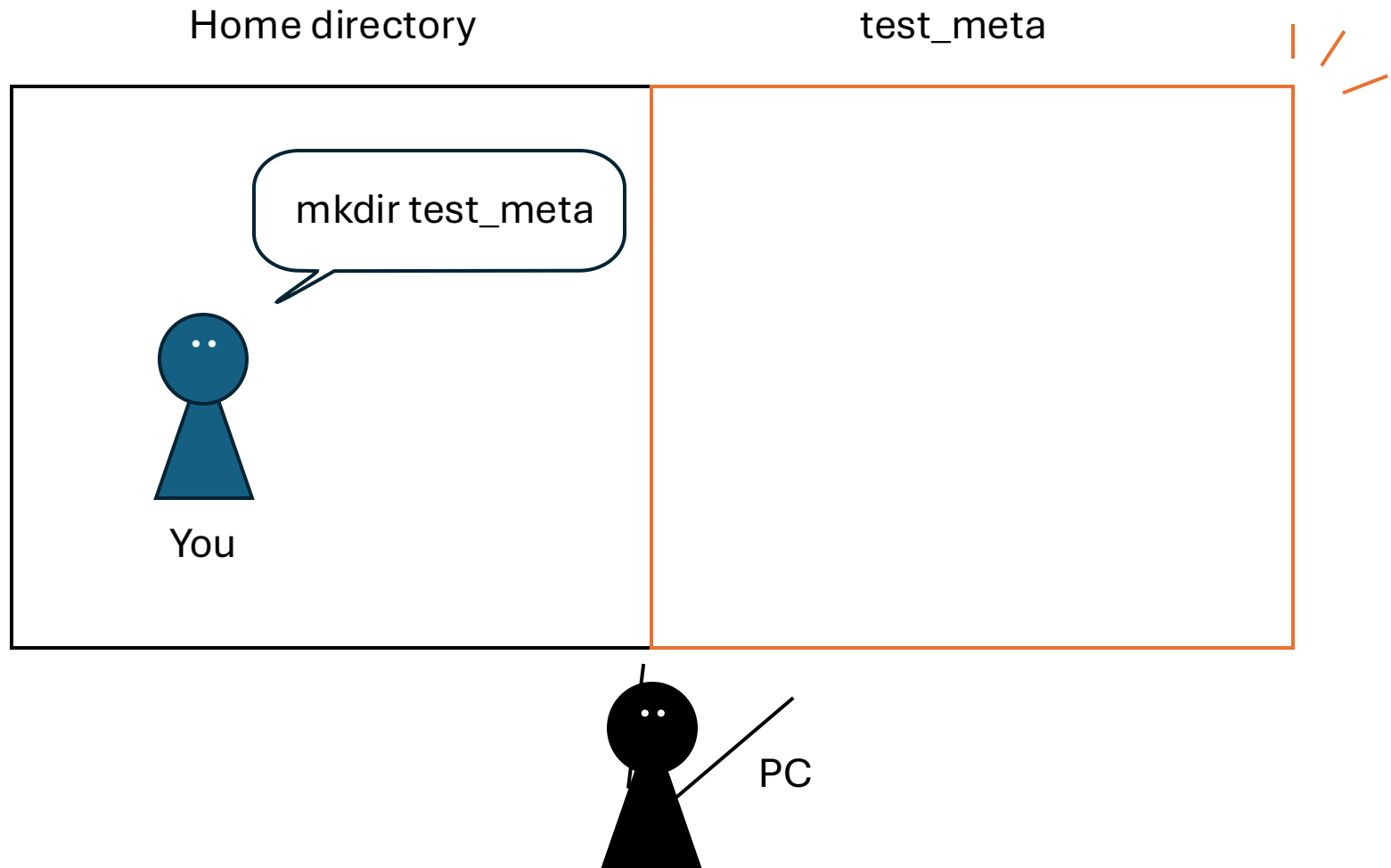
mkdir is a command to make a directory

What you did...



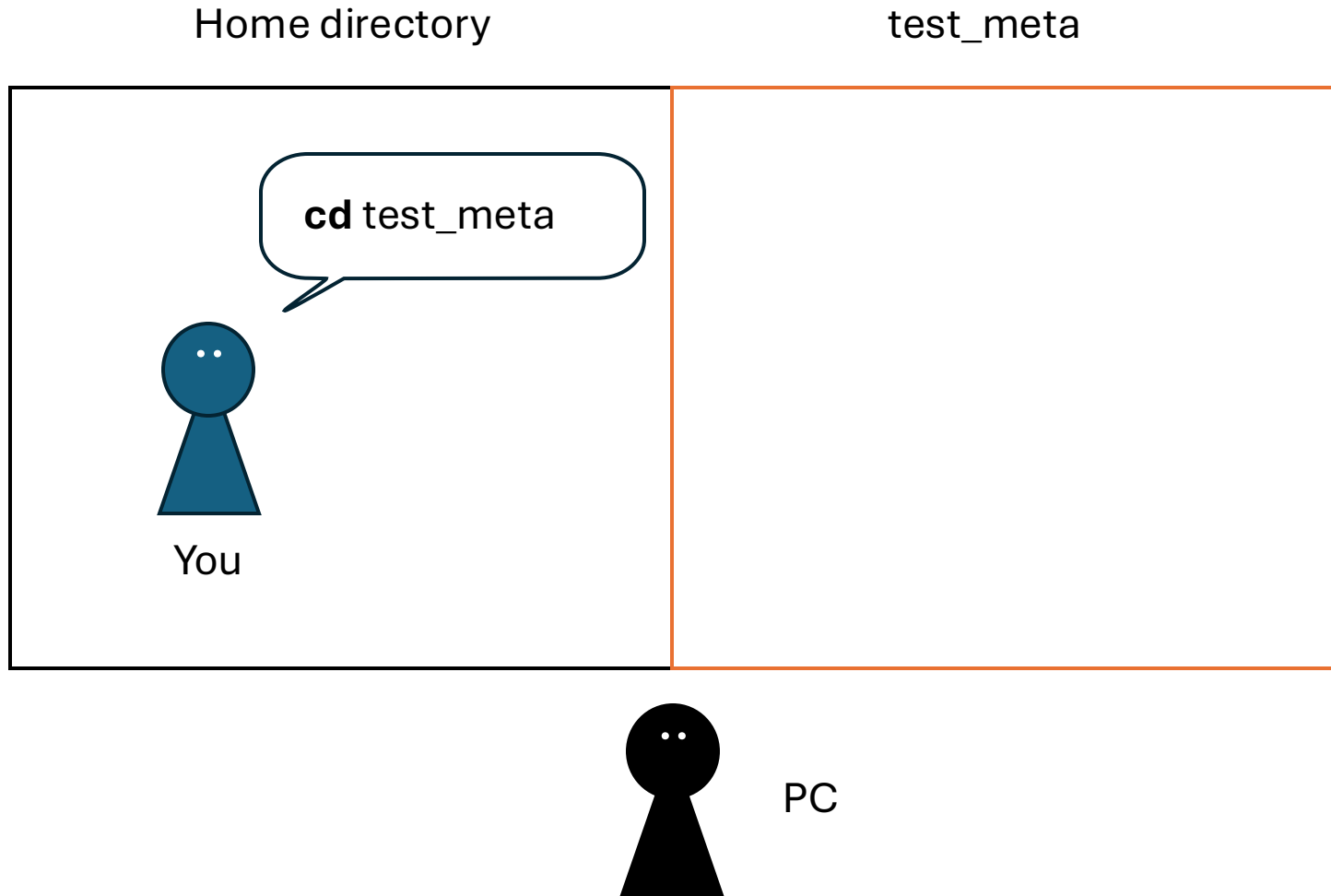
PC recognizes this command

What you did...



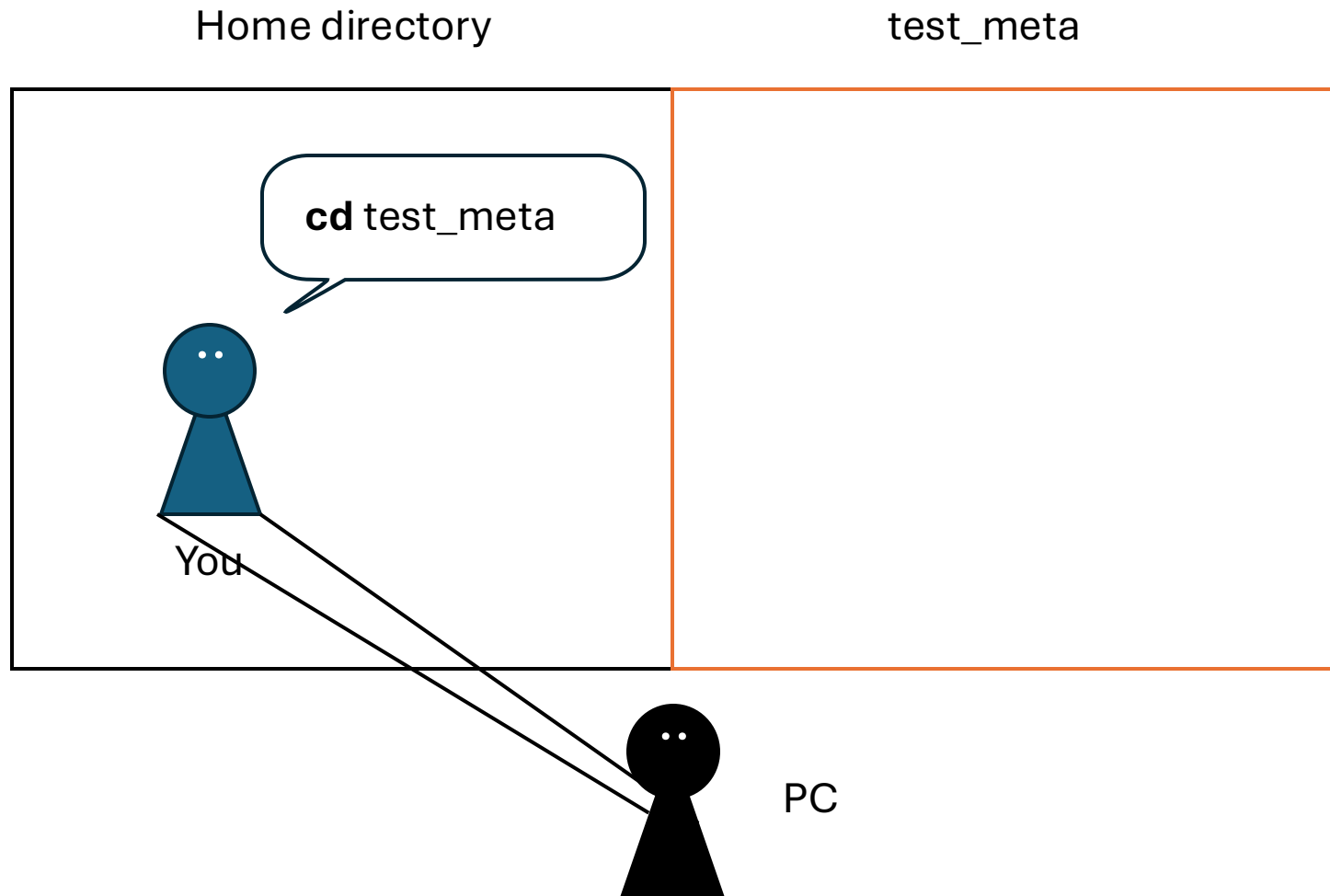
and made a directory

What you did...



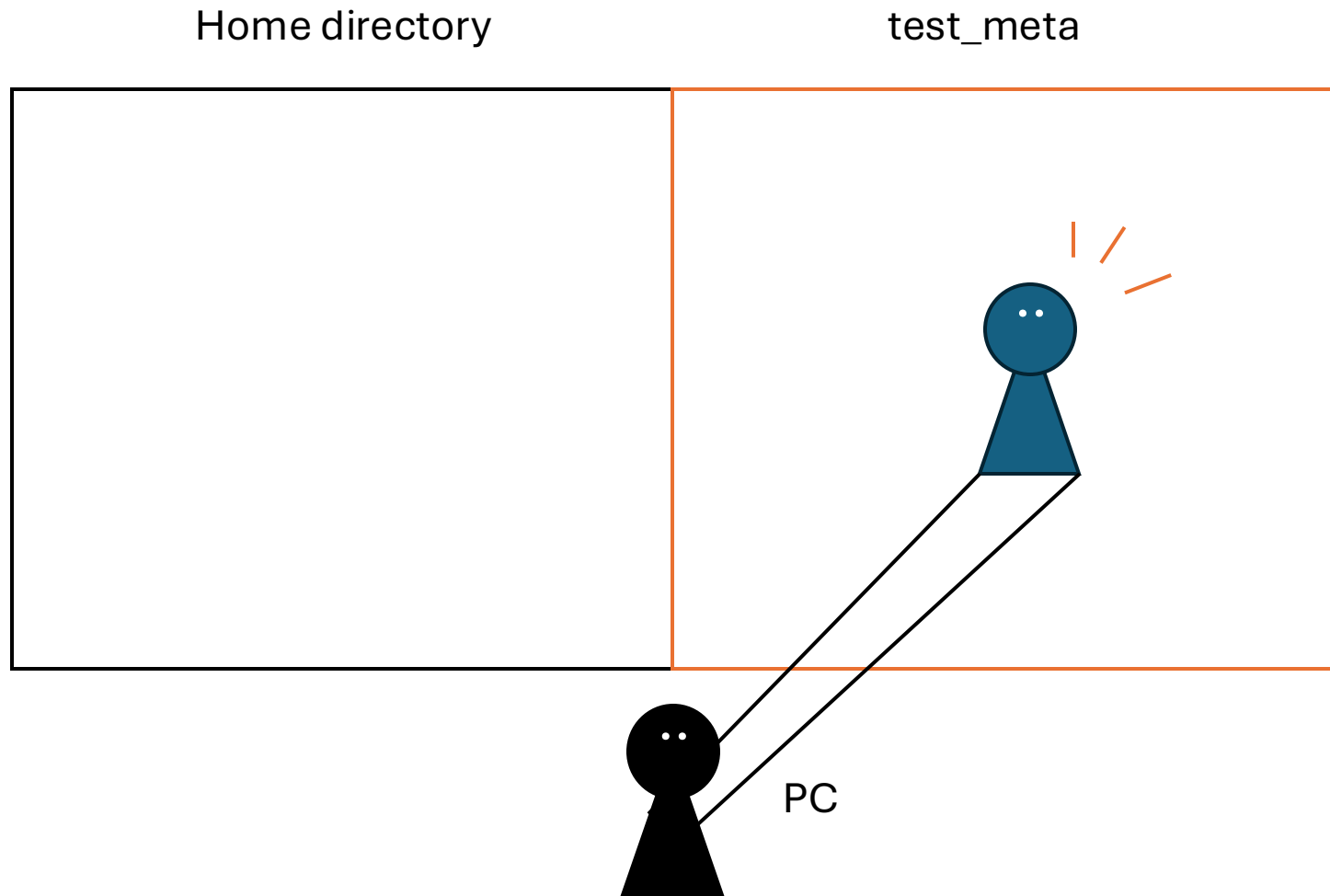
“cd” is “change directory”

What you did...

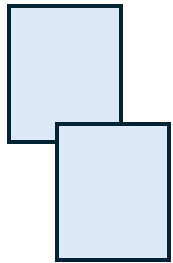


“cd” is “change directory”

What you did...



“cd” is “change directory”



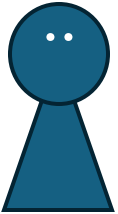
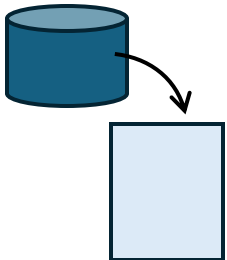
I wan to copy the
file

= cp



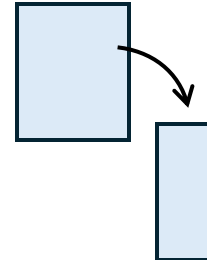
I wan to delete
the file

= rm



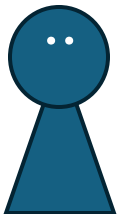
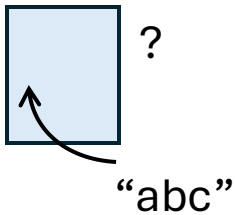
Download the
file from url

= wget



Edit the file
content

= awk



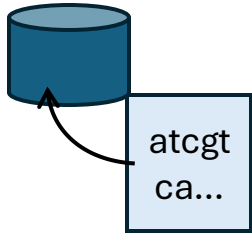
Search specific
words in the file

= grep

Various basic commands are
already prepared

See the official tutorial:

<https://ubuntu.com/tutorials/command-line-for-beginners#1-overview>



I want to make a
Blast database

= makeblastdb

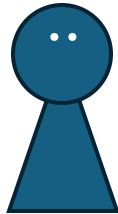
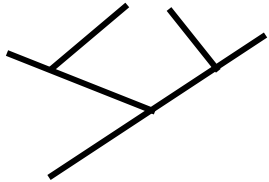
agctttta
atcgtca
...

atcgt
ca...



Search specific
sequences

= seqkit grep



Make a
phylogenetic tree

= raxml

Need to download specific
software for bioinformatic analysis

2. blast

See also <https://www.ncbi.nlm.nih.gov/books/NBK569861/>

```
wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
tar -xvzf ncbi-blast-2.16.0+-x64-linux.tar.gz
cd ncbi-blast-2.16.0+/bin
pwd
#Copy the displayed path!!
echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc
#Paste the path you copied to **YOUR PATH**!!

blastp -h
#If you see the description about Blast Search, then the installation worked.
```



All Databases

Search

NCBI Home

Resource List (A-Z)

All Resources
Chemicals & Bioassays
Data & Software
DNA & RNA
Domains & Structures
Genes & Expression
Genetics & Medicine
Genomes & Maps
Homology
Literature
Proteins
Sequence Analysis
Taxonomy
Training & Tutorials
Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

[About the NCBI](#) | [Mission](#) | [Organization](#) | [NCBI News & Blog](#)

Submit

Deposit data or manuscripts into NCBI databases



Download

Transfer NCBI data to your computer



Learn

Find help documents, attend a class or watch a tutorial



Develop

Use NCBI APIs and code libraries to build applications



Analyze

Identify an NCBI tool for your data analysis task



Research

Explore NCBI research and collaborative projects



Popular Resources

PubMed
Bookshelf
PubMed Central
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

NCBI News & Blog

NCBI Taxonomy Update Classification

Starting April 28, 2025 | 2024 was announced so

PubMed Central's Update Search Preview Now Available

As previously announced, we are announcing the PubMed Central's Update Search Preview Now Available

Coming Soon! Enhance your research with the new PubMed Central's Update Search Preview Now Available

Many people visit NCBI every day, multiple times

Software for blast search is available in the webpage of ncbi

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

[Learn more](#)

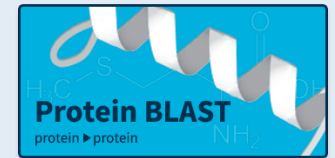
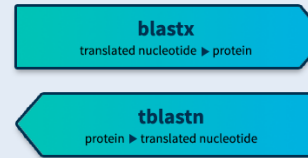
Mon, 17 Mar 2025

Improvements include upgrading to GCP Artifact Registry and better handling of job completion status in kubernetes version 1.30+.

ElasticBLAST 1.4.0 is now available!

[More BLAST news...](#)

Web BLAST



BLAST > [blast-help](#) > Download BLAST Software and Databases

Was this correct?

BLAST+ executables

What are the next steps?

Magic-BLAST

IgBLAST

SRPRISM

Databases

BLAST+ executables

Do you have difficulties running high volume BLAST searches? Do you have sequence data to search and cannot use the NCBI BLAST web site? Do you have your own server? Do you have your own research pipeline? Have security or sending searches outside of your organization? If you answered yes to any of these questions, read on!

The NCBI provides a suite of command-line tools to run BLAST called BLAST+. This allows users to perform BLAST searches on their own server without size, volume and database restrictions. BLAST+ can be used with a command line so it can be integrated directly into your workflow.

What are the next steps?

Download and install BLAST+. Installers and source code are available from <https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/>. Download the databases you need, (see database section below), or create your own. Start searching.

For more details, please see the [BLAST+ user manual](#), the [BLAST Help manual](#), the [BLAST releases notes](#), and the article in BMC Bioinformatics ([PubMed link](#)). See our [versioning policy](#).

The BLAST+ suite is the currently supported package. The older C toolkit executables are no longer supported. See our [versioning policy](#).

We are always listening and welcome your feedback at [BLAST Support Center](#).

BLAST Genomes

Enter organism common name, scientific name, or tax id

Search

Human

Mouse

Rat

Microbes

Standalone and API BLAST



Download BLAST

Get BLAST databases and executables



Use BLAST API

Call BLAST from your application



Use BLAST in the cloud

Start an instance at a cloud provider

```
wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
```



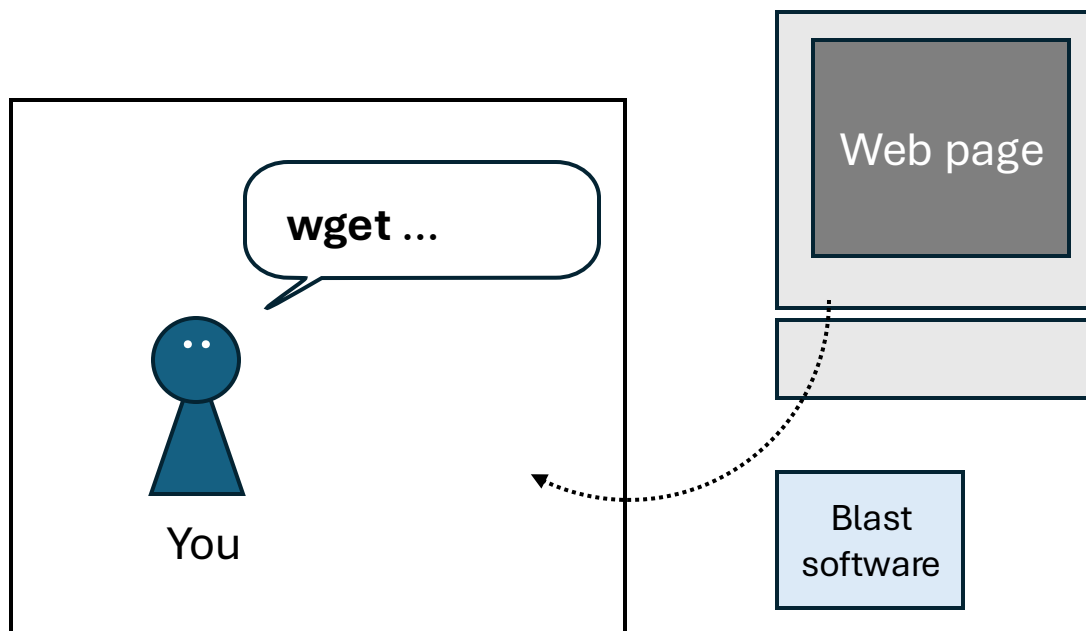
↓

```
shumpei_yamakawa@cloudshell:~/test_meta$ wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
--2025-06-04 13:38:44-- https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
Resolving ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)... 130.14.250.12, 130.14.250.13, 130.14.250.31, ...
Connecting to ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)|130.14.250.12|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 257516053 (246M) [application/x-gzip]
Saving to: 'ncbi-blast-2.16.0+-x64-linux.tar.gz'

ncbi-blast-2.16.0+-x64-linux.tar.gz      100%[=====] 245.59M  25.3MB/s   in 9.9s

2025-06-04 13:38:54 (24.9 MB/s) - 'ncbi-blast-2.16.0+-x64-linux.tar.gz' saved [257516053/257516053]

shumpei_yamakawa@cloudshell:~/test_meta$
```



```
wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
```



↓

```
shumpei_yamakawa@cloudshell:~/test_meta$ wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
--2025-06-04 13:38:44-- https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
Resolving ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)... 130.14.250.12, 130.14.250.13, 130.14.250.31, ...
Connecting to ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)|130.14.250.12|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 257516053 (246M) [application/x-gzip]
Saving to: 'ncbi-blast-2.16.0+-x64-linux.tar.gz'

ncbi-blast-2.16.0+-x64-linux.tar.gz      100%[=====>] 245.59M  25.3MB/s   in 9.9s

2025-06-04 13:38:54 (24.9 MB/s) - 'ncbi-blast-2.16.0+-x64-linux.tar.gz' saved [257516053/257516053]


shumpei_yamakawa@cloudshell:~/test_meta$
```

↓

Type “ls” (see the contents in the current directory)

```
shumpei_yamakawa@cloudshell:~/test_meta$ ls
ncbi-blast-2.16.0+-x64-linux.tar.gz
```

```
wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
```



```
shumpei_yamakawa@cloudshell:~/test_meta$ wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
--2025-06-04 13:38:44-- https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
Resolving ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)... 130.14.250.12, 130.14.250.13, 130.14.250.31, ...
Connecting to ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)|130.14.250.12|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 257516053 (246M) [application/x-gzip]
Saving to: 'ncbi-blast-2.16.0+-x64-linux.tar.gz'

ncbi-blast-2.16.0+-x64-linux.tar.gz      100%[=====>] 245.59M  25.3MB/s   in 9.9s

2025-06-04 13:38:54 (24.9 MB/s) - 'ncbi-blast-2.16.0+-x64-linux.tar.gz' saved [257516053/257516053]

shumpei_yamakawa@cloudshell:~/test_meta$
```



Type “ls” (see the contents in the current directory)

```
shumpei_yamakawa@cloudshell:~/test_meta$ ls
ncbi-blast-2.16.0+-x64-linux.tar.gz
```



Compressed archive file

```
wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
```



↓

```
shumpei_yamakawa@cloudshell:~/test_meta$ wget https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
--2025-06-04 13:38:44-- https://ftp.ncbi.nlm.nih.gov/blast/executables/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
Resolving ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)... 130.14.250.12, 130.14.250.13, 130.14.250.31, ...
Connecting to ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)|130.14.250.12|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 257516053 (246M) [application/x-gzip]
Saving to: 'ncbi-blast-2.16.0+-x64-linux.tar.gz'

ncbi-blast-2.16.0+-x64-linux.tar.gz      100%[=====>] 245.59M  25.3MB/s   in 9.9s

2025-06-04 13:38:54 (24.9 MB/s) - 'ncbi-blast-2.16.0+-x64-linux.tar.gz' saved [257516053/257516053]

shumpei_yamakawa@cloudshell:~/test_meta$
```

↓

Type “ls” (see the contents in the current directory)

```
shumpei_yamakawa@cloudshell:~/test_meta$ ls
ncbi-blast-2.16.0+-x64-linux.tar.gz
```

↑

Compressed archive file

↓

```
tar -xvzf ncbi-blast-2.16.0+-x64-linux.tar.gz
```

Command for decompressing

ncbi-blast-2.16.0+-x64-linux.tar.gz

shumpei_yamakawa@cloudshell:~/test_meta\$ tar -xvzf ncbi-blast-2.16.0+-x64-linux.tar.gz

ncbi-blast-2.16.0+/

ncbi-blast-2.16.0+/ChangeLog

ncbi-blast-2.16.0+/bin/

ncbi-blast-2.16.0+/bin/rpsblast

ncbi-blast-2.16.0+/bin/blastn_vdb

ncbi-blast-2.16.0+/bin/blast_vdb_cmd

ncbi-blast-2.16.0+/bin/makeprofiledb

ncbi-blast-2.16.0+/bin/blastp

ncbi-blast-2.16.0+/bin/deltablast

ncbi-blast-2.16.0+/bin/blastx

ncbi-blast-2.16.0+/bin/rpstblastn

ncbi-blast-2.16.0+/bin/psiblast

ncbi-blast-2.16.0+/bin/tblastx

ncbi-blast-2.16.0+/bin/tblastn_vdb

ncbi-blast-2.16.0+/bin/blast_formatter_vdb

ncbi-blast-2.16.0+/bin/segmasker

ncbi-blast-2.16.0+/bin/convert2blastmask

ncbi-blast-2.16.0+/bin/blastdbcmd

ncbi-blast-2.16.0+/bin/get_species_taxids.sh

ncbi-blast-2.16.0+/bin/dustmasker

ncbi-blast-2.16.0+/bin/cleanup-blastdb-volumes.py

ncbi-blast-2.16.0+/bin/blastn

ncbi-blast-2.16.0+/bin/windowmasker

ncbi-blast-2.16.0+/bin/makeblastdb

ncbi-blast-2.16.0+/bin/blastdb_aliastool

ncbi-blast-2.16.0+/bin/update_blastdb.pl

ncbi-blast-2.16.0+/bin/makembindex

ncbi-blast-2.16.0+/bin/blast_formatter

ncbi-blast-2.16.0+/bin/legacy_blast.pl

ncbi-blast-2.16.0+/bin/blastdbcheck

ncbi-blast-2.16.0+/bin/tblastn

ncbi-blast-2.16.0+/LICENSE

ncbi-blast-2.16.0+/BLAST_PRIVACY

ncbi-blast-2.16.0+/ncbi_package_info

ncbi-blast-2.16.0+/README

ncbi-blast-2.16.0+/doc/

ncbi-blast-2.16.0+/doc/README.txt

shumpei_yamakawa@cloudshell:~/test_meta\$ ls

ncbi-blast-2.16.0+ ncbi-blast-2.16.0+-x64-linux.tar.gz

shumpei_yamakawa@cloudshell:~/test_meta\$

Path set*

- ① `cd ncbi-blast-2.16.0+/bin`
- ② `pwd`
#Copy the displayed path!!
- ③ `echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc`
#Paste the path you copied to **YOUR PATH**!!

①

```
shumpei_yamakawa@cloudshell:~/test_meta$ cd ncbi-blast-2.16.0+/bin
```



②

```
shumpei_yamakawa@cloudshell:~/test_meta/ncbi-blast-2.16.0+/bin$ pwd
```

* If you want to know more about path setting, see the attached slides

Path set

- ① `cd ncbi-blast-2.16.0+/bin`
- ② `pwd`
#Copy the displayed path!!
- ③ `echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc`
#Paste the path you copied to **YOUR PATH**!!

①

```
shumpei_yamakawa@cloudshell:~/test_meta$ cd ncbi-blast-2.16.0+/bin
```



②

```
shumpei_yamakawa@cloudshell:~/test_meta/ncbi-blast-2.16.0+/bin$ pwd  
/home/shumpei_yamakawa/test_meta/ncbi-blast-2.16.0+/bin
```

↑
YOUR PATH

Path set

- ① `cd ncbi-blast-2.16.0+/bin`
- ② `pwd`
#Copy the displayed path!!
- ③ `echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc`
#Paste the path you copied to **YOUR PATH**!!

①

```
shumpei_yamakawa@cloudshell:~/test_meta$ cd ncbi-blast-2.16.0+/bin
```



②

```
shumpei_yamakawa@cloudshell:~/test_meta/ncbi-blast-2.16.0+/bin$ pwd  
/home/shumpei_yamakawa/test_meta/ncbi-blast-2.16.0+/bin
```



```
echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc
```

Path set

- ① `cd ncbi-blast-2.16.0+/bin`
- ② `pwd`
#Copy the displayed path!!
- ③ `echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc`
#Paste the path you copied to **YOUR PATH**!!

①

```
shumpei_yamakawa@cloudshell:~/test_meta$ cd ncbi-blast-2.16.0+/bin
```



②

```
shumpei_yamakawa@cloudshell:~/test_meta/ncbi-blast-2.16.0+/bin$ pwd  
/home/shumpei_yamakawa/test_meta/ncbi-blast-2.16.0+/bin
```



```
echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc
```



Substitute your path and remove ***

```
echo 'export PATH="/home/shu.../bin:$PATH"' >> ~/.bashrc; source ~/.bashrc
```

Path set

- ① `cd ncbi-blast-2.16.0+/bin`
- ② `pwd`
#Copy the displayed path!!
- ③ `echo 'export PATH="**YOUR PATH**:$PATH"' >> ~/.bashrc; source ~/.bashrc`
#Paste the path you copied to **YOUR PATH**!!

①

```
shumpei_yamakawa@cloudshell:~/test_meta$ cd ncbi-blast-2.16.0+/bin
```



②

```
shumpei_yamakawa@cloudshell:~/test_meta/ncbi-blast-2.16.0+/bin$ pwd  
/home/shumpei_yamakawa/test_meta/ncbi-blast-2.16.0+/bin
```



③

```
in$ echo 'export PATH="/home/shumpei_yamakawa/test_meta/ncbi-blast-2.16.0+/bin:$PATH"' >> ~/.bashrc; source ~/.bashrc
```

```
blastp -h
```

```
#If you see the description about Blast Search, then the installation worked.
```

```
shumpei_yamakawa@cloudshell:~/test_meta/ncbi-blast-2.16.0+/bin$ blastp -h
USAGE
  blastp [-h] [-help] [-import_search_strategy filename]
    [-export_search_strategy filename] [-task task_name] [-db database_name]
    [-dbsize num_letters] [-gilist filename] [-seqidlist filename]
    [-negative_gilist filename] [-negative_seqidlist filename]
    [-taxids taxids] [-negative_taxids taxids] [-taxidlist filename]
    [-negative_taxidlist filename] [-no_taxid_expansion] [-ipglist filename]
    [-negative_ipglist filename] [-entrez_query entrez_query]
    [-db_soft_mask filtering_algorithm] [-db_hard_mask filtering_algorithm]
    [-subject subject_input_file] [-subject_loc range] [-query input_file]
    [-out output_file] [-evaluate evaluate] [-word_size int_value]
    [-gapopen open_penalty] [-gapextend extend_penalty]
    [-qcov_hsp_perc float_value] [-max_hsps int_value]
    [-xdrop_ungap float_value] [-xdrop_gap float_value]
    [-xdrop_gap_final float_value] [-searchsp int_value] [-seg SEG_options]
    [-soft_masking soft_masking] [-matrix matrix_name]
    [-threshold float_value] [-culling_limit int_value]
    [-best_hit_overhang float_value] [-best_hit_score_edge float_value]
    [-subject_besthit] [-window_size int_value] [-lcase_masking]
    [-query_loc range] [-parse_deflines] [-outfmt format] [-show_gis]
    [-num_descriptions int_value] [-num_alignments int_value]
    [-line_length line_length] [-html] [-sorthits sort_hits]
    [-sorthsps sort_hsps] [-max_target_seqs num_sequences]
    [-num_threads int_value] [-mt_mode int_value] [-ungapped] [-remote]
    [-comp_based_stats compo] [-use_sw_tback] [-version]
```

DESCRIPTION

Protein-Protein BLAST 2.16.0+

Use '-help' to print detailed descriptions of command line arguments

```
shumpei_yamakawa@cloudshell:~/test_meta/ncbi-blast-2.16.0+/bin$
```

3. seqkit

The software for manipulating the sequence files. See also <https://bioinf.shenwei.me/seqkit/>

```
cd ~/test_meta
#move to the test directory
wget https://github.com/shenwei356/seqkit/releases/download/v2.10.0/seqkit_linux_amd64.tar.gz
tar -xvzf seqkit_linux_amd64.tar.gz
sudo cp seqkit /usr/local/bin/

seqkit -h
#If you see the description about Blast Search, then the installation worked.
```

4. update/developer environments

```
sudo apt update
sudo apt install -y \
    liblapack-dev \
    libblas-dev \
    gfortran \
    libpng-dev \
    libgsl-dev \
    libtiff5-dev \
    libjpeg-dev \
    libxml2-dev \
    libcurl4-openssl-dev \
    libxt-dev \
    libfftw3-dev \
    libreadline-dev \
    zlib1g-dev \
    libx11-dev \
    libncurses-dev \
    libbz2-dev \
    liblzma-dev
```

Simply follow the script...

5. R

R is a programming language and software environment for statistical computing, data analysis, and visualization. See also <https://www.r-project.org/>

```
cd ~/test_meta
#move to the test directory

# update indices
sudo apt update -qq
# install two helper packages we need
sudo apt install --no-install-recommends software-properties-common dirmngr
# add the signing key (by Michael Rutter) for these repos
# To verify key, run gpg --show-keys /etc/apt/trusted.gpg.d/cran_ubuntu_key.asc
# Fingerprint: E298A3A825C0D65DFD57CBB651716619E084DAB9
wget -qO- https://cloud.r-project.org/bin/linux/ubuntu/marutter_pubkey.asc | sudo tee -a /etc/apt/trusted.gpg.d/cran_
# add the repo from CRAN -- lsb_release adjusts to 'noble' or 'jammy' or ... as needed
sudo add-apt-repository "deb https://cloud.r-project.org/bin/linux/ubuntu $(lsb_release -cs)-cran40/"
# install R itself
sudo apt install --no-install-recommends r-base
```

During installing, you may see the following...

```
=xbQ3
-----END PGP PUBLIC KEY BLOCK-----
Repository: 'deb https://cloud.r-project.org/bin/linux/ubuntu noble-cran40/'
Description:
Archive for codename: noble-cran40/ components:
More info: https://cloud.r-project.org/bin/linux/ubuntu
Adding repository.
Press [ENTER] to continue or Ctrl-c to cancel.□
```

-> enter

```
libblas3 liblapack3 libpaper-utils libpaper1 libcurl3-gnutls libcurl3-nss libcurl4-openssl-dev libcurl4
r-cran-kernsmooth r-cran-lattice r-cran-mass r-cran-matrix r-cran-mgcv
0 upgraded, 27 newly installed, 0 to remove and 50 not upgraded.
Need to get 56.8 MB of archives.
After this operation, 94.2 MB of additional disk space will be used.
Do you want to continue? [Y/n] □
```

-> Y

```
shumpei_yamakawa@cloudshell:~$ R
```

Enter -> go to “R console”

```
shumpei_yamakawa@cloudshell:~$ R

R version 4.5.0 (2025-04-11) -- "How About a Twenty-Six"
Copyright (C) 2025 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

Start installing R packages

6. dada2: the R package for metabarcoding analysis

R provides a lot of the "packages" which are designed for specific analysis, and the package "dada2" performs to "infer exact amplicon sequence variants (ASVs) from amplicon data (<https://benjjneb.github.io/dada2/>)". This package needs to be installed in R console.

```
# install the softwares
install.packages(c("RcppEigen", "png", "deldir", "interp", "latticeExtra"))
if (!requireNamespace("BiocManager", quietly = TRUE))
  install.packages("BiocManager")
BiocManager::install("ShortRead")
BiocManager::install("dada2")
library(dada2)
packageVersion("dada2")
#Can you see the version of dada2? If so, dada2 was correctly installed!
```



```
shumpei_yamakawa@cloudshell:~$ R

R version 4.5.0 (2025-04-11) -- "How About a Twenty-Six"
Copyright (C) 2025 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> q()
Save workspace image? [y/n/c]: n
shumpei_yamakawa@cloudshell:~$
```

Type “q()” to escape from R console

Appendix

Public tutorial

<https://ubuntu.com/tutorials/command-line-for-beginners#1-overview>

<https://opensource.com/article/17/6/set-path-linux>

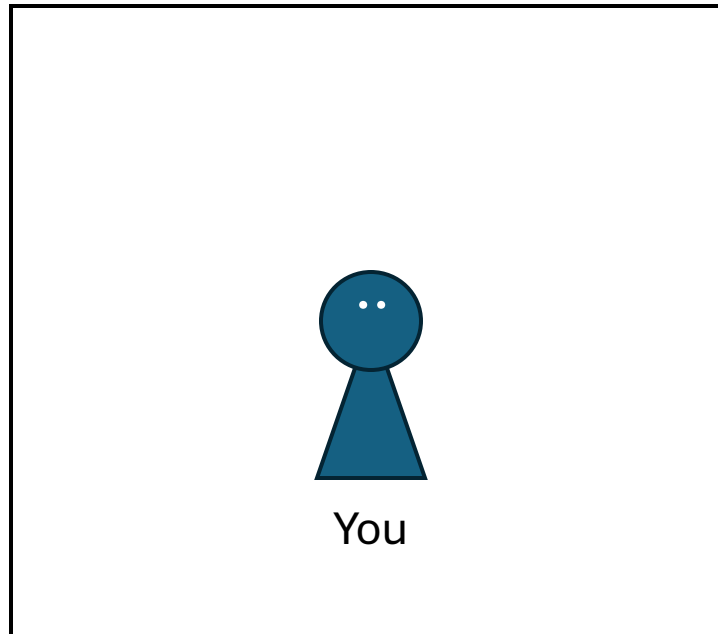
Illustrated guides about basic usage of linux

1. Location and directory structure
2. Installing software

1. Location and directory structure

```
Welcome to Cloud Shell! Type "help" to get started.  
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.  
You can view your projects by running `gcloud projects list`.  
Your home disk usage is at 95%.  
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.  
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.  
shumpei_yamakawa@cloudshell:~$
```

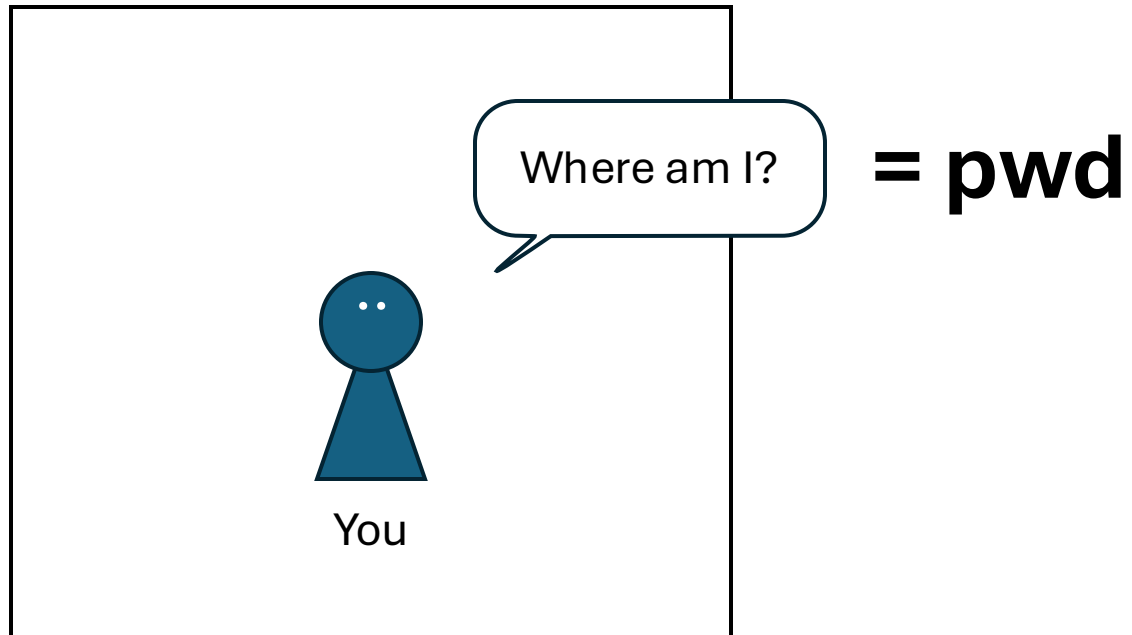
Home directory



“type pwd -> enter”

```
Welcome to Cloud Shell! Type "help" to get started.  
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.  
You can view your projects by running `gcloud projects list`.  
Your home disk usage is at 95%.  
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.  
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.  
shumpei_yamakawa@cloudshell:~$ pwd
```

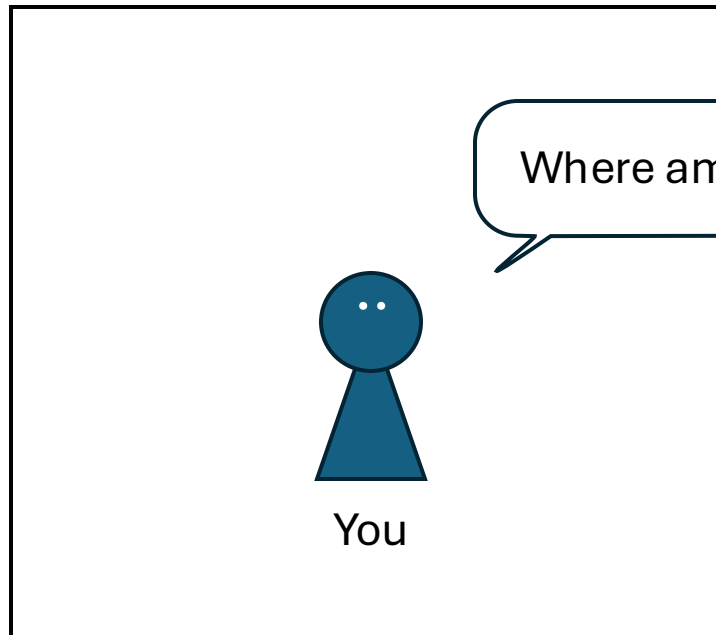
Home directory



```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
Your home disk usage is at 95%.
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.
shumpei_yamakawa@cloudshell:~$ pwd
/home/shumpei_yamakawa
shumpei_yamakawa@cloudshell:~$
```

your current address
(PATH)

Home directory

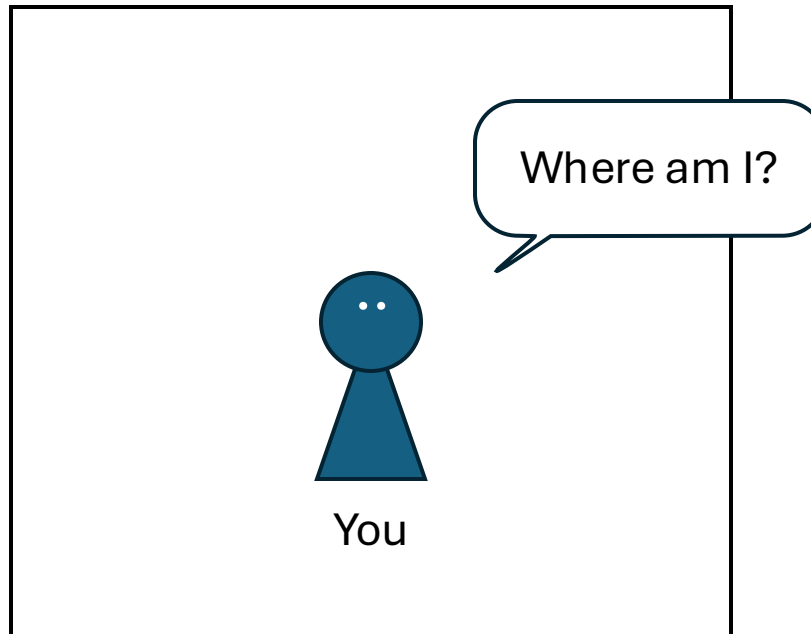


Where am I?

= **pwd**

```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
Your home disk usage is at 95%.
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.
shumpei_yamakawa@cloudshell:~$ pwd
/home/shumpei_yamakawa
shumpei_yamakawa@cloudshell:~$
```

Home directory:
/home/shumpei_yamakawa

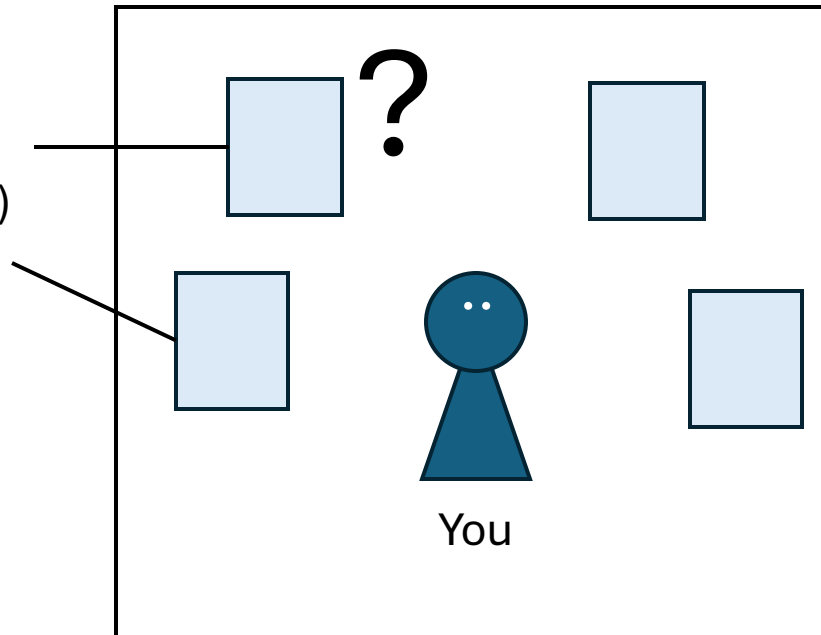


*the name of the directory depends on your account name

```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
Your home disk usage is at 95%.
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.
shumpei_yamakawa@cloudshell:~$ pwd
/home/shumpei_yamakawa
shumpei_yamakawa@cloudshell:~$
```

Home directory:
/home/shumpei_yamakawa

Files
(ex. text files)

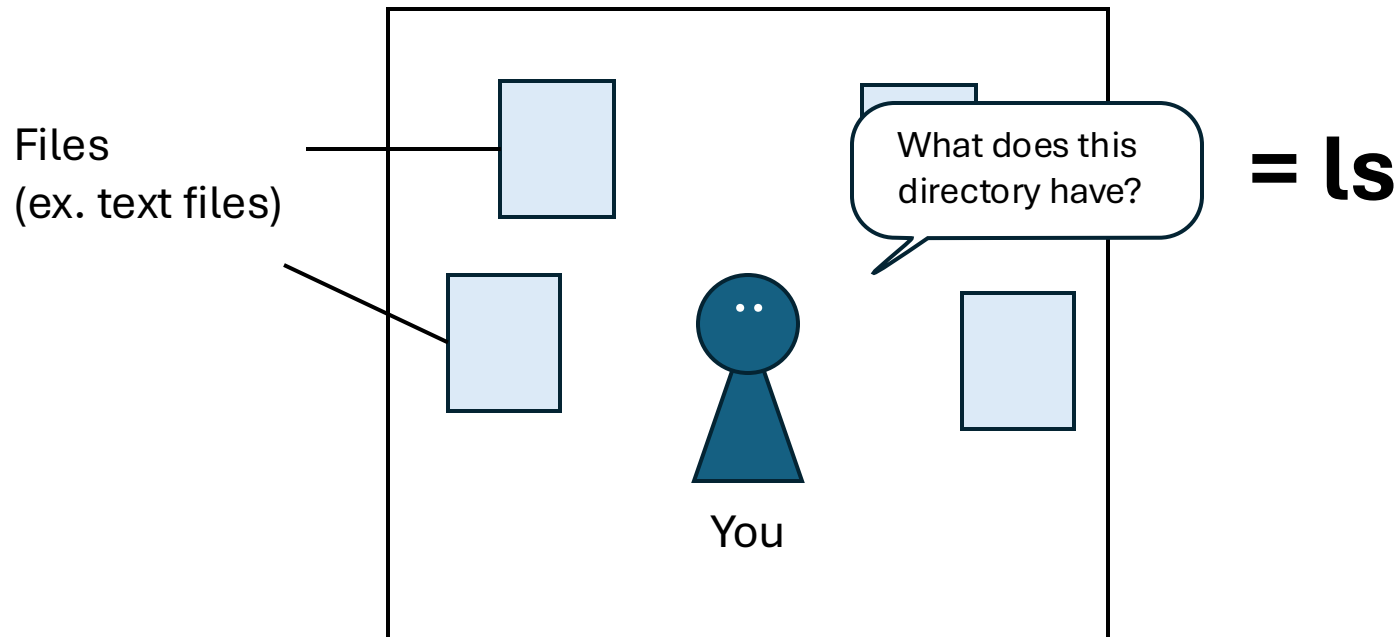


*the name of the directory depends on your account name

“type ls -> enter”

```
Welcome to Cloud Shell! Type "help" to get started.  
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.  
You can view your projects by running `gcloud projects list`.  
Your home disk usage is at 95%.  
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.  
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.  
shumpei_yamakawa@cloudshell:~$ pwd  
/home/shumpei_yamakawa  
shumpei_yamakawa@cloudshell:~$ ls
```

Home directory:
/home/shumpei_yamakawa

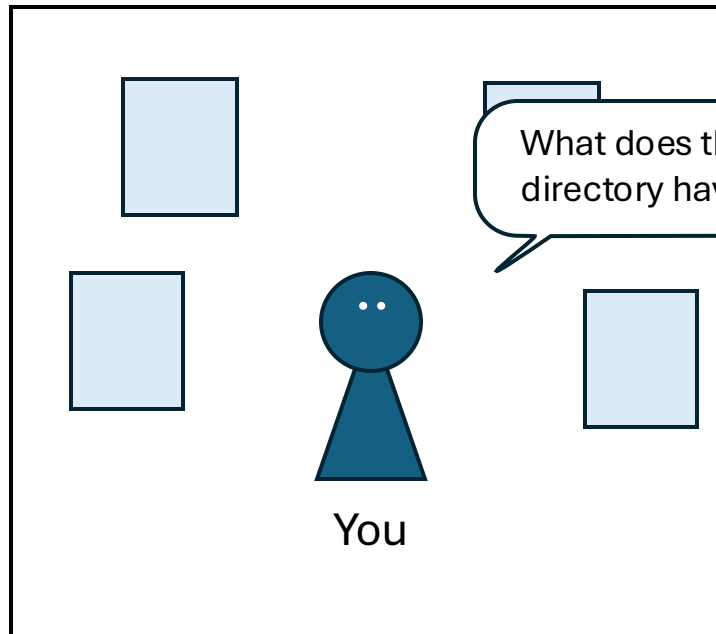


*the name of the directory depends on your account name


```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
Your home disk usage is at 95%.
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.
shumpei_yamakawa@cloudshell:~$ pwd
/home/shumpei_yamakawa
shumpei_yamakawa@cloudshell:~$ ls
README-cloudshell.txt
shumpei_yamakawa@cloudshell:~$
```

Home directory:
/home/shumpei_yamakawa

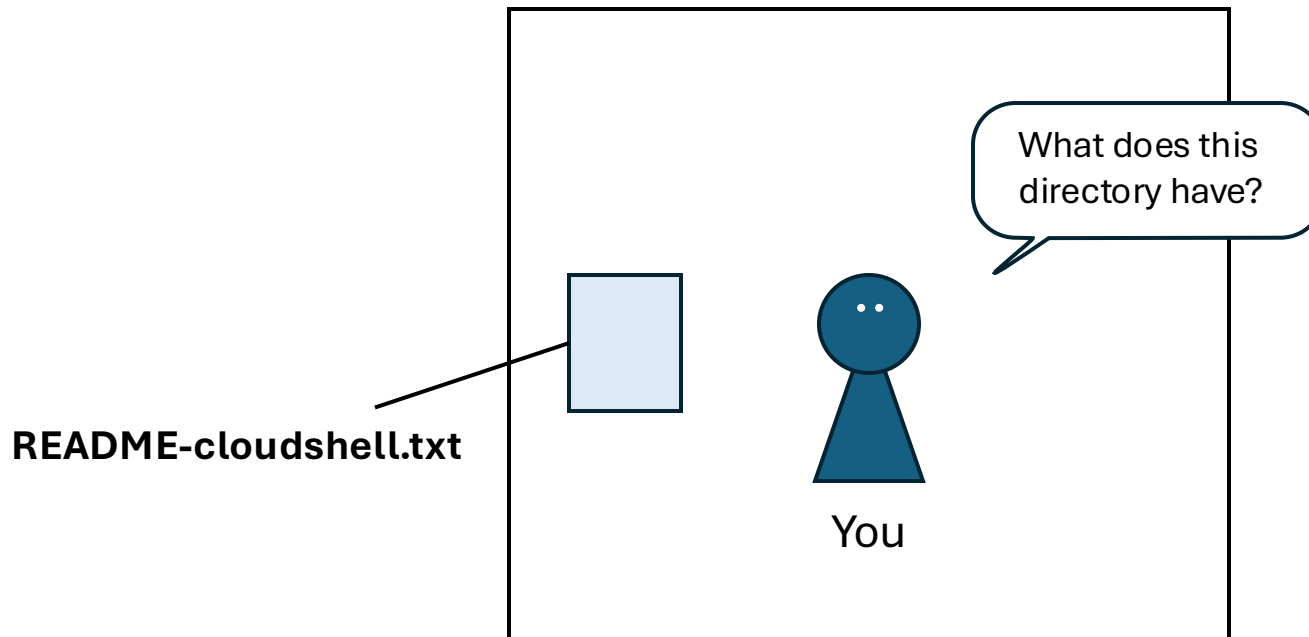
You have
“README-cloudshell.txt”



= ls

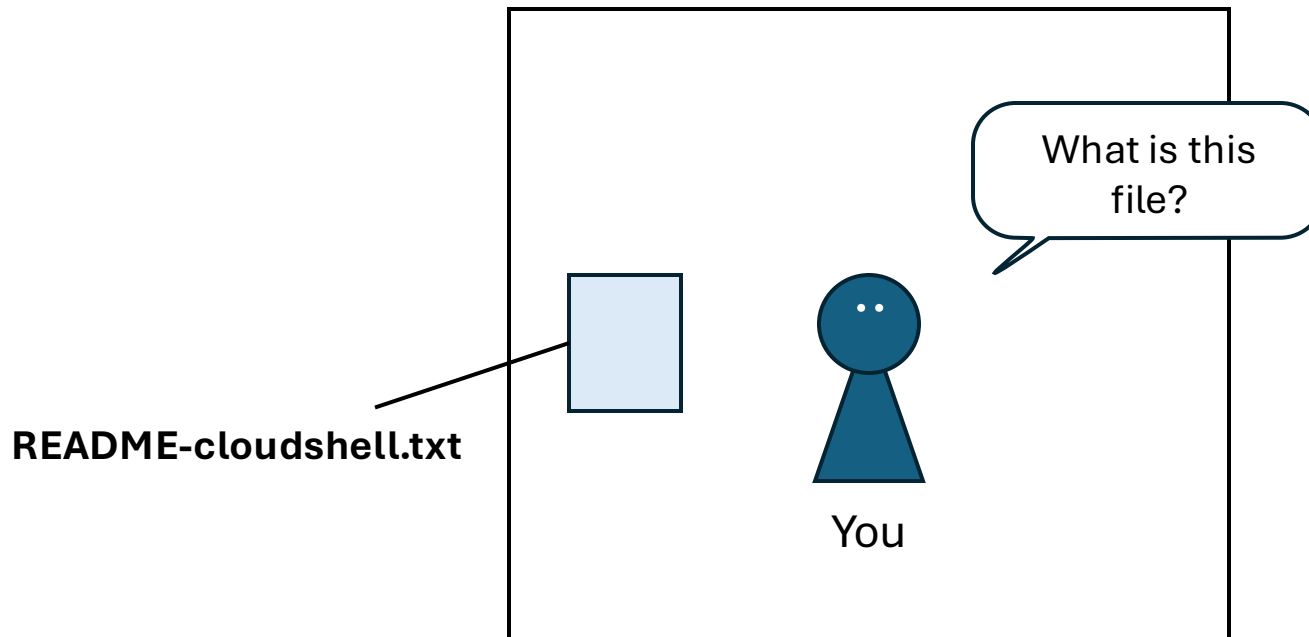
```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
Your home disk usage is at 95%.
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.
shumpei_yamakawa@cloudshell:~$ pwd
/home/shumpei_yamakawa
shumpei_yamakawa@cloudshell:~$ ls
README-cloudshell.txt
shumpei_yamakawa@cloudshell:~$
```

Home directory:
/home/shumpei_yamakawa



```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
Your home disk usage is at 95%.
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.
shumpei_yamakawa@cloudshell:~$ pwd
/home/shumpei_yamakawa
shumpei_yamakawa@cloudshell:~$ ls
README-cloudshell.txt
shumpei_yamakawa@cloudshell:~$
```

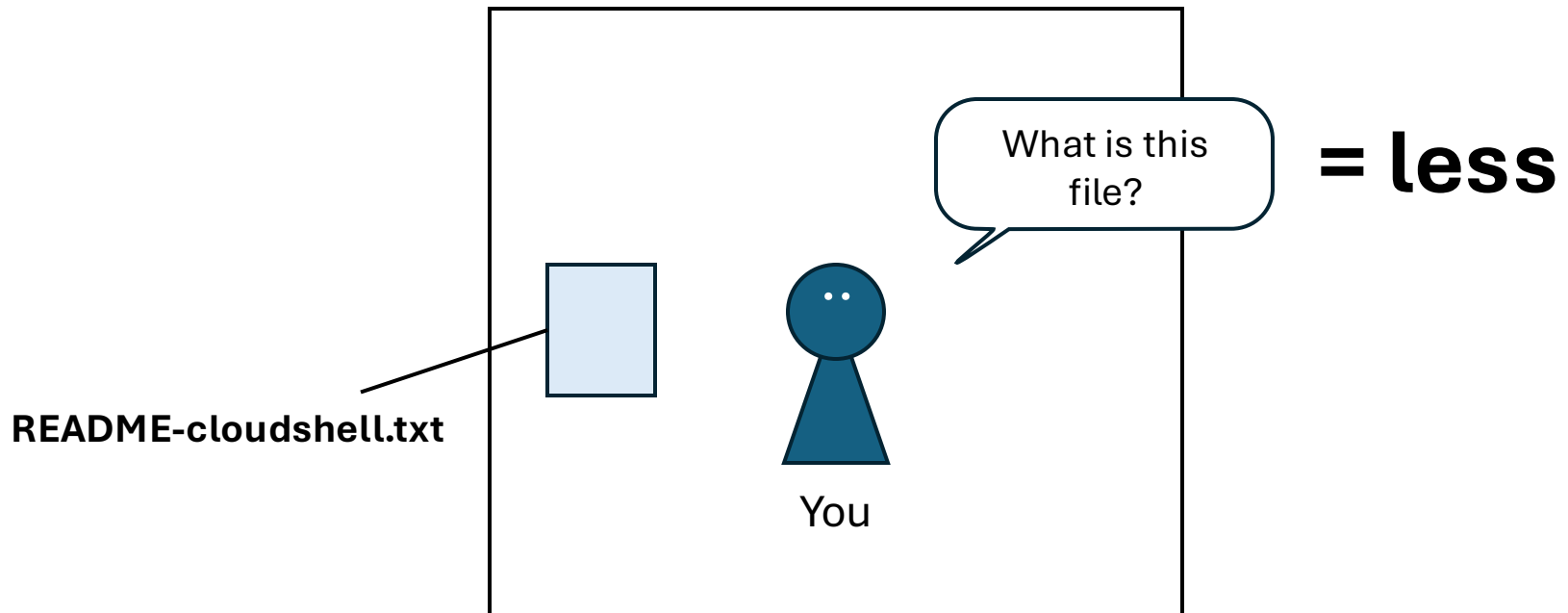
Home directory:
/home/shumpei_yamakawa



Type “less {file name}” and enter

```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
Your home disk usage is at 95%.
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing_disk_space.
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.
shumpei_yamakawa@cloudshell:~$ pwd
/home/shumpei_yamakawa
shumpei_yamakawa@cloudshell:~$ ls
README-cloudshell.txt test
shumpei_yamakawa@cloudshell:~$ less README-cloudshell.txt
```

Home directory:
/home/shumpei_yamakawa



```
Welcome to Cloud Shell! Type "help" to get started.
To set your Cloud Platform project in this session use `gcloud config set project [PROJECT_ID]`.
You can view your projects by running `gcloud projects list`.
Your home disk usage is at 95%.
You can find suggestions to clear space at https://cloud.google.com/shell/docs/quotas-limits#clearing\_disk\_space.
Upgrade to Cloud Workstations for a secure development environment without these limits: https://cloud.google.com/workstations.
shumpei_yamakawa@cloudshell:~$ pwd
/home/shumpei_yamakawa
shumpei_yamakawa@cloudshell:~$ ls
README-cloudshell.txt  test
shumpei_yamakawa@cloudshell:~$ less README-cloudshell.txt
```

enter

```
Welcome to Google Cloud Shell, a tool for managing resources hosted on Google Cloud Platform!
The machine comes pre-installed with the Google Cloud SDK and other popular developer tools.

Your 5GB home directory will persist across sessions, but the VM is ephemeral and will be reset
approximately 20 minutes after your session ends. No system-wide change will persist beyond that.

Type "gcloud help" to get help on using Cloud SDK. For more examples, visit
https://cloud.google.com/shell/docs/quickstart and https://cloud.google.com/shell/docs/examples

Type "cloudshell help" to get help on using the "cloudshell" utility. Common functionality is
aliased to short commands in your shell, for example, you can type "dl <filename>" at Bash prompt to
download a file. Type "cloudshell aliases" to see these commands.

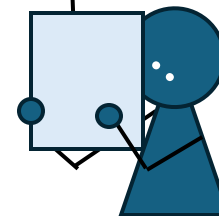
Type "help" to see this message any time. Type "builtin help" to see Bash interpreter help.

README-cloudshell.txt (END)
```

Type "q"

```
shumpei_yamakawa@cloudshell:~$ less README-cloudshell.txt
shumpei_yamakawa@cloudshell:~$
```

README-cloudshell
.txt



What is this
file?

“cat” is also an option to look at the file content

```
shumpei_yamakawa@cloudshell:~$ cat README-cloudshell.txt
```

```
Welcome to Google Cloud Shell, a tool for managing resources hosted on Google Cloud Platform!  
The machine comes pre-installed with the Google Cloud SDK and other popular developer tools.
```

```
Your 5GB home directory will persist across sessions, but the VM is ephemeral and will be reset  
approximately 20 minutes after your session ends. No system-wide change will persist beyond that.
```

```
Type "gcloud help" to get help on using Cloud SDK. For more examples, visit  
https://cloud.google.com/shell/docs/quickstart and https://cloud.google.com/shell/docs/examples
```

```
Type "cloudshell help" to get help on using the "cloudshell" utility. Common functionality is  
aliased to short commands in your shell, for example, you can type "dl <filename>" at Bash prompt to  
download a file. Type "cloudshell aliases" to see these commands.
```

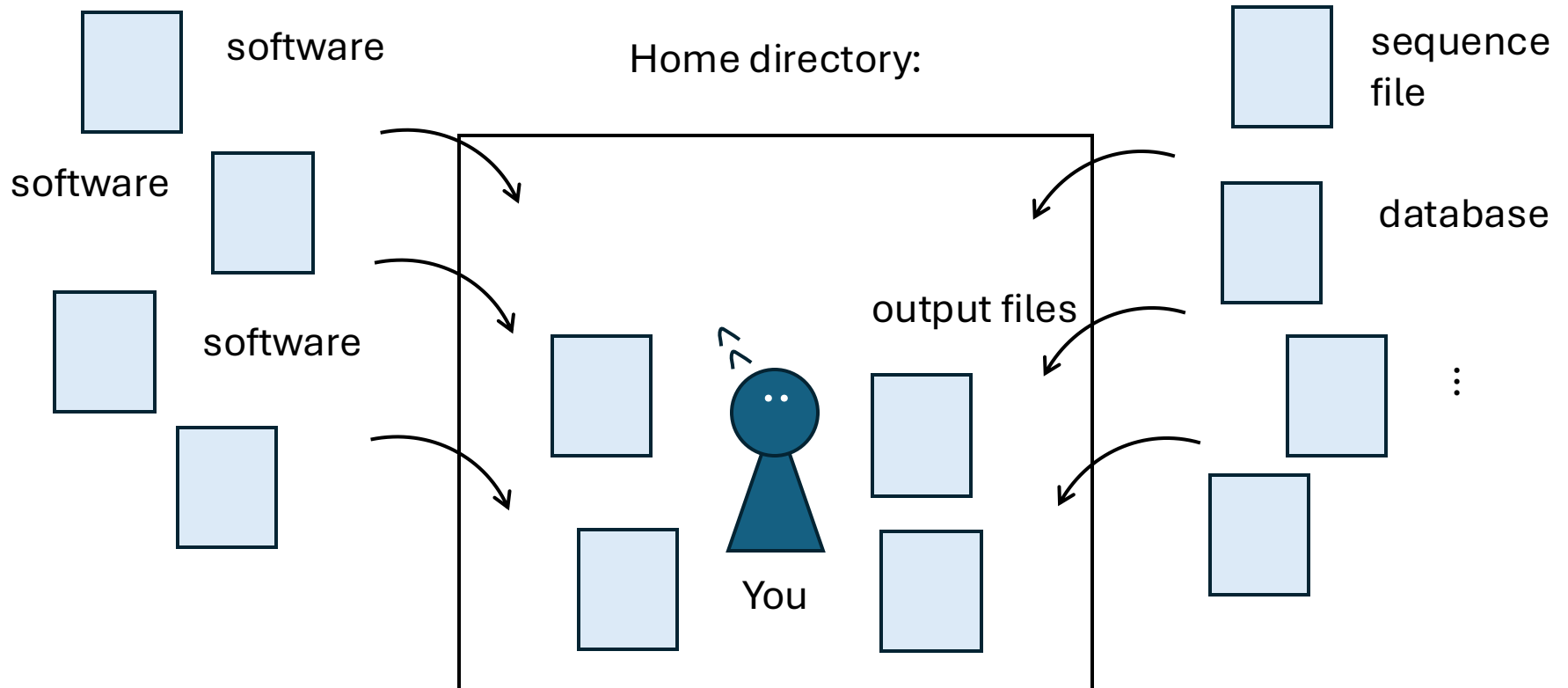
```
Type "help" to see this message any time. Type "builtin help" to see Bash interpreter help.
```

```
shumpei_yamakawa@cloudshell:~$ █
```

Less vs cat

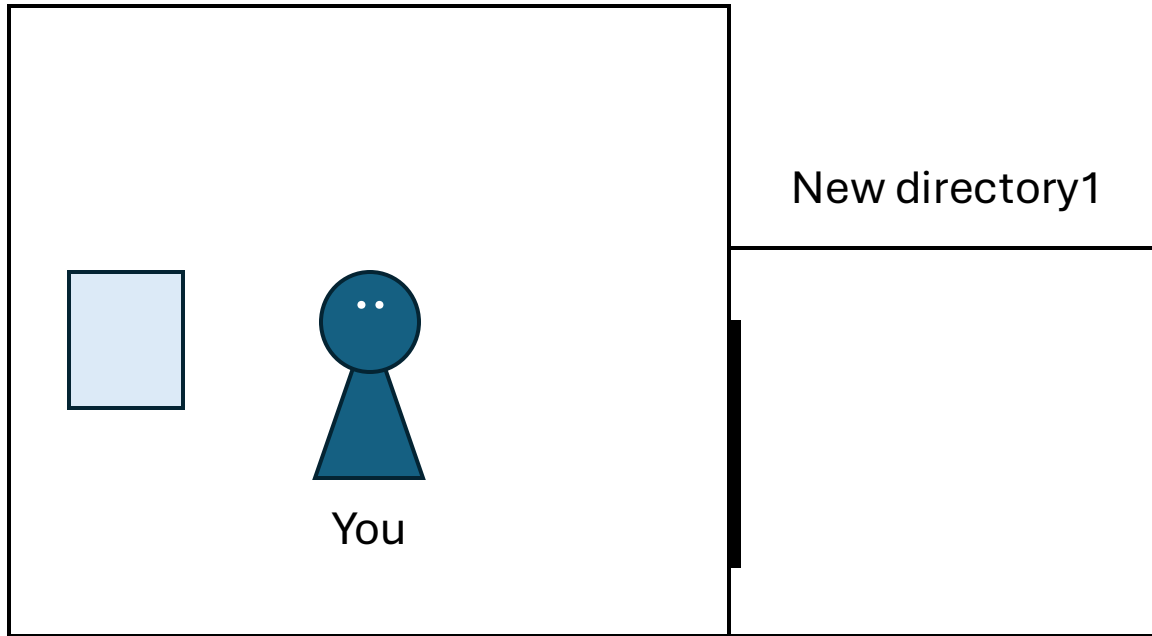
- less: in different output page For big data
- cat: in standard output For small data and to “concatenate”

Do not stack too many files in the home directly



Hierarchical structure is ideal

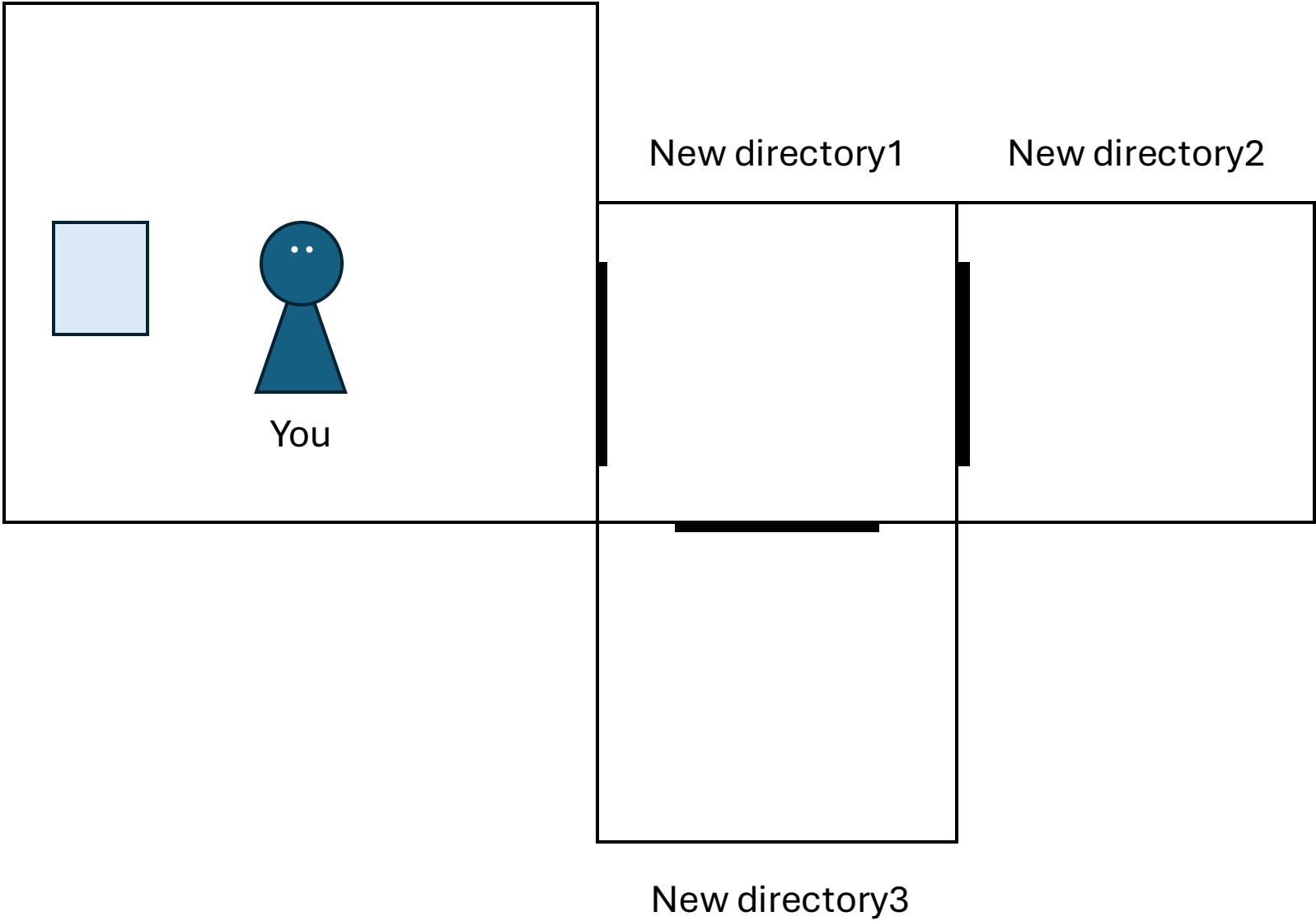
Home directory



New directory1

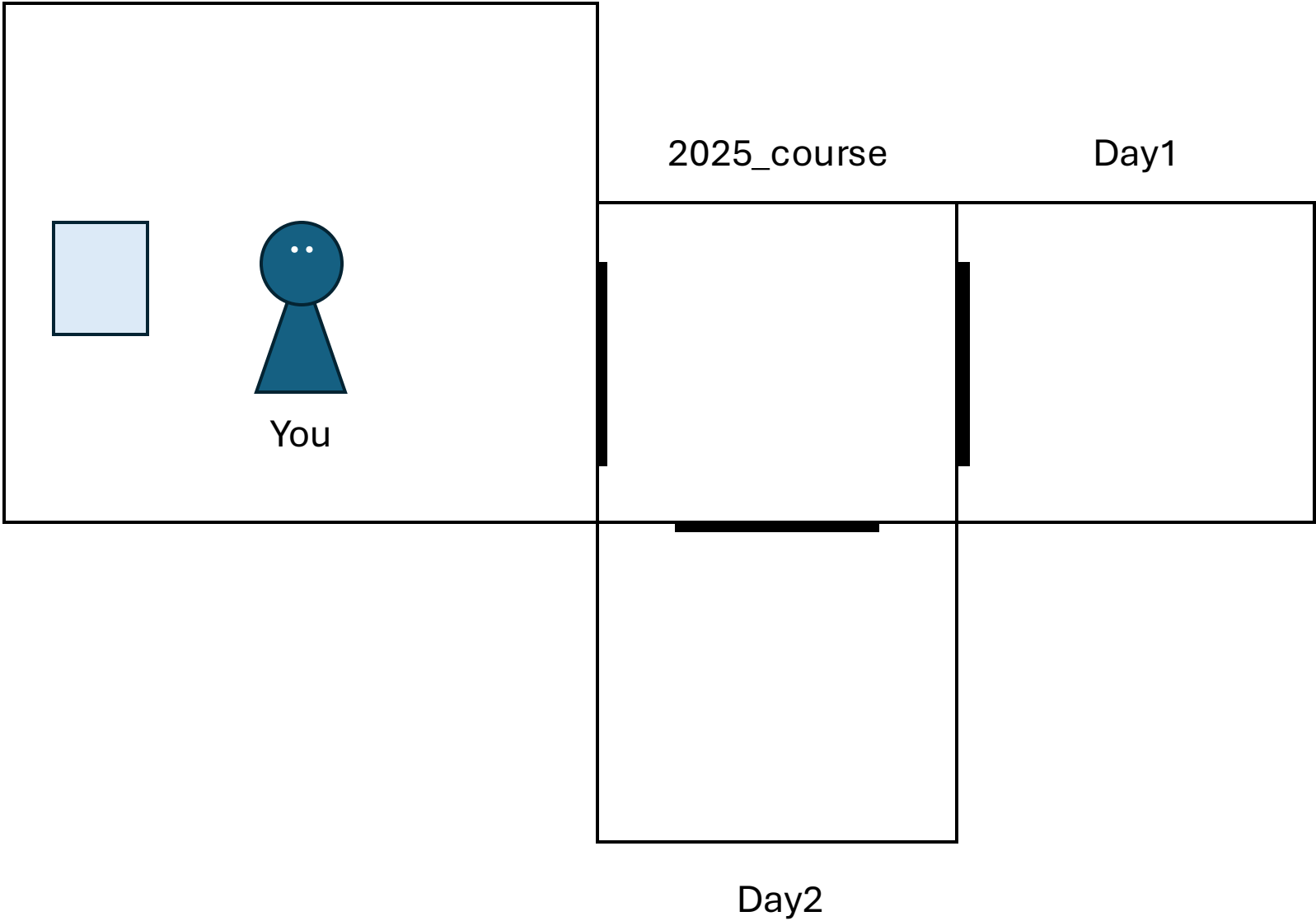
Hierarchical structure is ideal

Home directory



Hierarchical structure is ideal

Home directory



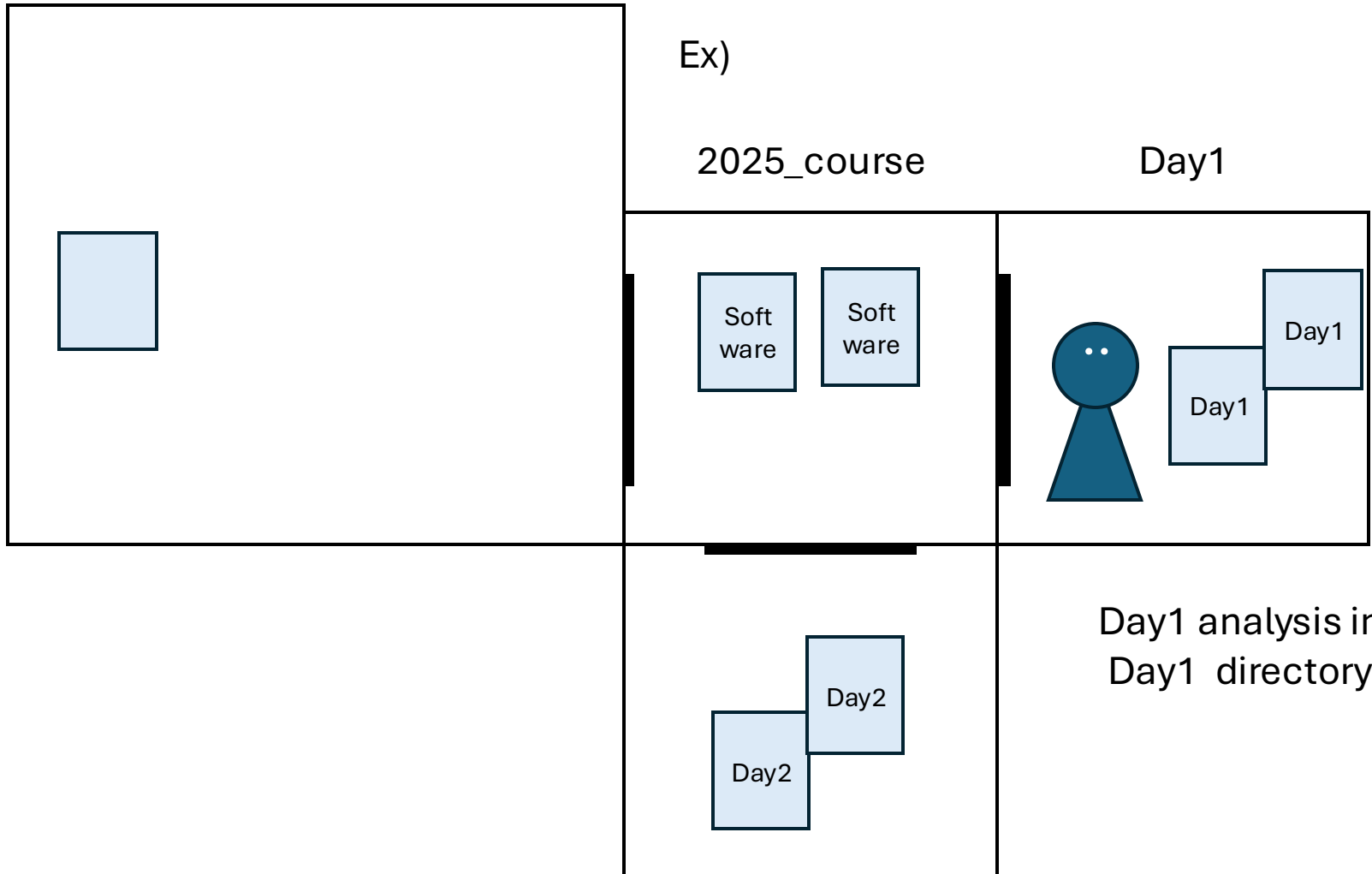
Hierarchical structure is ideal

Home directory

Ex)

2025_course

Day1



Day1 analysis in
Day1 directory

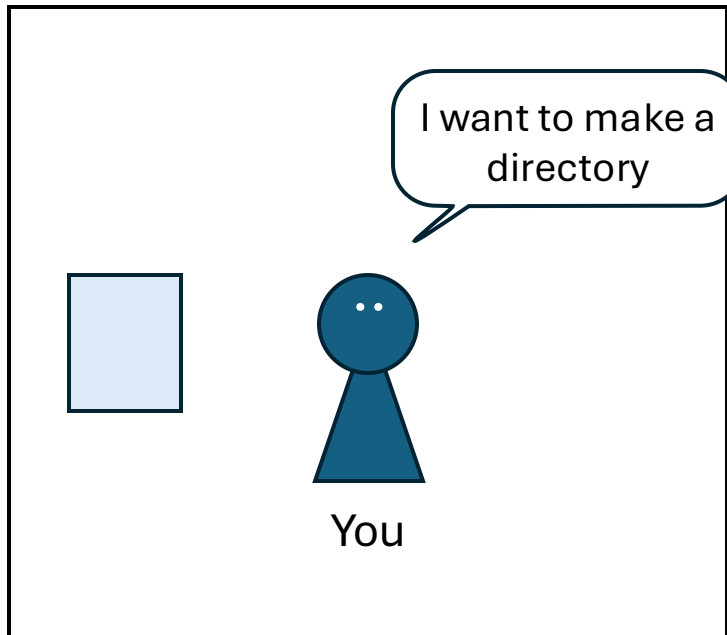
Day2

```
shumpei_yamakawa@cloudshell:~$ mkdir New_directory1
```



Home directory

Any name is okay

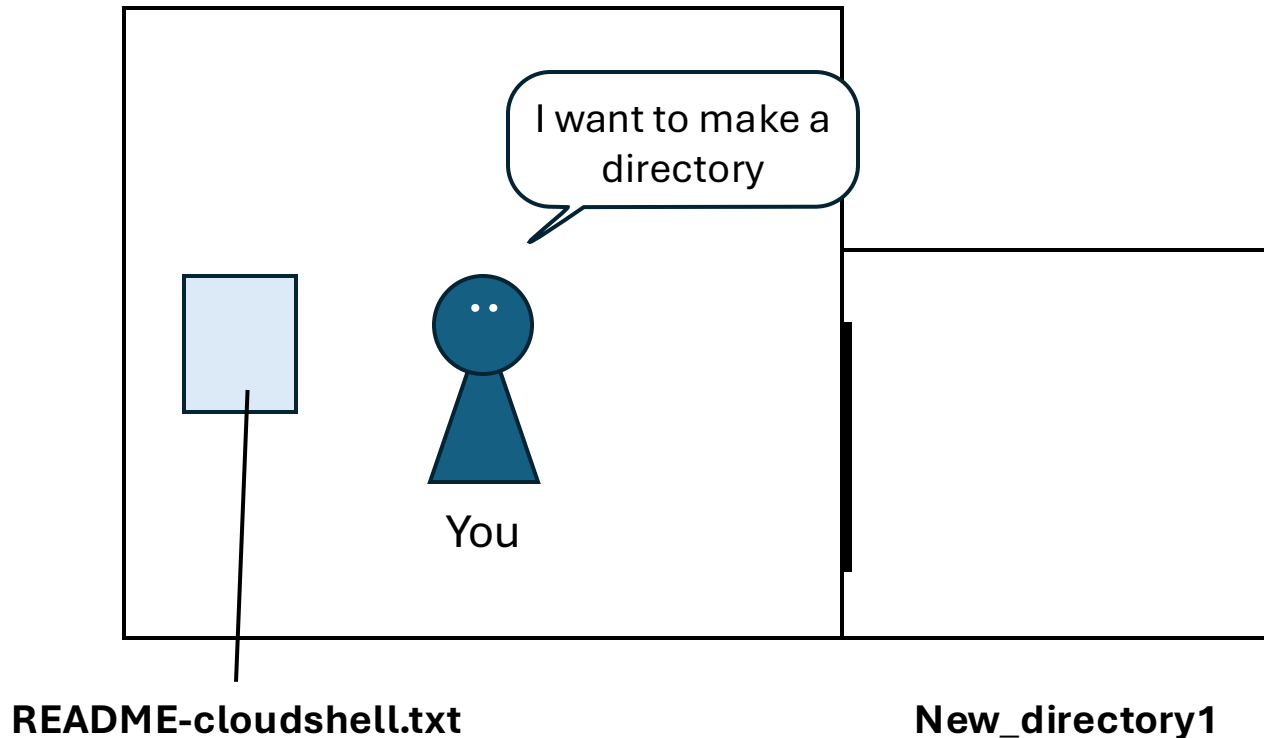


= mkdir

Check the directory by the command ls

```
shumpei_yamakawa@cloudshell:~$ mkdir New_directory1  
shumpei_yamakawa@cloudshell:~$ ls  
New_directory1  README-cloudshell.txt
```

Home directory



Check the directory by the command ls

```
shumpei_yamakawa@cloudshell:~$ cd New_directory1
```

↑
Directory or PATH that
you want to go

Home directory

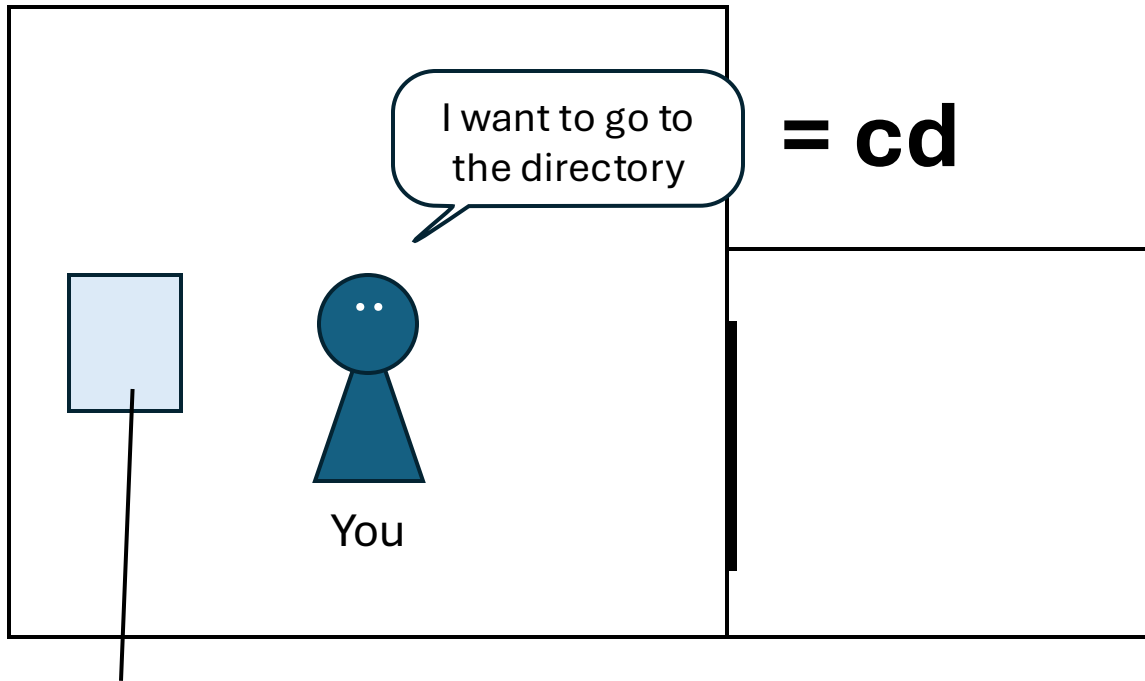
I want to go to
the directory

= cd

You

README-cloudshell.txt

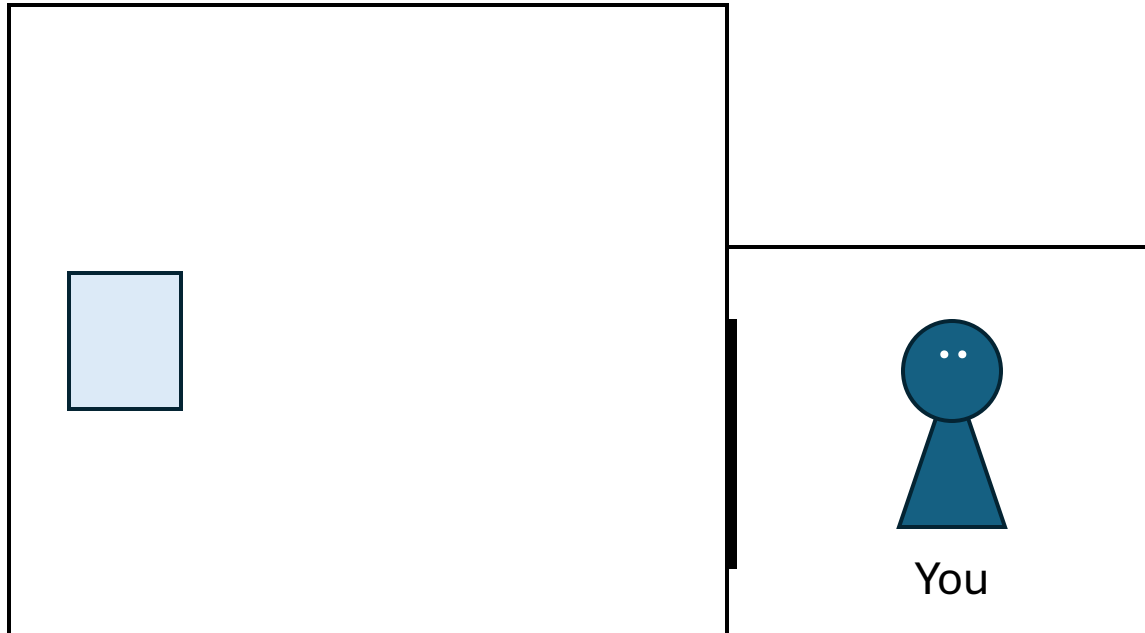
New_directory1



Check the directory by the command ls

```
shumpei_yamakawa@cloudshell:~$ cd New_directory1/  
shumpei_yamakawa@cloudshell:~/New_directory1$ pwd  
/home/shumpei_yamakawa/New_directory1
```

Home directory



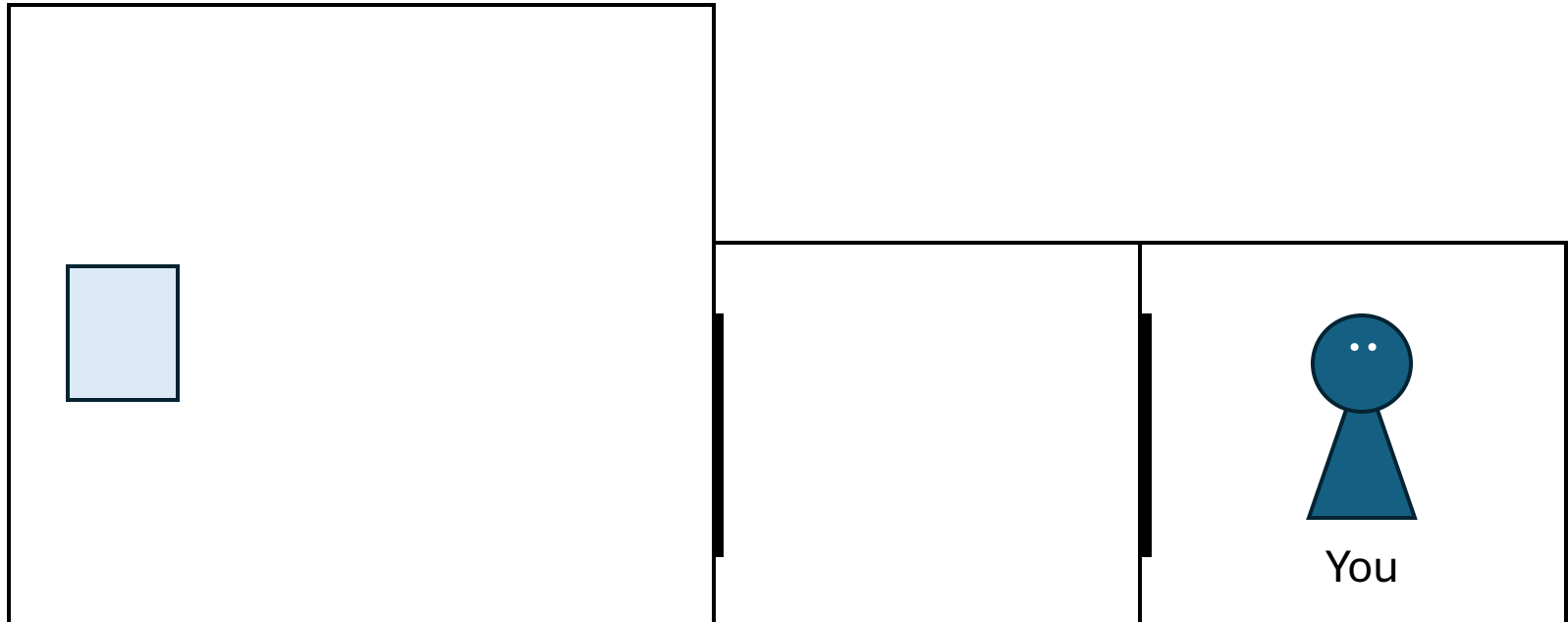
New_directory1

**/home/shumpei_yama
kawa/**

**/home/shumpei_yama
kawa/New_directory1**

Exercise1

Make a new directory and move into there



Home directory

/home/shumpei_yama
kawa/

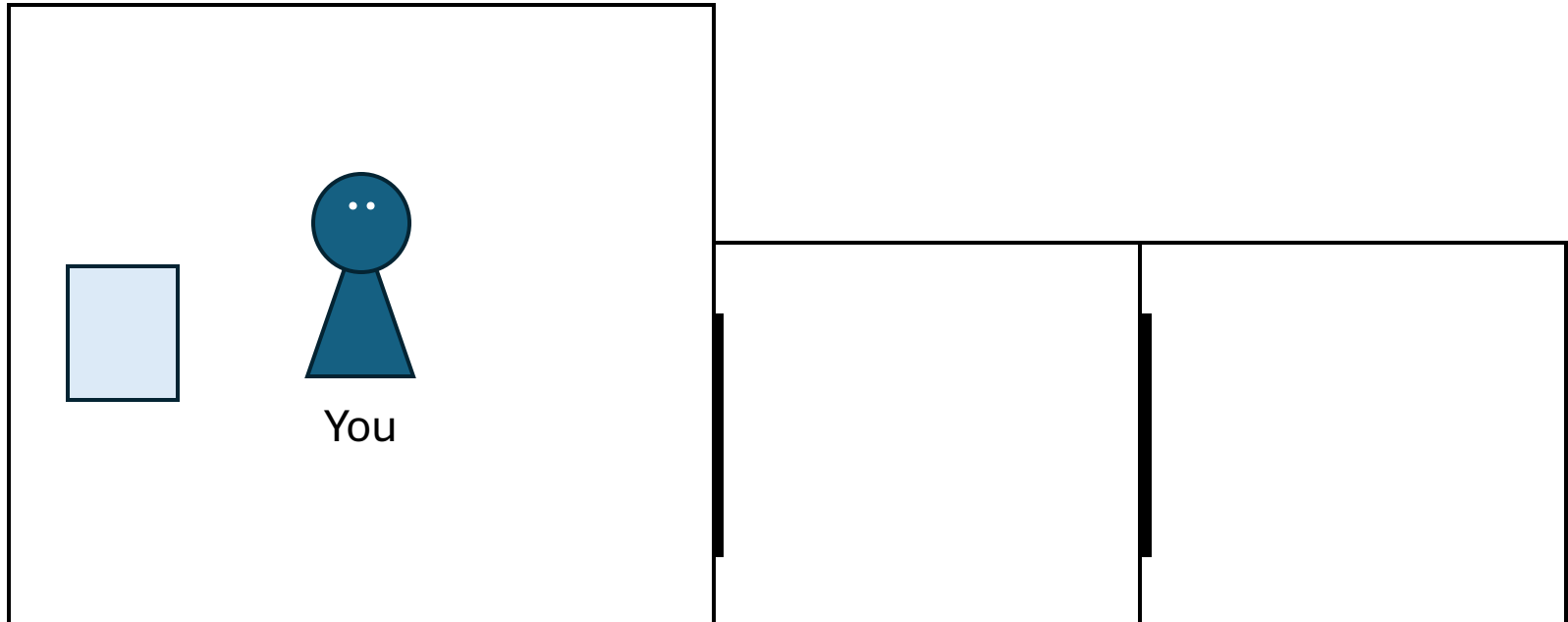
New_directory1

/home/shumpei_yama
kawa/New_directory1

New_directory2

Exercise2

Go back to the home directory



Home directory

/home/shumpei_yama
kawa/

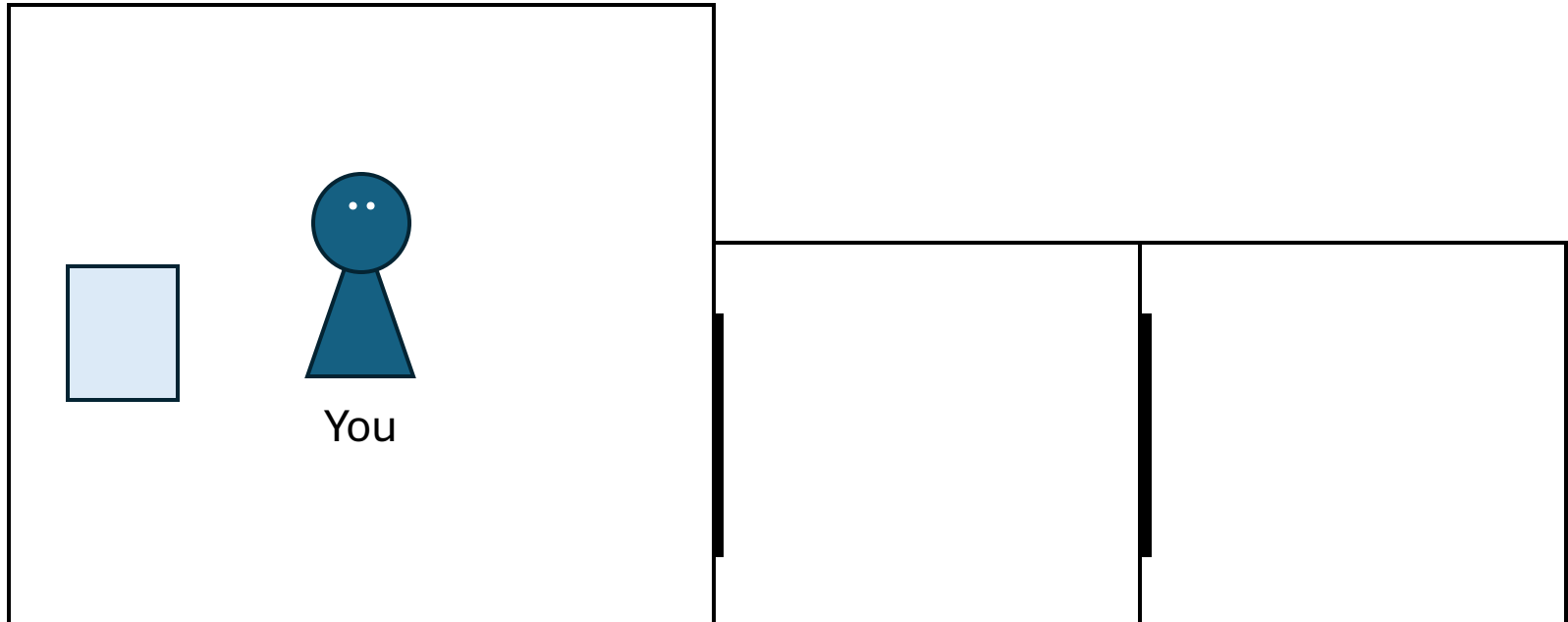
New_directory1

/home/shumpei_yama
kawa/New_directory1

New_directory2

Exercise2

Go back to the home directory



Home directory

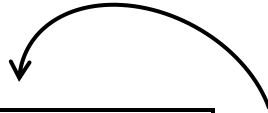
/home/shumpei_yama
kawa/

New_directory1

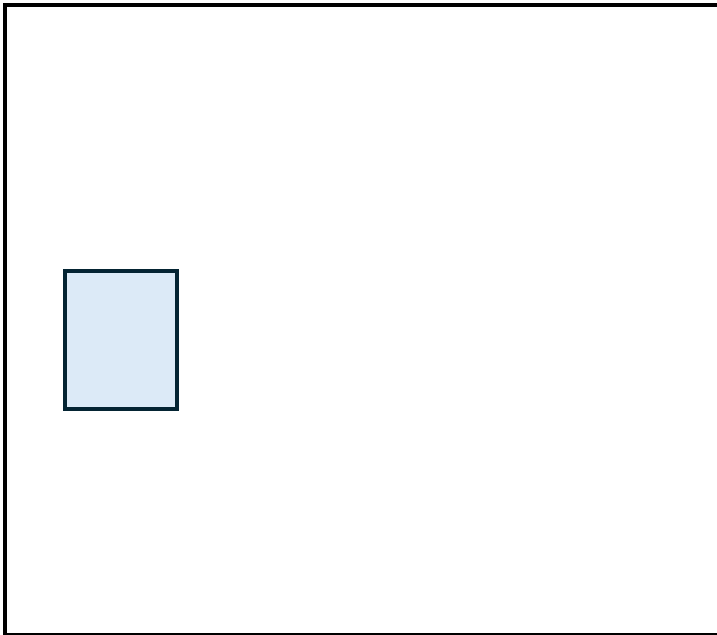
/home/shumpei_yama
kawa/New_directory1

New_directory2

cd ..

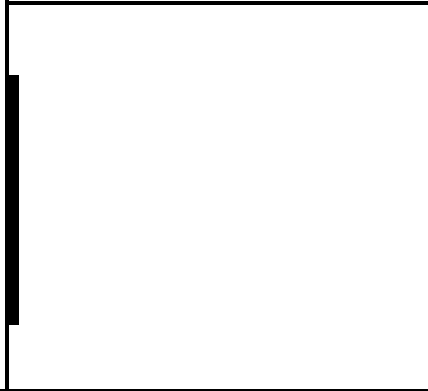


cd ..



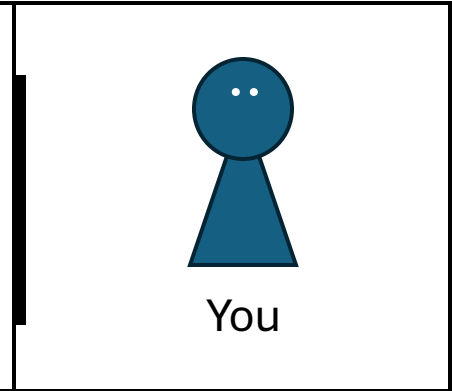
Home directory

/home/shumpei_yama
kawa/



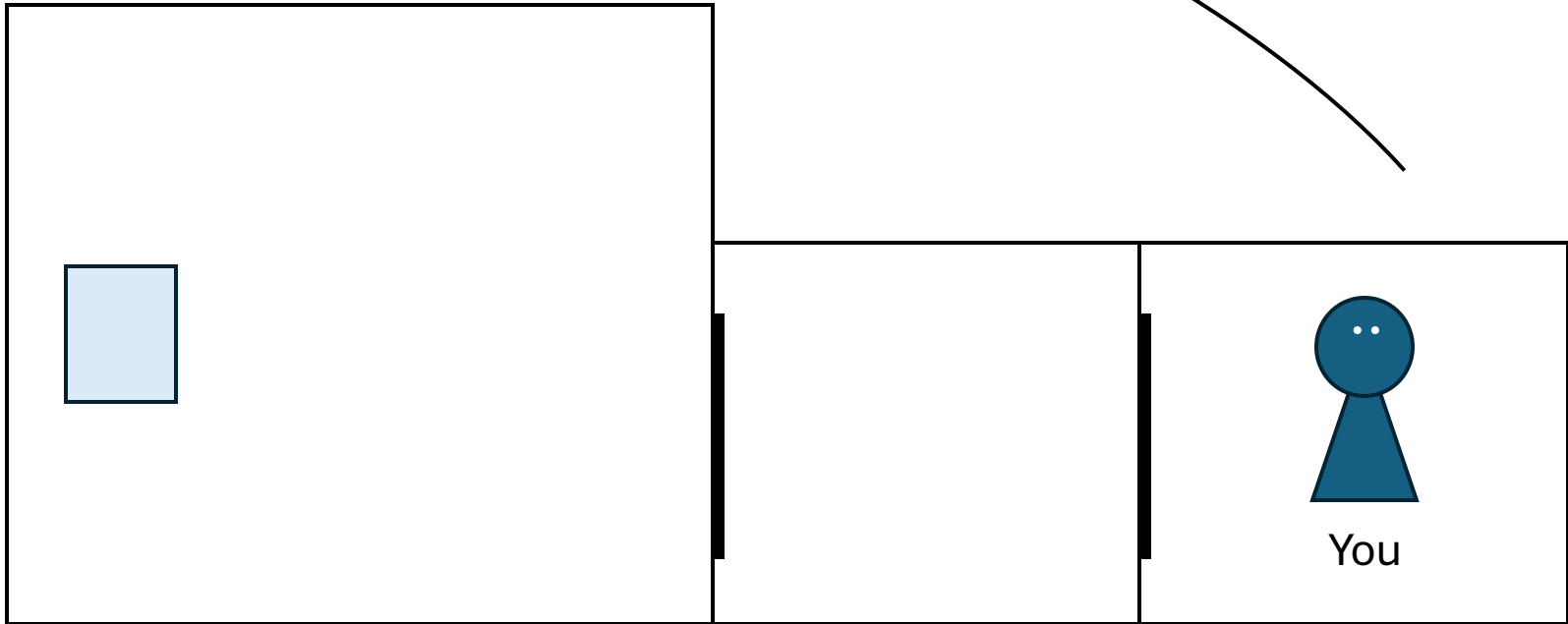
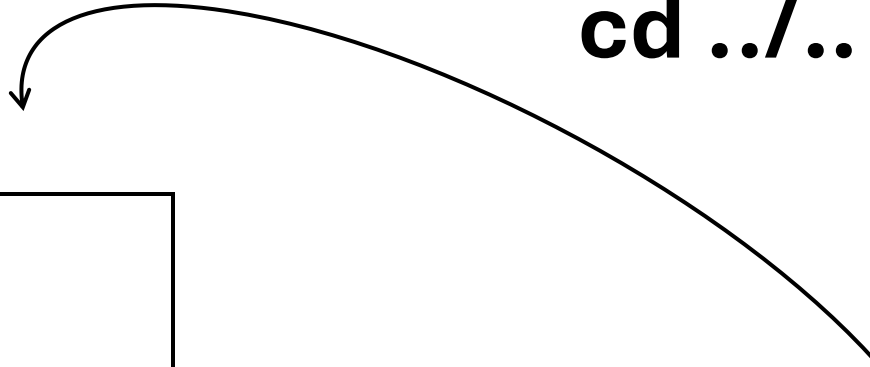
New_directory1

/home/shumpei_yama
kawa/New_directory1



New_directory2

cd ../..



Home directory

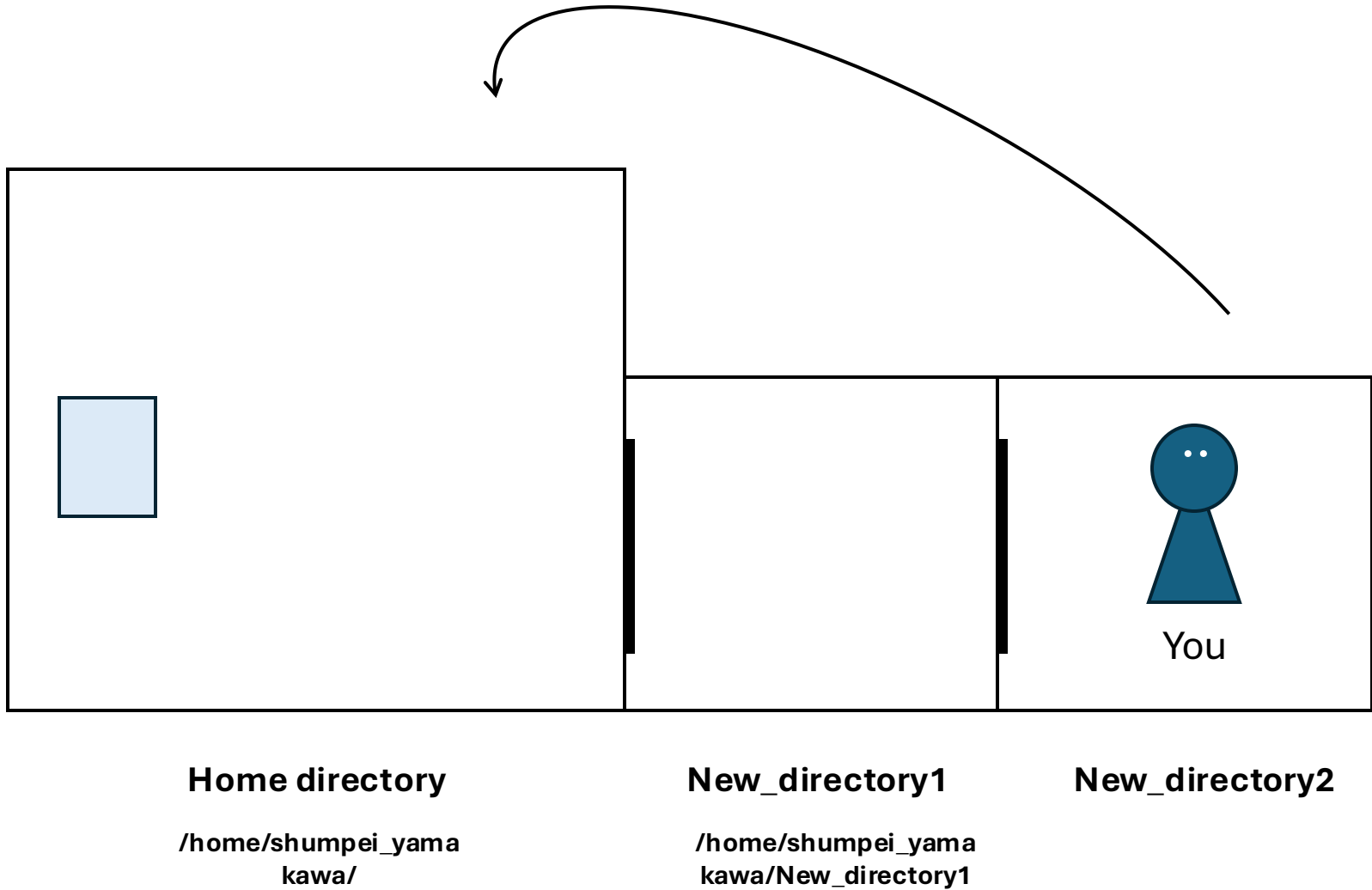
/home/shumpei_yama
kawa/

New_directory1

/home/shumpei_yama
kawa/New_directory1

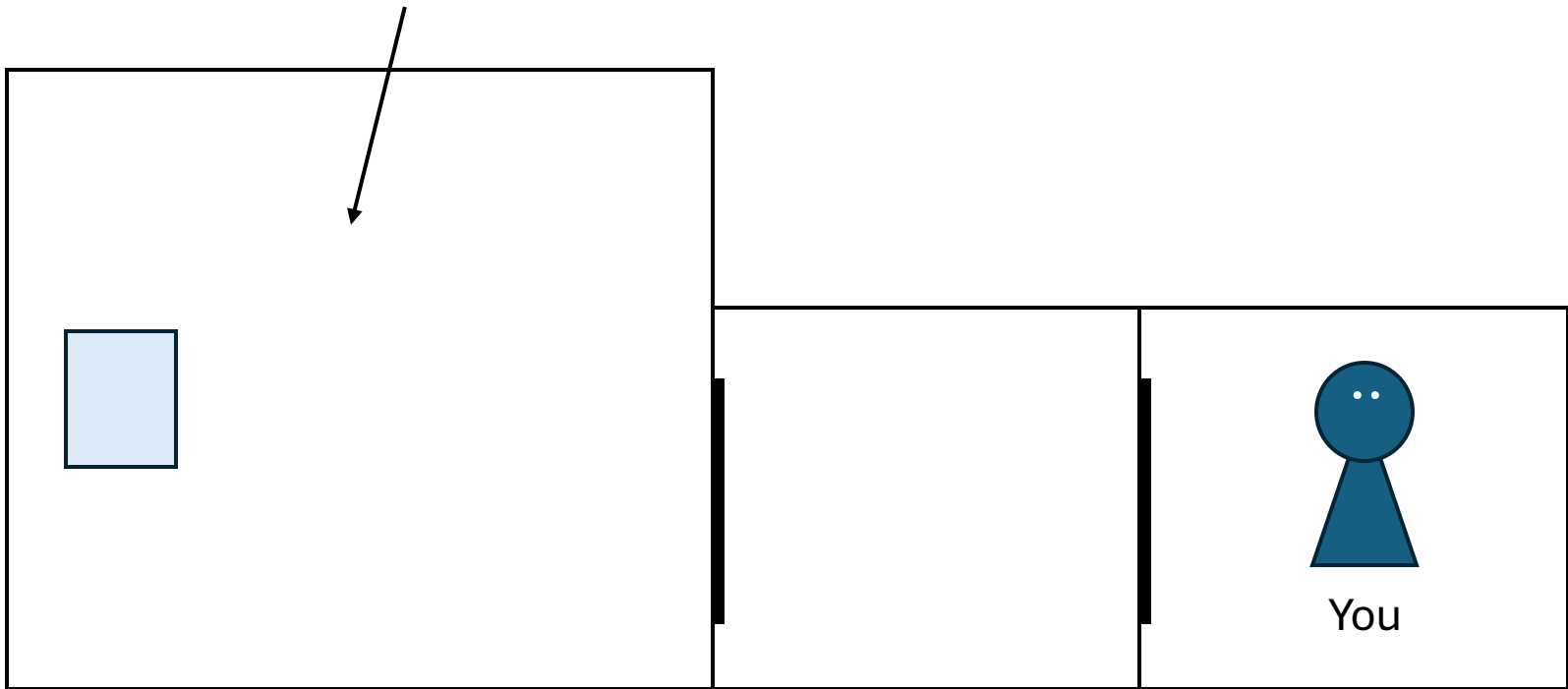
New_directory2

cd /home/shumpei_yamakawa



Absolute path `../..`

Relative path `/home/shumpei_yamakawa`



Home directory

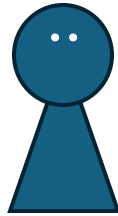
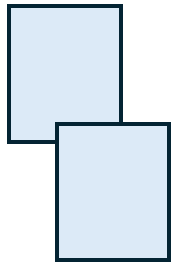
`/home/shumpei_yama
kawa/`

New_directory1

`/home/shumpei_yama
kawa/New_directory1`

New_directory2

2. Basic commands and specific analysis software



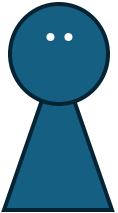
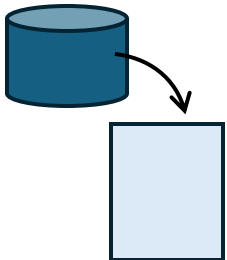
I wan to copy the
file

= cp



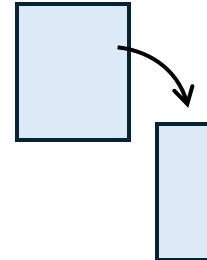
I wan to delete
the file

= rm



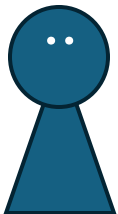
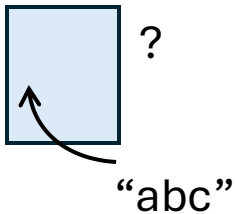
Download the
file from url

= wget



Edit the file
content

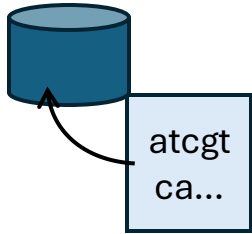
= awk



Search specific
words in the file

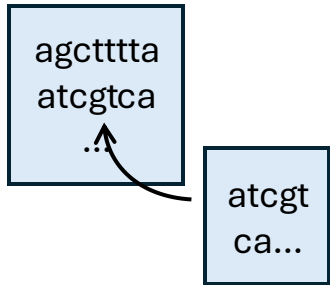
= grep

Various basic commands
are already prepared



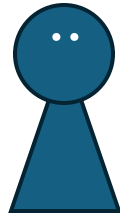
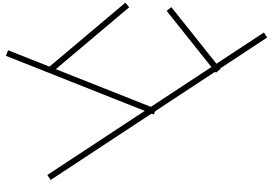
I want to make a
Blast database

= makeblastdb



Search specific
sequences

= seqkit grep




Make a
phylogenetic tree

= raxml

Need to download
specific software for
bioinformatic analysis

**Executable files
(binary)**



You

```
/usr/bin/home/
```

Files for the basic commands such as Cat, less, mkdir, pwd etc are included in this directory

Files for the basic commands such as Cat, less, mkdir, pwd etc are included in this directory

/usr/bin/

Executable files (binary)

```
aa-enabled          enc2as              leasgrog            pinentry-curses     ss
aa-essc             encguess            libnetcfg            ping                 ssh
aa-features-abi     env                 libtoolize            ping4                ssh-add
aclocal             envsubst            link                  ping6                 ssh-agent
aclocal-1.16         eqn                  linux32                pinky                 ssh-argv0
acutils             esb                  linux64                pip                   ssh-argv1
add-apt-repository   errno                linux-check-removal    pip3                  ssh-copy-id
addpart              add2line             linux-update-symlinks pip3.12                ssh-keygen
add2line             alioydb-auth-proxy  logname                 pkaction              ssh-keyscan
anthoscli            apropos              locale                  pkcheck               stat
apt                  apt-get              locale-check            pkgconf               statbuf
apt-add-repository   apt-cache            localelect              pkgtar                 strace
apt-cdrom            apt-config            local-extract           pkill                  strace-log-merge
apt-get              apt-key              logger                   pkill                  steamrip
apt-mark             apt-mark              login                    pldd                   strings
ar                   ar                    logintcl                 pm2                     strip
arch                 arch                  logname                  pod2html               stty
autoconf             autoconf              look                      pod2man                sudo
as                   as                     ls                         pod2text                sudoedit
as-headers            as-headers            lsattr                   pod2usage               sudoreplay
as-headers            as-headers            lscfg                     ps                       supervisorctl
as-headers            as-headers            lscfg                      ps                       supervisorord
as-headers            as-headers            lscfg                      ps                       sync
as-headers            as-headers            lscfg                      ps                       syntax_suggest3.2
as-headers            as-headers            lscfg                      ps                       systemctl
as-headers            as-headers            lscfg                      ps                       systemd
as-headers            as-headers            lscfg                      ps                       systemd-ac-power
as-headers            as-headers            lscfg                      ps                       systemd-analyze
as-headers            as-headers            lscfg                      ps                       systemd-ask-passw
as-headers            as-headers            lscfg                      ps                       systemd-cat
as-headers            as-headers            lscfg                      ps                       systemd-cgls
as-headers            as-headers            lscfg                      ps                       systemd-cgroup
as-headers            as-headers            lscfg                      ps                       systemd-confext
as-headers            as-headers            lscfg                      ps                       systemd-creds
as-headers            as-headers            lscfg                      ps                       systemd-cryptenro
as-headers            as-headers            lscfg                      ps                       systemd-cryptsetup
as-headers            as-headers            lscfg                      ps                       systemd-daemon
as-headers            as-headers            lscfg                      ps                       systemd-detect-vi
as-headers            as-headers            lscfg                      ps                       systemd-escape
as-headers            as-headers            lscfg                      ps                       systemd-firstboot
as-headers            as-headers            lscfg                      ps                       systemd-hwdb
as-headers            as-headers            lscfg                      ps                       systemd-ld128
```

mkdir

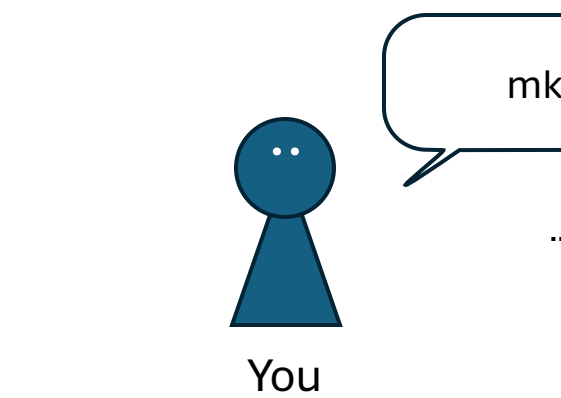


You

/usr/bin/home/


```
shumpei_yamakawa@cloudshell:~$ mkdir
```

**Executable files
(binary)**




A diagram illustrating a user interaction. On the left, a blue icon of a person's head and shoulders is shown, with the word "You" written below it. To the right of the person is a white speech bubble with a dark blue outline. Inside the speech bubble, the command "mkdir" is written in a dark blue, monospaced font. A dotted line extends from the right side of the speech bubble towards the right edge of the diagram.


A diagram illustrating a user interaction. On the left, a blue icon of a person's head and shoulders is shown, with the word "You" written below it. To the right of the person is a white speech bubble with a dark blue outline, containing the text "mkdir". A dotted line extends from the right side of the speech bubble towards the right edge of the diagram.



mkdir



Ok, I will look for it in /usr/bin



Ok, I will look for it in /usr/bin

aa-enabled	emc2ms	leagroup	pinentry-curses	ss
aa-exec	emcquags	libnetcfg	pingd	ss
aa-features-abi	env	libtoolize	pinkeyd	ssh-add
aclocal	envsubst	link	pinmg6	ssh-agent
aclocal-1.16	epn	linux32	pinky	ssh-argv0
acrylic	esb	linux64	pip	ssh-copy-id
add-apt-repository	esb3.2	linux-check-removal	pip3	ssh-keygen
addpart	arbo	linux-update-symlinks	pip3.12	ssh-keyscan
add2line	etags	linux-version	phabricator	stat
alloydb-auth-proxy	etags.emacs	in	pkchack	stdbuf
anthoscli	expand	lnstat0	pkgconf	strace
apropos	expm	lnstat	pkg-config	strace-log-merge
apt	expm	locale	ptail	streamrip
apt-add-repository	expm	locale-check	pktyagent	strings
apt-cache	factor	localaclt	plpmp	strip
apt-cdrom	faillog	localdef	pldd	stty
apt-config	faillocate	local-extract	pmap	su
apt-get	false	logger	pod2html	sudo
apt-key	fc-cache	login	pod2man	sudedit
apt-mark	fc-cat	logintctl	pod2text	sudoersplay
ar	fc-confliat	logname	pod2usage	sum
arch	fc-list	look	podchecker	supervisorctl
as	fc-match	ls	preconv	supervisor
autoconf	fc-pattern	lsattr	printenv	sync
autoheader	fc-query	lsblk	printf	syntax_suggest3.2
automake	fc-scan	lsb_release	prlimit	systemd
automake	fc-validate	lsgroup	protoc	systemd-ac-power
automake-1.16	fdp	lscpa	prove	systemd-analyze
autoreconf	fdpgrp	lsinitramfs	prstat	systemd-ac-pasae
autoscan	find	lsnipe	prune	systemd-cat
autoupdate	find	lslocks	ps	systemd-cpfs
awk	findmnt	lspgins	pslog	systemd-cgtop
b2sum	flock	lsmem	psql	systemd-confext
base32	fmt	lsmem	ptar	systemd-cryptenr
base64	fold	lspgpt	ptardiff	systemd-cryptntr
basenano	free	lsasbays	ptatdrip	systemd-delta
basenc	funsip	lto-dump	ptatdrip	systemd-delta-vi
bash	fuser	lto-dump-13	ptx	systemd-escape
bashbug	g++	lxc-attach	pwd	systemd-firstboot
base1	g++13	lxc-autostart	pwdx	systemd-id128
bccomp	gccgo	lxc-checkconfig	pwsh	systemd-hwdb
bison_yacc	gccgo	lxc-checkconfig		

**Executable files
(binary)**

A diagram illustrating a user interaction. On the left, a blue icon of a person is labeled "You" below it. To the right of the person is a speech bubble containing the text "mkdir". Below the speech bubble, there are two horizontal dotted lines, with a left-pointing arrow above the top line, indicating a sequence of actions or a process flow.

A diagram illustrating a user interaction. On the left, a blue icon of a person is labeled "You". To the right of the person is a speech bubble containing the text "mkdir". Below the speech bubble, there are two horizontal dotted lines, with the first one starting from a left-pointing arrowhead.


mkdir

Yes, found it.
Let's execute it


Yes, found it.
Let's execute it

A black silhouette of a person's head and shoulders. To the left of the head is a speech bubble containing two horizontal dotted lines, indicating speech or a thought.


**Executable files
(binary)**



You



A diagram illustrating a simple interaction. On the left, a blue stick figure labeled "You" stands inside a large white rectangle. To the right of this rectangle is a smaller white rectangle. To the right of the smaller rectangle is a black stick figure labeled "PC". A speech bubble from the PC says "Here you go". Three orange lines are positioned above the gap between the two rectangles, indicating a transfer or action.



Here you go

aa-enabled	emc2ss	leagrow	pinentry-curses	ss
aa-exec	enoughss	libnetcfg	ping	ssh
aa-features-abi	evv	libnetc	pininfo	ssh-add
aclocal	envsubst	link	pinimg	ssh-agent
aclocal-1.16	epn	linux32	pinky	ssh-argv0
acrylic	erb	linux44	pip	ssh-copy-id
add-apt-repository	erfb.2	linux-check-removal	pip3	ssh-keygen
addpart	erno	linux-update-symlinks	pip3.12	ssh-keyscan
add2line	etags	linux-version	placeholder	stat
alloydb-auth-proxy	etags.emacs	in	pkcheck	stdbuf
antosci	in	inneto	pkconf	strace
apropos	expand	innetat	pkconfig	strace-log-merge
apt	gromacs	locale	ptill	streammap
apt-add-repository	empr	locale-check	pktyagent	strings
apt-cache	factor	localeacl	p12pm	strip
apt-cdrom	faillog	localedef	plid	stty
apt-config	faillocate	local-extract	psmp	su
apt-get	false	logger	pod2html	sudo
apt-key	fc-cache	login	pod2man	sudoedit
apt-mark	fc-cat	logintcl	pod2text	sudoreplay
ar	fc-confilist	logname	pod2usage	sum
arch	fc-list	look	podchecker	supervisordctl
as	fc-match	ls	pr	supervisord
autoconf	lattr	lsblk	preconv	sync
autoheader	fc-query	lsb-release	printenv	sysctl-suggest3.2
automake	fc-scan	lsb-release	printit	sysctlctl
automake	fc-validate	lsbgroup	prlimit	systemd
automake-1.16	fdp	lscpu	proto	systemd-ask-power
autoreconf	fgrep	lsinitramfs	prove	systemd-analyze
autoscan	find	lsipc	prstat	systemd-ask-passw
autoupdate	file	lslocks	prune	systemd-cat
avx	findmnt	lslogins	ps	systemd-cgls
b2num	flock	lsmem	pslog	systemd-cgtop
base32	fmt	lsmem	psql	systemd-confext
base64	fold	lscn	psutils	systemd-creds
basename	free	lspopopt	ptrees.kill	systemd-cryptenro
basenc	funzip	lsusbys	ptar	systemd-cryptstatu
bash	fwac	lto-dump	ptardiff	systemd-id128
bashbug	fwacount	lto-dump-13	ptargrep	systemd-detact-vi
base1	g++	lxc-attach	ptx	systemd-escape
bcnaps	gr-rs-13	lxc-autosetab	pwd	systemd-firstboot
bison	g++-cgroup	lxc-cgroup	pwdx	systemd-hack
bison_yacc	gc	lxc-checkconfig	pwsh	systemd-id128

/usr/bin/

Executable files
(binary)

```
aa-enabled          enc2as              lscfg              pinentry-curses    ss
aa-esc              encguess            libnetcfg          ping               ssh
aa-features-abi     env                 libtoolize         ping4              ssh-add
aclocal              envsubst            link                ping6              ssh-agent
aclocal-1.16         eqn                 linux32             pinky              ssh-argv0
acpkg               adb                 linux64             pip                ssh-copy-id
add-apt-repository   ar3.2               linux-check-removal pip3.12            ssh-keygen
addpart             arno                linux-update-symlinks pkaction           ssh-keyscan
add2line            atlogb-auth-proxy  ls                  pkcheck            stat
anthoscli            atags               lna                 pkgconf            strace
apropos              atags.amans         ln                   pkg-config          strace-log-merge
apt                  atags               locale               pkil               steamrip
apt-add-repository   atags               locale-check        pkttysagent        strings
apt-cache            atags               localelect          pl2pm              strip
apt-cdrom            atags               localedef           pldd               strty
apt-config            atags               local-extract       pmap               su
apt-get              atags               logger              pod2html           sudo
apt-key              atags               login                pod2man            sudoedit
apt-mark             atags               logintcl            pod2text            sudoreplay
ar                   atags               logname             pod2usage           sum
arch                  atags               look                 podchecker          supervisorctl
as                     atags               ls                   ps                  supervisorord
autoconf              atags               lsattr              preconv            sync
autoheader            atags               lsbk                 printenv            syntax_suggest3.2
automite              atags               lsb_release          printf              systemd
automake               atags               lscgroup             printit             systemd
automake-1.16         atags               lscpu                protoc              systemd-ac-power
autoreconf             atags               lsmnt                prove               systemd-analyze
autoscan               atags               lsipc                 ptstat              systemd-ask-passw
autoupdate             atags               lslocks               prune               systemd-cat
awk                     atags               lsmnt                 ps                  systemd-cgls
b2sum                  atags               flock                 rsync               systemd-cgtop
base32                  atags               fmt                   rsync               systemd-confext
base64                  atags               fold                  lane                 systemd-creds
basenr                  atags               free                  lppgpt              systemd-cryptenro
basenc                  atags               fsumip               lsduhys              systemd-cryptsetup
bash                     atags               fuser                 lto-dump             systemd-delta
bashbug                  atags               gcc                   lto-dump-13          systemd-detect-vi
base1                    atags               gcc++13               lxc-autostart         systemd-escape
bcowsps                  atags               gccapplication        lxc-cgroup            systemd-firstboot
bison                    atags               gc                     lxc-cgroup            systemd-hwdb
bison.yacc               atags               gc                     lxc-checkconfig       systemd-ld128
```

makeblastdb


Ok, I will look for
it in /usr/bin

PC


You

/usr/bin/home/

**Executable files
(binary)**



A diagram showing a blue stick figure representing a user. Below the figure is the text "You". To the right of the figure is a speech bubble containing the text "makeblastdb".



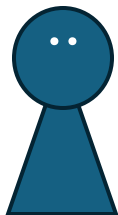
A diagram showing a blue stick figure representing a user. Below the figure is the text "You". To the right of the figure is a speech bubble containing the text "makeblastdb".

```
graph TD
    A[makeblastdb] --> B[blastn]
    B --> C[blastp]
```


No, I cannot find it...

No, I cannot find it...

**Executable files
(binary)**



You



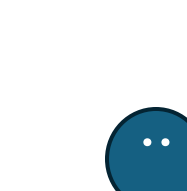
blast

**Executable file of
blast**

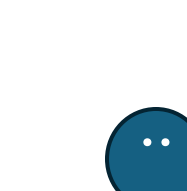


Place the file into different directory


**Executable files
(binary)**



A diagram showing a blue person icon with a speech bubble. The speech bubble contains the text "makebl". Below the icon is the label "You".



A diagram showing a blue person icon with a speech bubble. The speech bubble contains the text "makebl". Below the icon is the label "You".

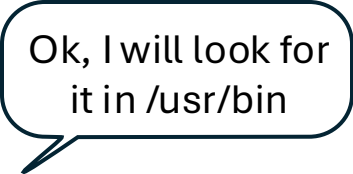


```
graph LR; A[makeblastdb] --> B[blastn]
```

**Executable file of
blast**


**Executable file of
blast**

**Executable file of
blast**

[illegible]

Ok, I will look for it in /usr/bin

**Executable files
(binary)**

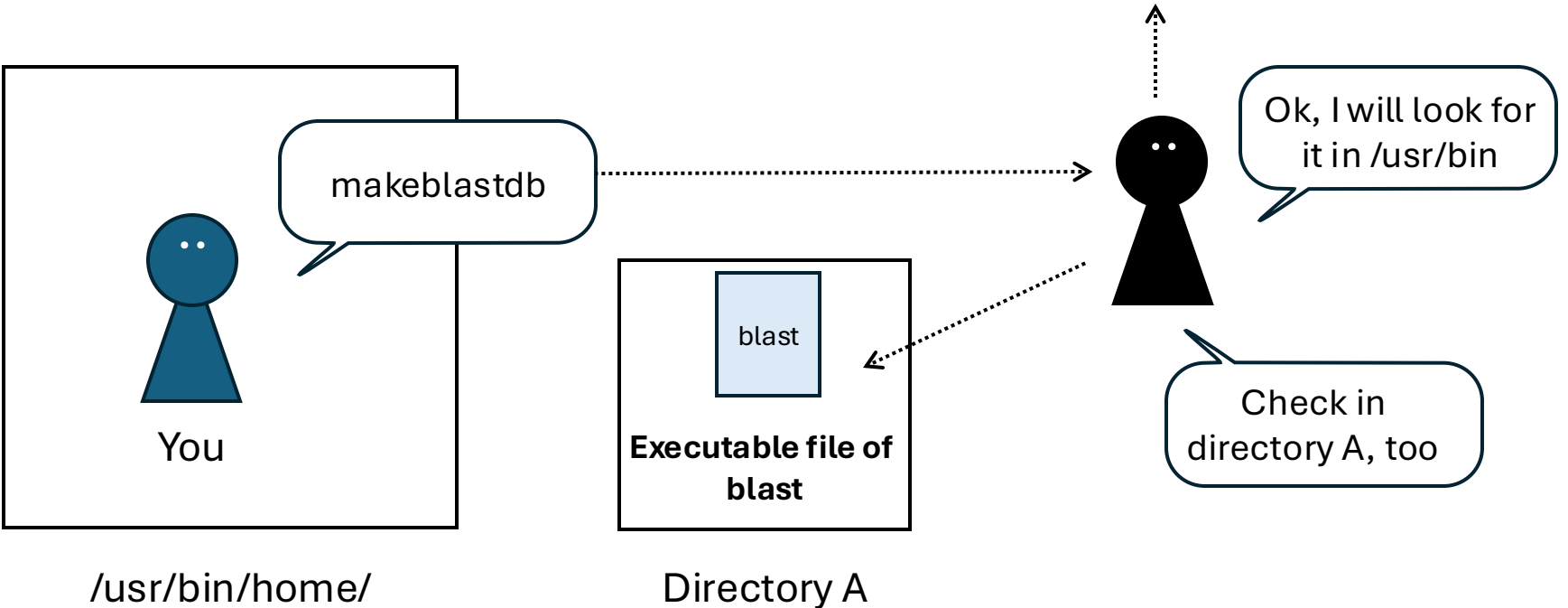


A diagram showing a person icon (a blue circle head with two dots for eyes, and a blue trapezoid body) labeled "You" below it. To the right of the person is a speech bubble containing the text "makebl".


blast

Executable file of
blast

aa-enabled	aaen25s	laargrog	panenary-curses	ss
aa-sock	aaenogless	lilinetog	ping	st
aa-features-abi	aanv	liblollis	ping6	stab-add
aclocal	anvsubst	link	ping6s	stab-agent
aclocal-1.16	anv	linux32	pinky	ssh-argv0
acyclic	arb	linux64	pip	ssh-copy-id
add-apt-repository	arkb.2	linux-check-removal	pip3	ssh-keygen
addpart	ararno	linux-update-symlinks	pip3.12	ssh-keyscan
add22line	atags	linux-version	pkaction	stat
allioydb-auth-proxy	atags_emacs	in	pkcheck	stdufb
anthoscli	ax	inmato	pkconf	strace
apt	axpend	inmatat	pk-config	strace-log-merge
apt-add-repository	axp416	locale	pkill	streamrip
apt-cache	axpr	locale-check	pktyagent	strings
apt-cdrom	factor	localec1	pl2pm	strip
apt-config	falllog	localedef	pldd	stty
apt-get	falllocate	local-extract	pmap	su
apt-key	false	logger	pod2html	sudo
apt-mark	fc-cache	login	pod2man	sudedit
ar	fc-cat	logintel	pod2text	sudoreplay
arch	fc-confliat	logname	pod2usage	sum
	fc-list	look	podchecker	supervisordcli
as	fc-match	ls	pr	supervisord
autoconf	fc-pattern	lsattr	preconv	sync
autoheader	fc-query	lsblk	printenv	sysbench_suggest3.2
autom4te	fc-scan	lsb_release	printf	systemctl
automake	fc-validate	lsgroup	prlimit	systemd
automake-1.16	rdp	lscpu	protoc	systemd-ac-power
autoreconf	gppp	lsn1transf	prove	systemd-analyze
autocan	file	lsipc	prstat	systemd-ask-passw
autopatch	find	lslocks	prune	systemd-cat
	findmt	lslogins	ps	systemd-cgls
b2sum	flock	lsmem	palog	systemd-cgtop
base32	fmt	lsmem	psql	systemd-confext
base64	fold	lms	ptcrce	systemd-creds
basenane	free	lpgpgot	ptcrce.kill	systemd-cryptenq
basenc	funsip	lsabays	ptar	systemd-cryptntr
bash	funsb	lto-dump	ptardiff	systemd-del1
bashbug	fuysermount	lto-dump-13	ptargrep	systemd-detect-vl
bazel	g++	lxc-attach	pts	systemd-escape
bcnaps	g++-13	lxc-autostart	pwd	systemd-firstboot
bison	gc	lxc-cgroup	rwk	systemd-hwdb
bison.yacc	gc	lxc-checkconfig	pwsh	systemd-id128



**Executable files
(binary)**

[illegible]A blue stylized figure representing 'You'. It consists of a circular head with two small white dots for eyes, and a triangular body. The figure is centered within a square frame.

You

```
/usr/bin/home/
```

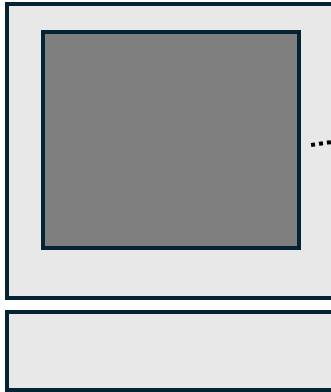
➔ but, the directory is for the basic command lines and may cause conflict with them...

“not recommended”

3. Installing the software

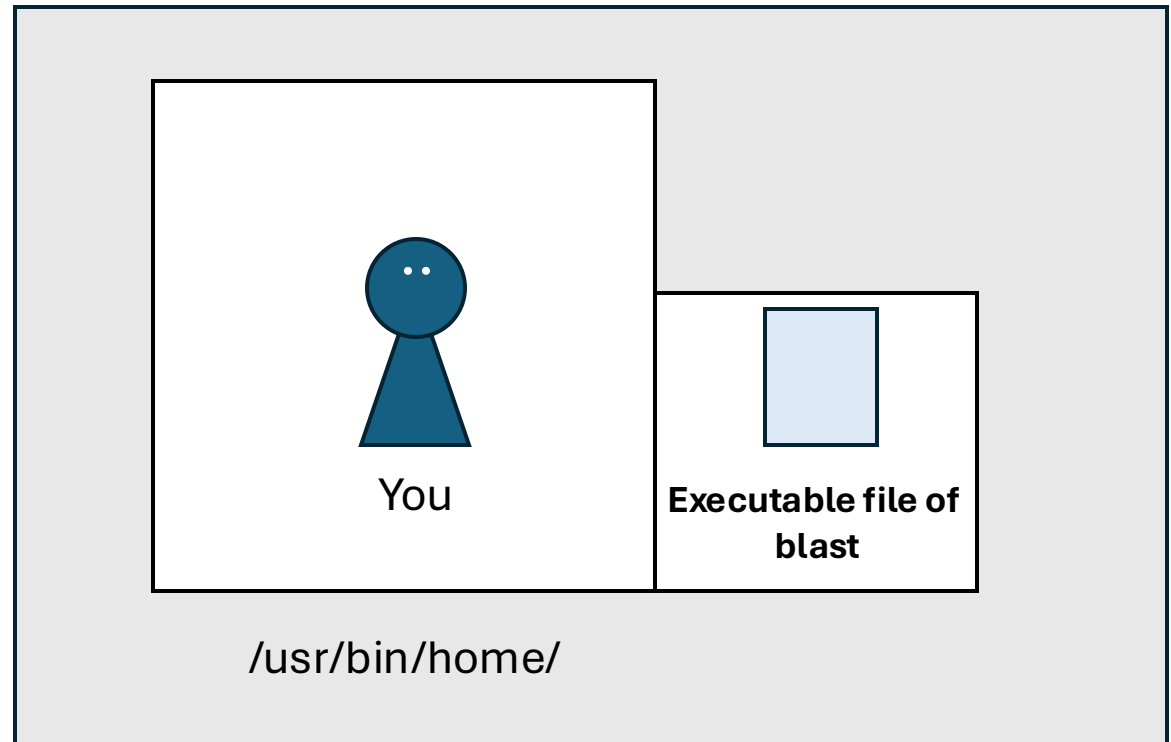
Installing the software

Web online

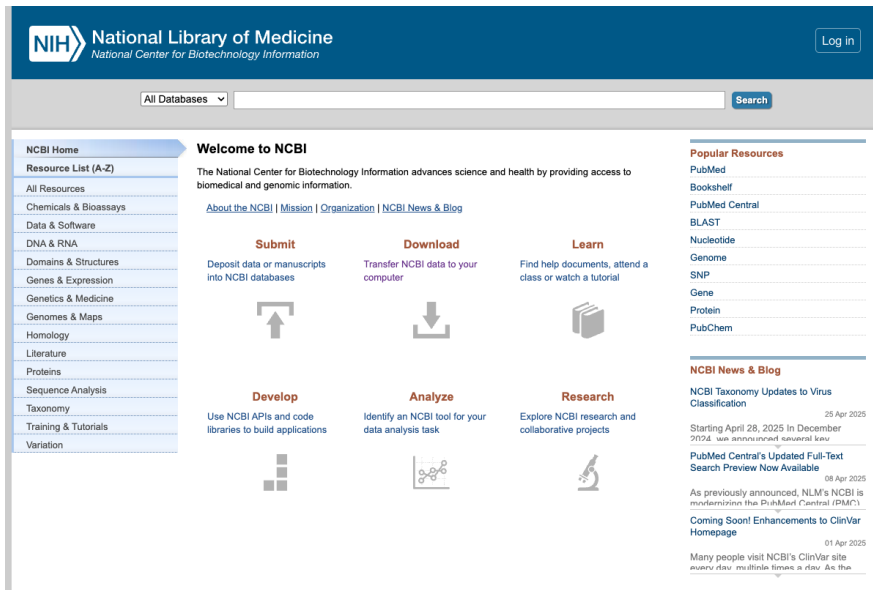


1. **Download the software**
2. **Add a directory to PATH**

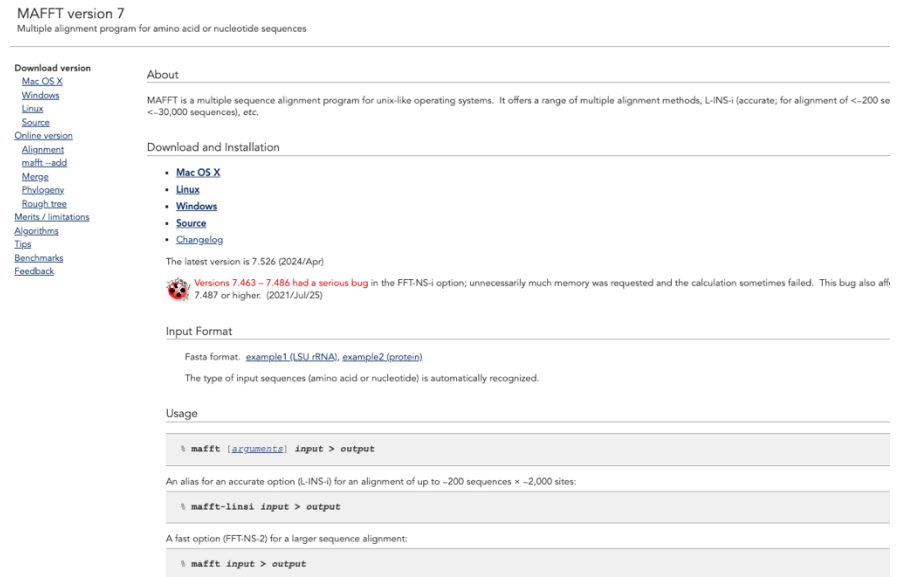
Your local PC (=Cloud Shell)



1. Download the software



Ex) NCBI provides a lot of the tools such as blast, sra-tools, and so on...



Ex) The webpage of MAFFT, an alignment tool

Go to the webpage of the software

All Databases

Search

NCBI Home

Resource List (A-Z)

All Resources
Chemicals & Bioassays
Data & Software
DNA & RNA
Domains & Structures
Genes & Expression
Genetics & Medicine
Genomes & Maps
Homology
Literature
Proteins
Sequence Analysis
Taxonomy
Training & Tutorials
Variation

Welcome to NCBI

The National Center for Biotechnology Information advances science and health by providing access to biomedical and genomic information.

[About the NCBI](#) | [Mission](#) | [Organization](#) | [NCBI News & Blog](#)

Submit

Deposit data or manuscripts into NCBI databases



Download

Transfer NCBI data to your computer



Learn

Find help documents, attend a class or watch a tutorial



Develop

Use NCBI APIs and code libraries to build applications



Analyze

Identify an NCBI tool for your data analysis task



Research

Explore NCBI research and collaborative projects



Popular Resources

PubMed
Bookshelf
PubMed Central
BLAST
Nucleotide
Genome
SNP
Gene
Protein
PubChem

NCBI News & Blog

NCBI Taxonomy Update Classification

Starting April 28, 2025 | 2024 was announced so PubMed Central's Update Search Preview Now At

As previously announced, we are announcing the PubMed Central's Update Search Preview Now At

Many people visit NCBI every day, multiple times

Follow the web page...

Basic Local Alignment Search Tool

BLAST finds regions of similarity between biological sequences. The program compares nucleotide or protein sequences to sequence databases and calculates the statistical significance.

[Learn more](#)

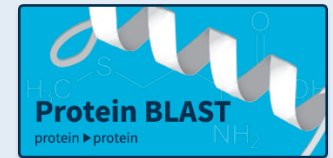
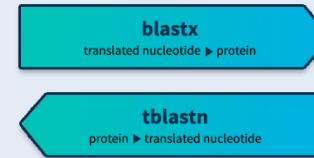
Mon, 17 Mar 2025

Improvements include upgrading to GCP Artifact Registry and better handling of job completion status in kubernetes version 1.30+.

ElasticBLAST 1.4.0 is now available!

[More BLAST news...](#)

Web BLAST



BLAST > [blast-help](#) > Download BLAST Software and Databases

Was this cor

BLAST+ executables

What are the next steps?

Magic-BLAST

IgBLAST

SRPRISM

Databases

BLAST+ executables

Do you have difficulties running high volume BLAST searches? Do you have sequence data to search and cannot use the NCBI BLAST web site? Do you have your own server? Do you have your own research pipeline? Have security or sending searches outside of your organization? If you answered yes to any of these questions, read on!

The NCBI provides a suite of command-line tools to run BLAST called BLAST+. This allows users to perform BLAST searches on their own server without size, volume and database restrictions. BLAST+ can be used with a command line so it can be integrated directly into your workflow.

What are the next steps?

Download and install BLAST+. Installers and source code are available from <https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/>. Download the databases you need, (see database section below), or create your own. Start searching.

For more details, please see the [BLAST+ user manual](#), the [BLAST Help manual](#), the [BLAST releases notes](#), and the article in BMC Bioinformatics ([PubMed link](#)). See our [versioning policy](#).

The BLAST+ suite is the currently supported package. The older C toolkit executables are no longer supported. See our [versioning policy](#).

We are always listening and welcome your feedback at [BLAST Support Center](#).

Standalone and API BLAST



Download BLAST

Get BLAST databases and executables



Use BLAST API

Call BLAST from your application



Use BLAST in the cloud

Start an instance at a cloud provider

Index of /blast/executables/blast+/LATEST

Name	Last modified	Size
Parent Directory		-
ChangeLog	2024-06-25 14:34	85
ncbi-blast-2.16.0+-1.src.rpm	2024-06-25 14:31	21M
ncbi-blast-2.16.0+-1.src.rpm.md5	2024-06-25 14:35	63
ncbi-blast-2.16.0+-1.x86_64.rpm	2024-06-25 14:31	202M
ncbi-blast-2.16.0+-1.x86_64.rpm.md5	2024-06-25 14:35	66
ncbi-blast-2.16.0+-aarch64-linux.tar.gz	2024-07-30 11:04	225M
ncbi-blast-2.16.0+-aarch64-linux.tar.gz.md5	2024-07-30 11:04	74
ncbi-blast-2.16.0+-aarch64-macosx.tar.gz	2024-06-25 14:33	191M
ncbi-blast-2.16.0+-aarch64-macosx.tar.gz.md5	2024-06-25 14:35	75
ncbi-blast-2.16.0+-aarch64.dmg	2024-06-25 14:33	193M
ncbi-blast-2.16.0+-aarch64.dmg.md5	2024-06-25 14:35	65
ncbi-blast-2.16.0+-src.tar.gz	2024-06-25 14:35	27M
ncbi-blast-2.16.0+-src.tar.gz.md5	2024-06-25 14:35	64
ncbi-blast-2.16.0+-src.zip	2024-06-25 14:35	31M
ncbi-blast-2.16.0+-src.zip.md5	2024-06-25 14:35	61
ncbi-blast-2.16.0+-universal-macosx.tar.gz	2024-06-25 14:44	398M
ncbi-blast-2.16.0+-universal-macosx.tar.gz.md5	2024-06-25 14:44	76
ncbi-blast-2.16.0+-universal.dmg	2024-06-25 14:43	400M
ncbi-blast-2.16.0+-universal.dmg.md5	2024-06-25 14:44	66
ncbi-blast-2.16.0+-win64.exe	2024-06-25 14:30	129M
ncbi-blast-2.16.0+-win64.exe.md5	2024-06-25 14:35	63
ncbi-blast-2.16.0+-x64-linux.tar.gz	2024-06-25 14:33	246M
ncbi-blast-2.16.0+-x64-linux.tar.gz.md5	2024-06-25 14:35	70
ncbi-blast-2.16.0+-x64-macosx.tar.gz	2024-06-25 14:35	206M
ncbi-blast-2.16.0+-x64-macosx.tar.gz.md5	2024-06-25 14:35	71
ncbi-blast-2.16.0+-x64-win64.tar.gz	2024-06-25 14:31	133M
ncbi-blast-2.16.0+-x64-win64.tar.gz.md5	2024-06-25 14:35	70
ncbi-blast-2.16.0+-x86_64.dmg	2024-06-25 14:34	208M
ncbi-blast-2.16.0+-x86_64.dmg.md5	2024-06-25 14:35	64

FTP
(File Transfer Protocol)

Index of /blast/executables/blast+/LATEST

Name	Last modified	Size
Parent Directory		-
ChangeLog	2024-06-25 14:34	85
ncbi-blast-2.16.0+-1.src.rpm	2024-06-25 14:31	21M
ncbi-blast-2.16.0+-1.src.rpm.md5	2024-06-25 14:35	63
ncbi-blast-2.16.0+-1.x86_64.rpm	2024-06-25 14:31	202M
ncbi-blast-2.16.0+-1.x86_64.rpm.md5	2024-06-25 14:35	66
ncbi-blast-2.16.0+-aarch64-linux.tar.gz	2024-07-30 11:04	225M
ncbi-blast-2.16.0+-aarch64-linux.tar.gz.md5	2024-07-30 11:04	74
ncbi-blast-2.16.0+-aarch64-macosx.tar.gz	2024-06-25 14:33	191M
ncbi-blast-2.16.0+-aarch64-macosx.tar.gz.md5	2024-06-25 14:35	75
ncbi-blast-2.16.0+-aarch64.dmg	2024-06-25 14:33	193M
ncbi-blast-2.16.0+-aarch64.dmg.md5	2024-06-25 14:35	65
ncbi-blast-2.16.0+-src.tar.gz	2024-06-25 14:35	27M
ncbi-blast-2.16.0+-src.tar.gz.md5	2024-06-25 14:35	64
ncbi-blast-2.16.0+-src.zip	2024-06-25 14:35	31M
ncbi-blast-2.16.0+-src.zip.md5	2024-06-25 14:35	61
ncbi-blast-2.16.0+-universal-macosx.tar.gz	2024-06-25 14:44	398M
ncbi-blast-2.16.0+-universal-macosx.tar.gz.md5	2024-06-25 14:44	76
ncbi-blast-2.16.0+-universal.dmg	2024-06-25 14:43	400M
ncbi-blast-2.16.0+-universal.dmg.md5	2024-06-25 14:44	66
ncbi-blast-2.16.0+-win64.exe	2024-06-25 14:30	129M
ncbi-blast-2.16.0+-win64.exe.md5	2024-06-25 14:35	63
ncbi-blast-2.16.0+-x64-linux.tar.gz	2024-06-25 14:33	246M
ncbi-blast-2.16.0+-x64-linux.tar.gz.md5	2024-06-25 14:35	70
ncbi-blast-2.16.0+-x64-macosx.tar.gz	2024-06-25 14:35	206M
ncbi-blast-2.16.0+-x64-macosx.tar.gz.md5	2024-06-25 14:35	71
ncbi-blast-2.16.0+-x64-win64.tar.gz	2024-06-25 14:31	133M
ncbi-blast-2.16.0+-x64-win64.tar.gz.md5	2024-06-25 14:35	70
ncbi-blast-2.16.0+-x86_64.dmg	2024-06-25 14:34	208M
ncbi-blast-2.16.0+-x86_64.dmg.md5	2024-06-25 14:35	64

FTP
(File Transfer Protocol)

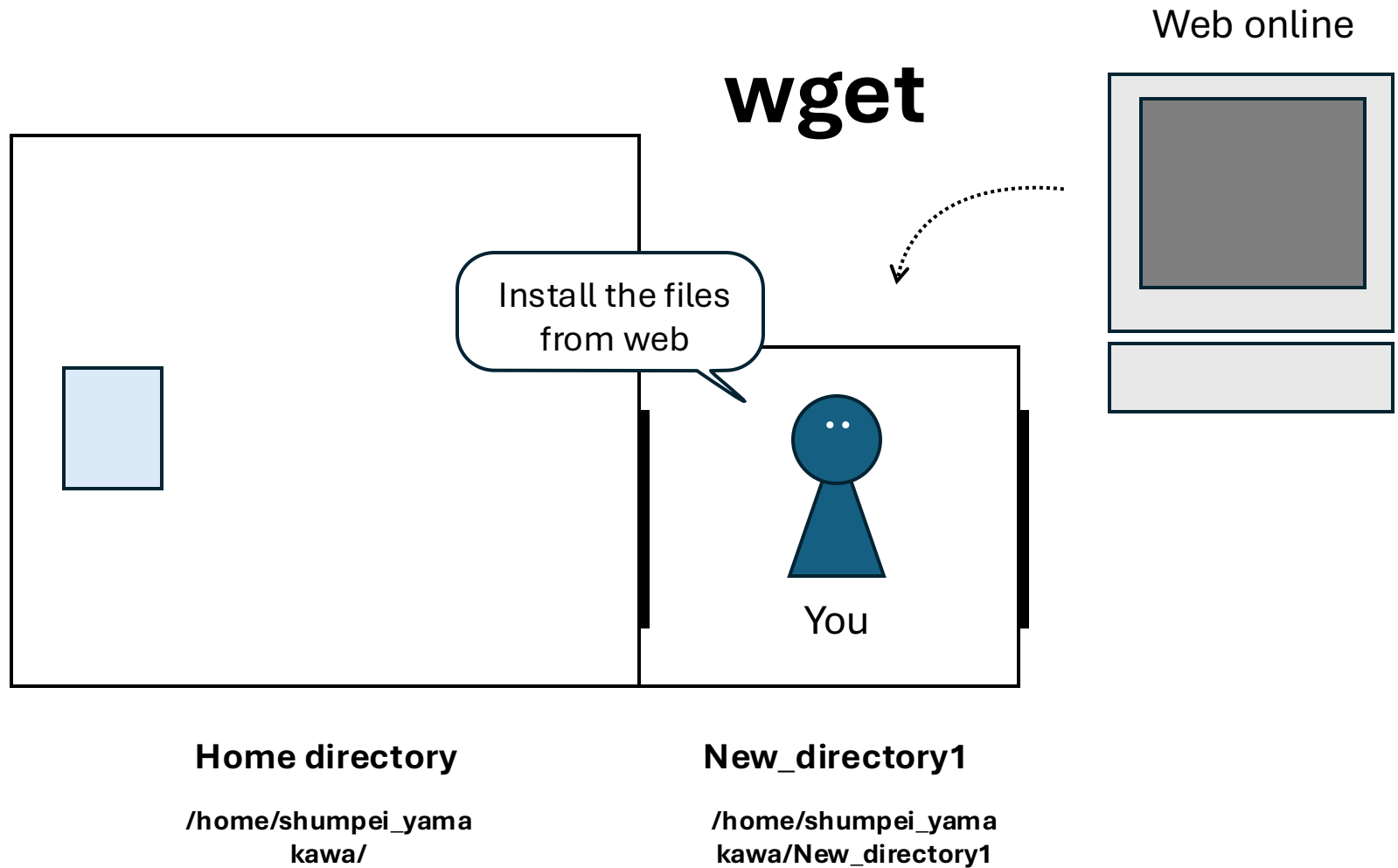
Index of /blast/executables/blast+/LATEST

Name	Last modified	Size
Parent Directory		-
ChangeLog	2024-06-25 14:34	85
ncbi-blast-2.16.0+-1.src.rpm	2024-06-25 14:31	21M
ncbi-blast-2.16.0+-1.src.rpm.md5	2024-06-25 14:35	63
ncbi-blast-2.16.0+-1.x86_64.rpm	2024-06-25 14:31	202M
ncbi-blast-2.16.0+-1.x86_64.rpm.md5	2024-06-25 14:35	66
ncbi-blast-2.16.0+-aarch64-linux.tar.gz	2024-07-30 11:04	225M
ncbi-blast-2.16.0+-aarch64-linux.tar.gz.md5	2024-07-30 11:04	74
ncbi-blast-2.16.0+-aarch64-macosx.tar.gz	2024-06-25 14:33	191M
ncbi-blast-2.16.0+-aarch64-macosx.tar.gz.md5	2024-06-25 14:35	75
ncbi-blast-2.16.0+-aarch64.dmg	2024-06-25 14:33	193M
ncbi-blast-2.16.0+-aarch64.dmg.md5	2024-06-25 14:35	65
ncbi-blast-2.16.0+-src.tar.gz	2024-06-25 14:35	27M
ncbi-blast-2.16.0+-src.tar.gz.md5	2024-06-25 14:35	64
ncbi-blast-2.16.0+-src.zip	2024-06-25 14:35	31M
ncbi-blast-2.16.0+-src.zip.md5	2024-06-25 14:35	61
ncbi-blast-2.16.0+-universal-macosx.tar.gz	2024-06-25 14:44	398M
ncbi-blast-2.16.0+-universal-macosx.tar.gz.md5	2024-06-25 14:44	76
ncbi-blast-2.16.0+-universal.dmg	2024-06-25 14:43	400M
ncbi-blast-2.16.0+-universal.dmg.md5	2024-06-25 14:44	66
ncbi-blast-2.16.0+-win64.exe	2024-06-25 14:30	129M
ncbi-blast-2.16.0+-win64.exe.md5	2024-06-25 14:35	63
ncbi-blast-2.16.0+-x64-linux.tar.gz	2024-06-25 14:33	246M
ncbi-blast-2.16.0+-x64-linux.tar.gz.md5	2024-06-25 14:35	70
ncbi-blast-2.16.0+-x64-macosx.tar.gz	2024-06-25 14:35	206M
ncbi-blast-2.16.0+-x64-macosx.tar.gz.md5	2024-06-25 14:35	71
ncbi-blast-2.16.0+-x64-win64.tar.gz	2024-06-25 14:31	133M
ncbi-blast-2.16.0+-x64-win64.tar.gz.md5	2024-06-25 14:35	70
ncbi-blast-2.16.0+-x86_64.dmg	2024-06-25 14:34	208M
ncbi-blast-2.16.0+-x86_64.dmg.md5	2024-06-25 14:35	64

Copy link address

<https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz>

```
~$ wget https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
```

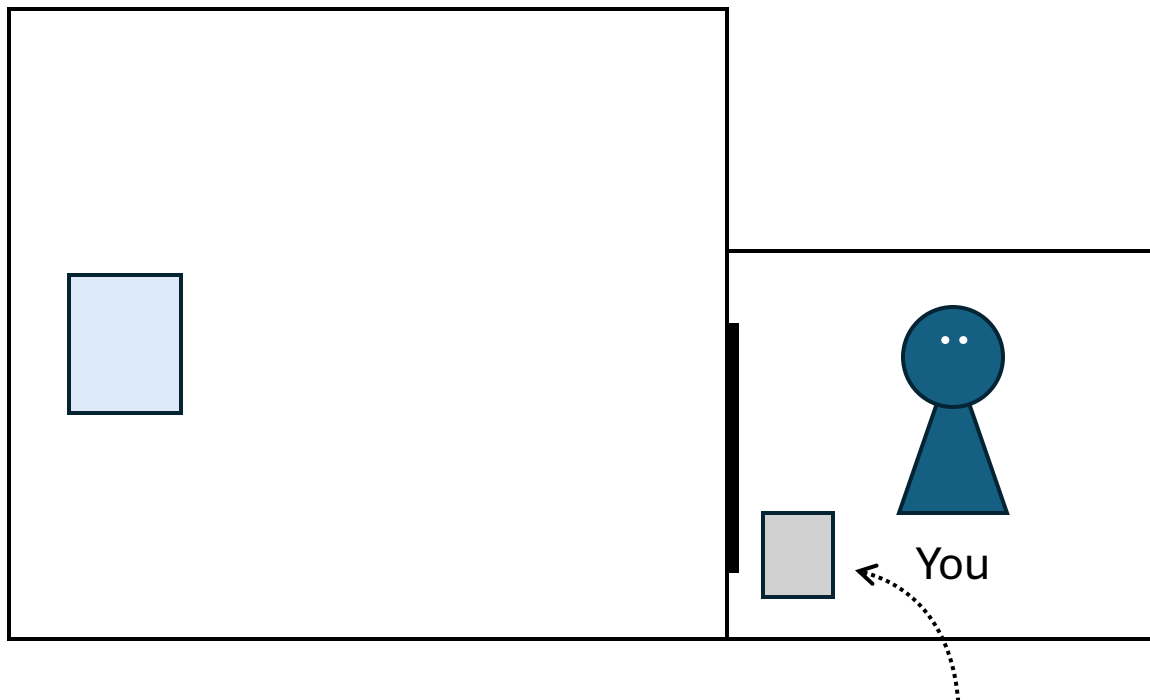


```
shumpei_yamakawa@cloudshell:~$ wget https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
--2025-05-14 13:21:21-- https://ftp.ncbi.nlm.nih.gov/blast/executables/blast+/LATEST/ncbi-blast-2.16.0+-x64-linux.tar.gz
Resolving ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)... 130.14.250.13, 130.14.250.31, 130.14.250.7, ...
Connecting to ftp.ncbi.nlm.nih.gov (ftp.ncbi.nlm.nih.gov)|130.14.250.13|:443... connected.
HTTP request sent, awaiting response... 200 OK
Length: 257516053 (246M) [application/x-gzip]
Saving to: 'ncbi-blast-2.16.0+-x64-linux.tar.gz'

ncbi-blast-2.16.0+-x64-linux.tar.gz      100%[=====>] 245.59M  14.4MB/s   in 13s

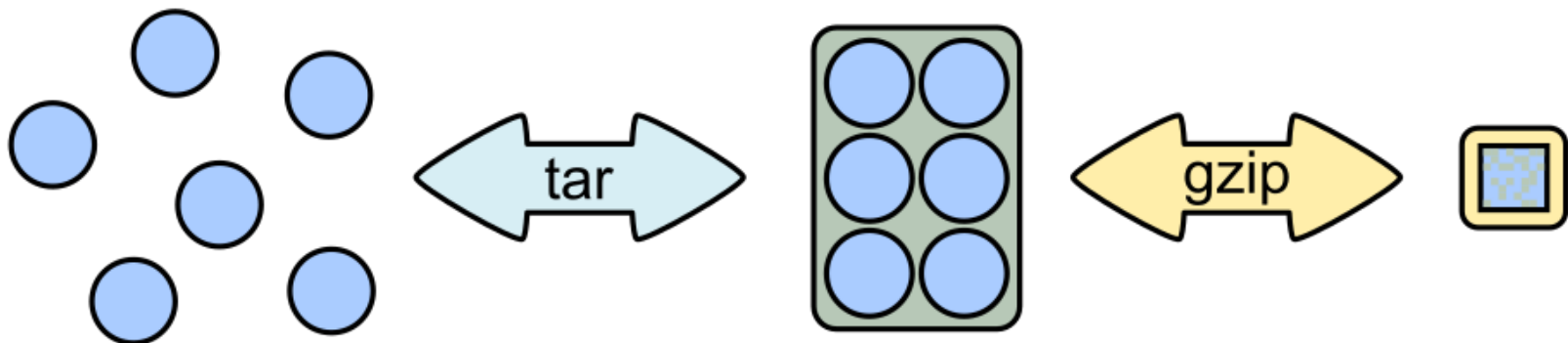
2025-05-14 13:21:35 (18.4 MB/s) - 'ncbi-blast-2.16.0+-x64-linux.tar.gz' saved [257516053/257516053]

shumpei_yamakawa@cloudshell:~$ ls
ncbi-blast-2.16.0+-x64-linux.tar.gz  New directory  README-cloudshell.txt  test
```



**ncbi-blast-2.16.0+-
x64-linux.tar.gz**

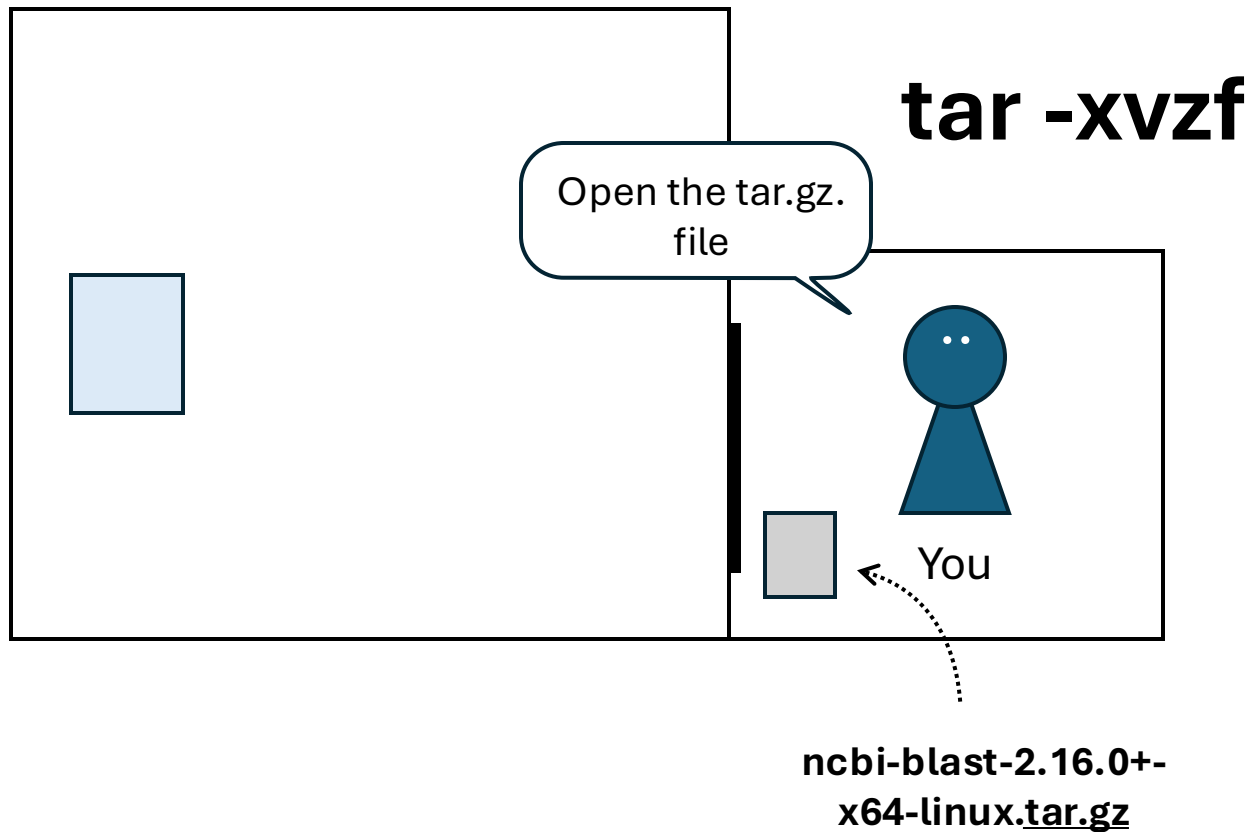
Archive and compress



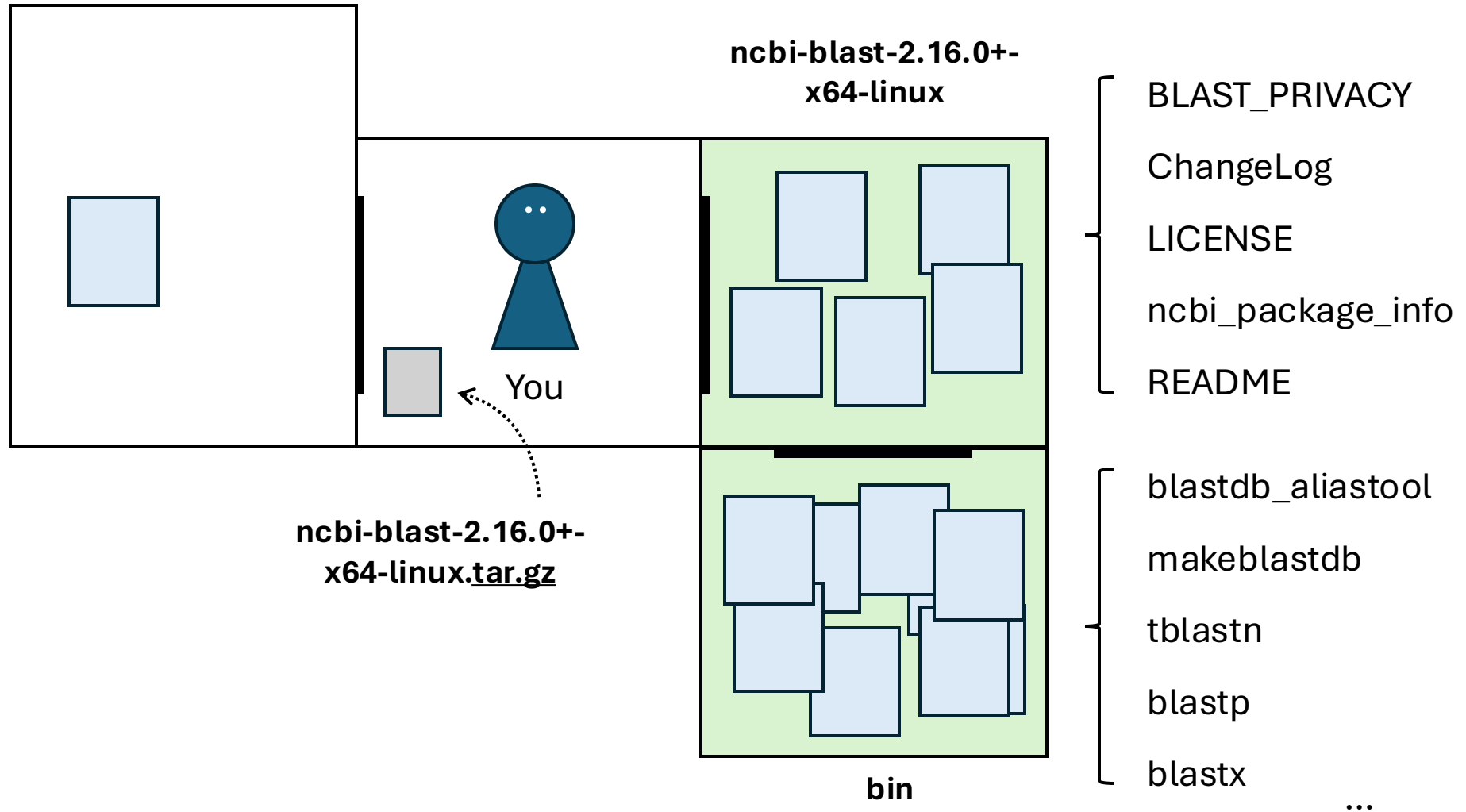
archive

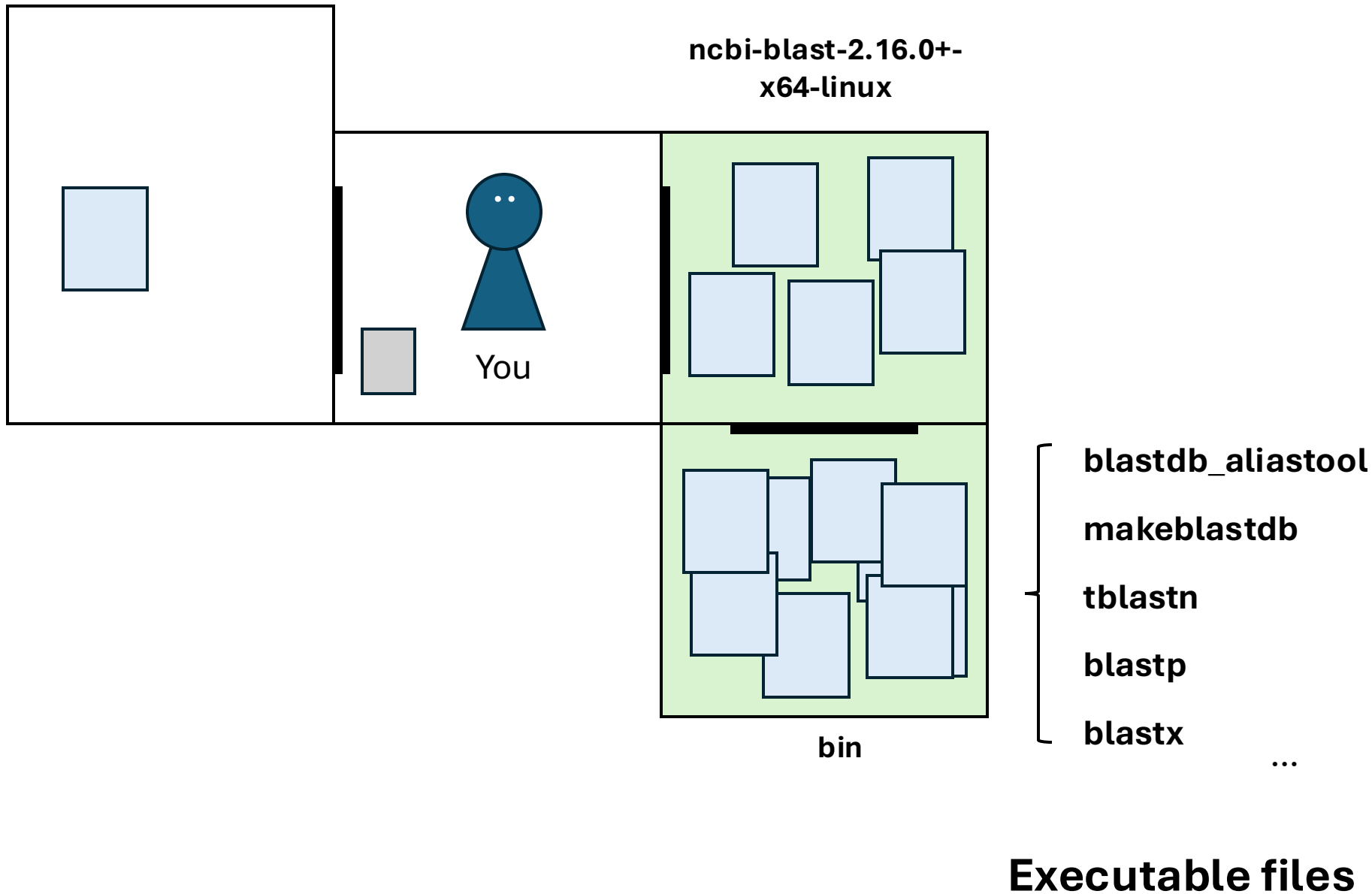
compress

```
~$ tar -xvzf ncbi-blast-2.16.0+-x64-linux.tar.gz
```



```
shumpei_yamakawa@cloudshell:~$ tar -xvzf ncbi-blast-2.16.0+-x64-linux.tar.gz
ncbi-blast-2.16.0+/
ncbi-blast-2.16.0+/ChangeLog
ncbi-blast-2.16.0+/bin/
ncbi-blast-2.16.0+/bin/rpsblast
tar: ncbi-blast-2.16.0+/bin/rpsblast: Wrote only 6656 of 10240 bytes
```





Not always so easy....

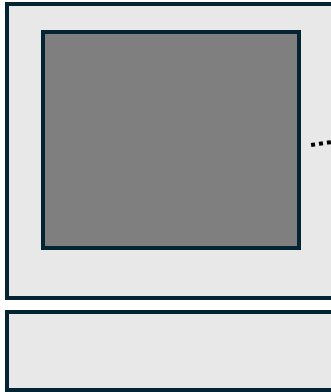
RxML

```
wget https://github.com/stamatak/standard-RxML.git
unzip master.zip
cd standard-RxML-master/
make -f Makefile.gcc
rm *.o
make -f Makefile.SSE3.gcc
rm *.o
make -f Makefile.PTHREADS.gcc
rm *.o
make -f Makefile.SSE3.PTHREADS.gcc
echo 'export PATH="/home/shumpei_yamakawa/test/standard-RxML-master:$PATH"' >> ~/.bashrc; source ~/.bashrc
```



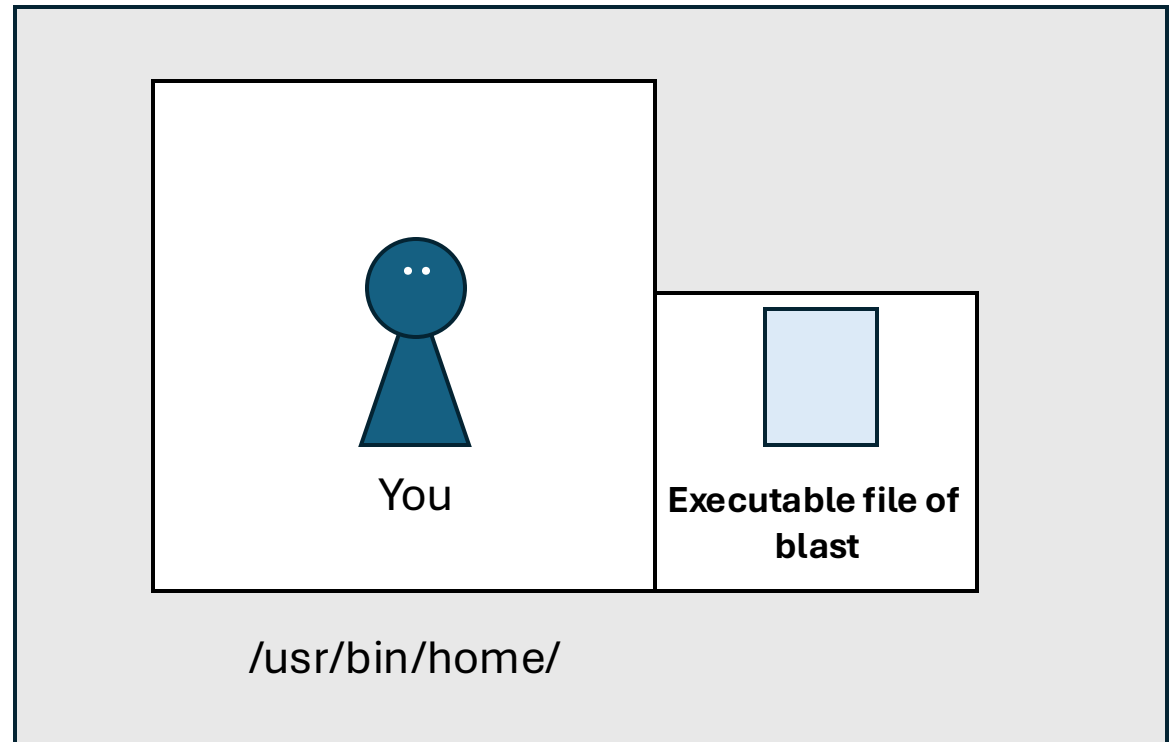
Installing the software

Web online




1. **Download the software**
2. **Add a directory to PATH**

Your local PC (=Cloud Shell)



**Executable files
(binary)**

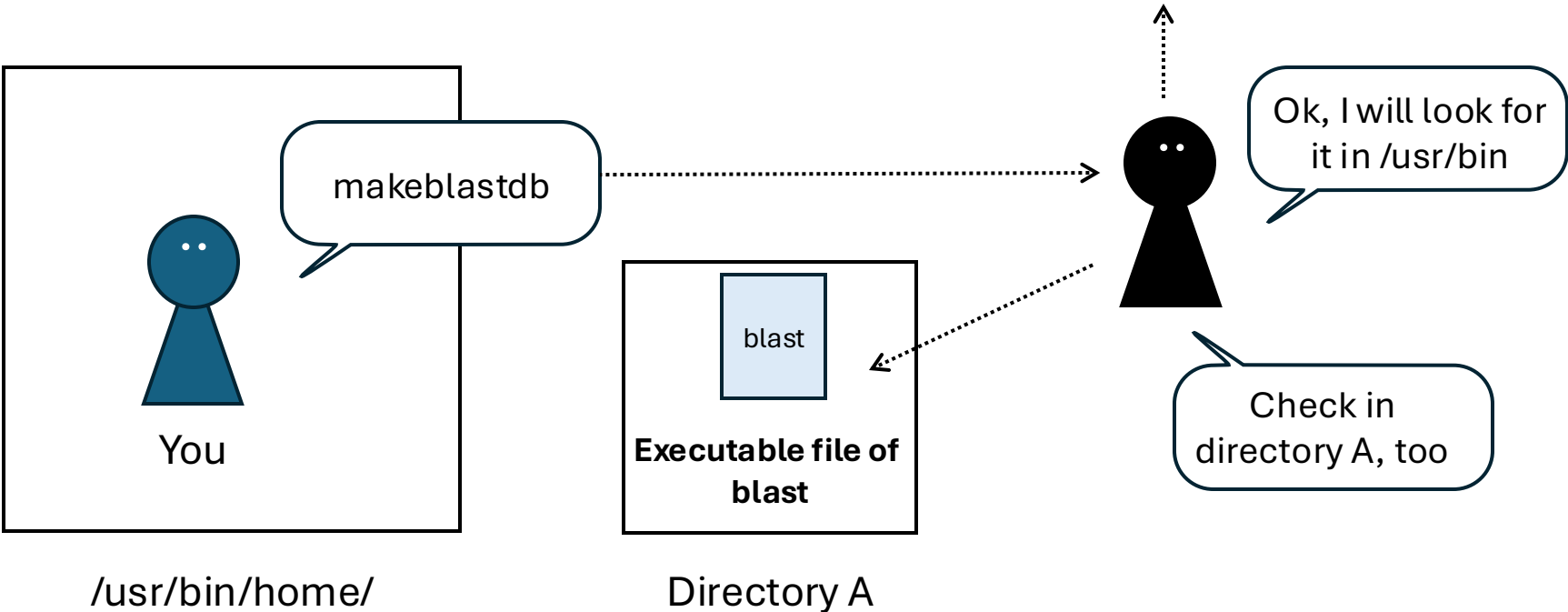


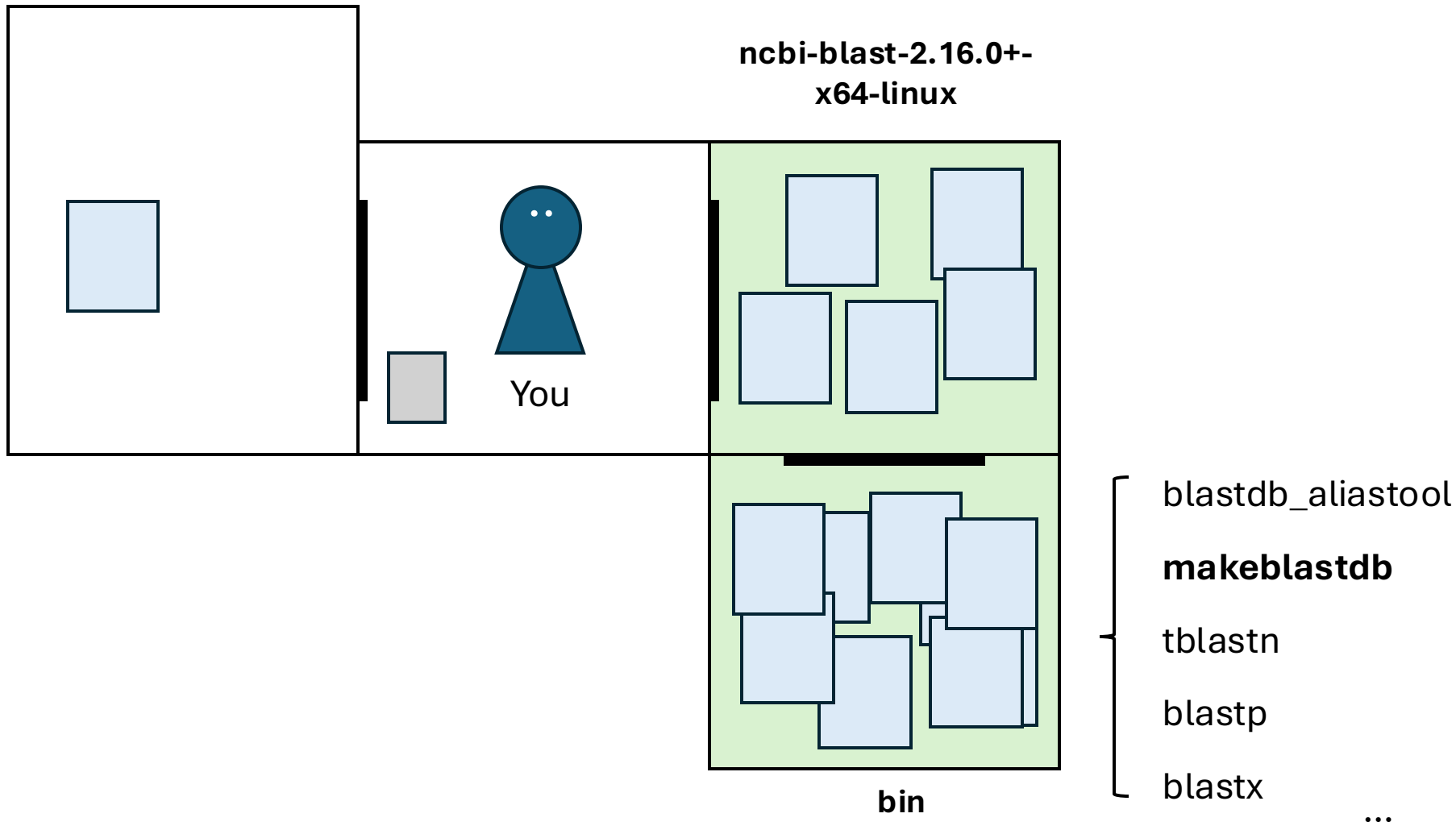
A diagram showing a person icon (a blue circle head with two dots for eyes, and a blue trapezoid body) labeled "You" below it. To the right of the person is a speech bubble containing the text "makebl".

blast

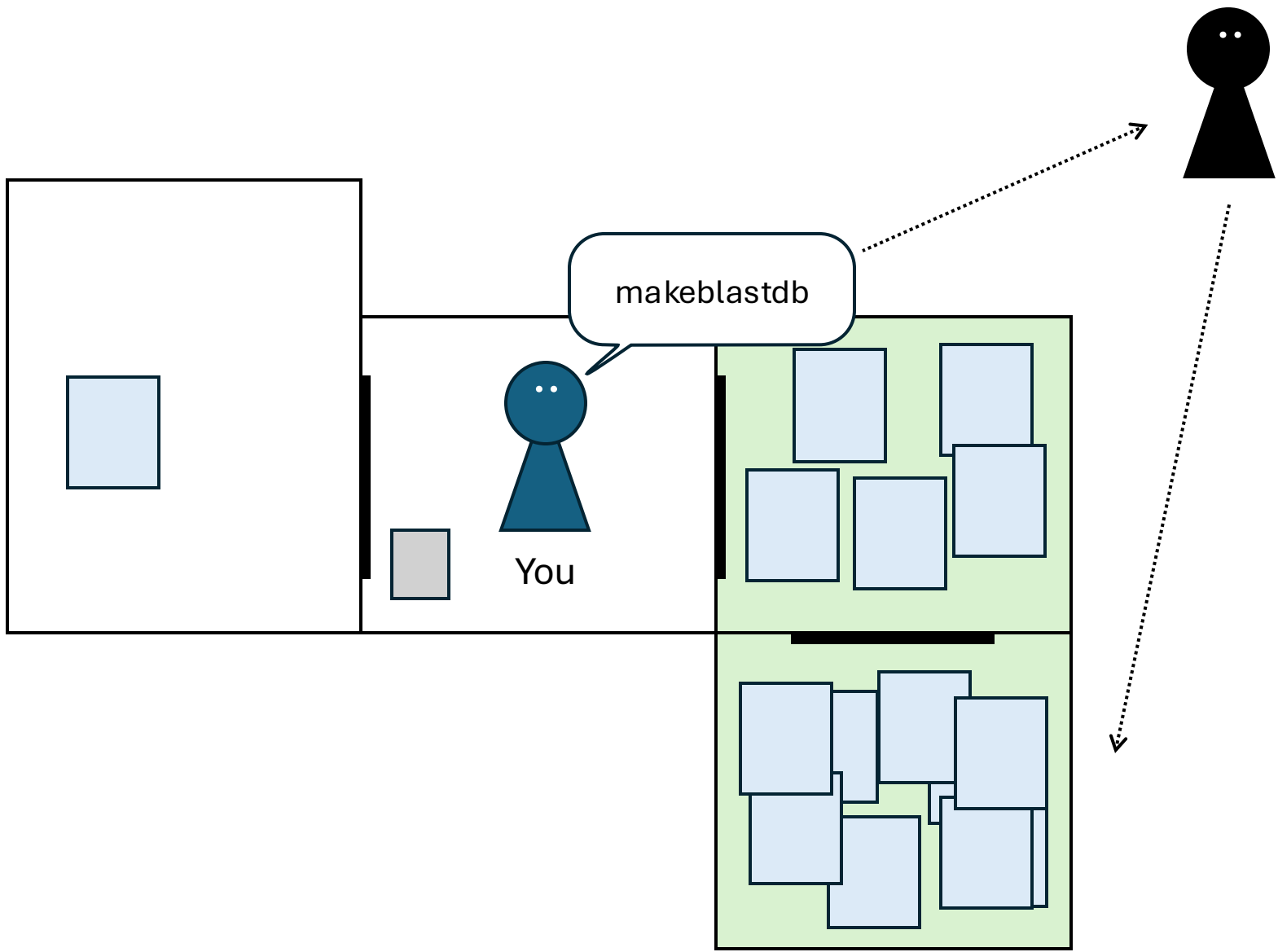
**Executable file of
blast**

an-enabled	cnchks	lswgrog	pinentry-curses	ss
an-features-abi	cnquess	libbrotli	ping	ssh
an-local	enqvcs	libtoolize	ping6	ssh-add
an-local-1.16	envubst	link	ping6s	ssh-agent
an-syscall	eqn	linux25	pinky	ssh-argv0
add-apt-repository	esb	linux64	pip	ssh-copy-id
addpart	esb3.2	linux-check-removal	pip3	ssh-keygen
addxline	errno	linux-update-symlinks	pip3.12	ssh-keyscan
alloydb-auth-proxy	etags	linux-version	pkaction	stat
antioscli	etags.emacs	in	pkcheck	stdufb
atropos	ek	lmeato	pkconf	strace
apt	expand	lmetat	pkconfig	strace-log-merge
apt-add-repository	exmp	locale	pkkill	streamrip
apt-factor	exmp	locale-check	pkktyagent	strings
apt-cdrom	faillog	locale2	plasma	strip
apt-config	faillog	localedef	pldd	stty
apt-get	fallocatc	local-extract	pmap	stty
apt-key	false	logger	pod2html	sudo
apt-mark	fc-cache	login	pod2man	sudoedit
arch	fc-cat	logintcl	pod2test	sudoreplay
as	fc-conflict	logname	pod2usage	sum
autoconf	fc-list	look	podchecker	supervisord
autoheader	fc-match	ls	pr	supervisord
automake	fc-pattern	lstrtr	preconv	sync
automake-1.16	fc-query	libbit	printf	synops_suggests.2
autoscan	fc-scan	lab-release	prlimit	systemctl
autoupdate	fc-validate	lscgrop	protoc	systemd
awk	fdp	lscups	protoe	systemd-ac-power
base28	fdp	lstdntrans	prove	systemd-analyze
base64	file	lsipc	prstat	systemd-anal-panels
b2sum	find	lslocks	prune	systemd-cat
base32	findmt	lsofcpns	ps	systemd-cgls
base64	flock	lsmem	pslog	systemd-cgtop
basenc	fat	lsmem	psql	systemd-confext
basenc	fold	lsmem	psrcs	systemd-creds
bashbug	free	lspgpot	ptree.111	systemd-cryptenro
basel	funzip	lsuhsays	ptar	systemd-cryptsetup
base16	fuser	lto-dump	ptardiff	systemd-delta
base16	g++	lto-dump-13	ptargrep	systemd-detect-vi
base16	g++	lxc-attach	pts	systemd-escape
base16	g++-13	lxc-autostart	pwd	systemd-escape
base16	gc	lxc-cgroup	pwd	systemd-firstboot
base16	gc	lxc-checkconfig	pwd	systemd-id128





Executable files



**/home/shumpei_yamakawa/n
cbi-blast-2.16.0+/bin**

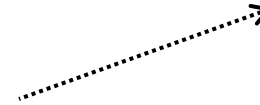
PATH: Search path for executable commands



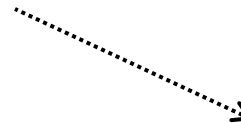
PATH

```
/home/usr/directoryA:  
/home/usr/direcotryB:  
/home/usr/direcotryC:
```

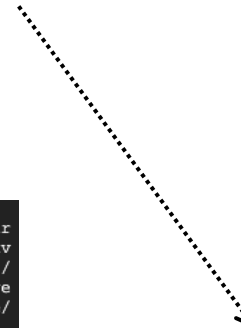
≡ a directory list



directory A



directory B

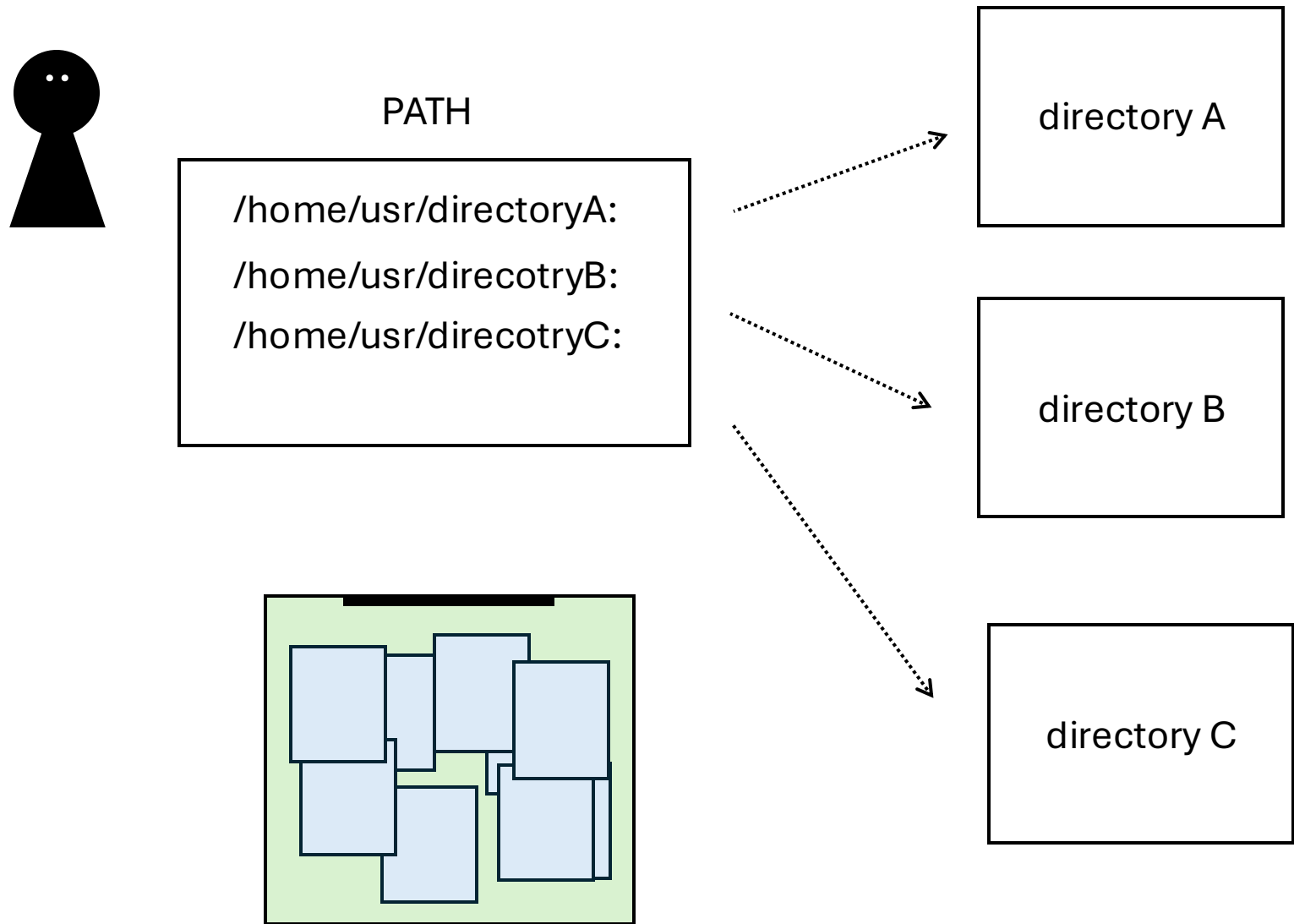


directory C

Ex)

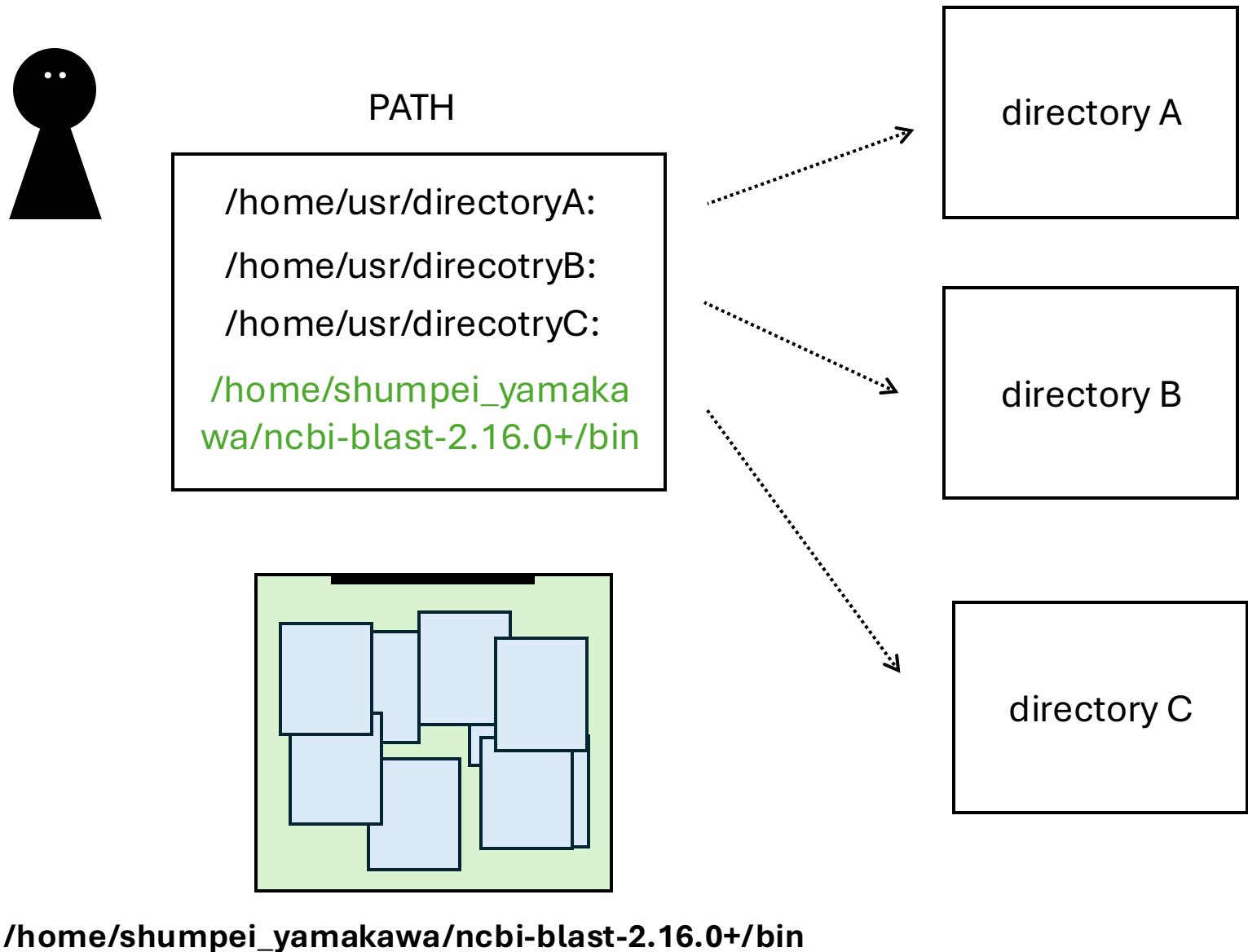
```
shumpei_yamakawa@cloudshell:~$ echo $PATH  
/home/shumpei_yamakawa/test/standard-RAXML-master:/home/shumpei_yamakawa/test/trimal-tr  
imal/source:/home/shumpei_yamakawa/test/ncbi-blast-2.16.0+/bin:/opt/gradle/bin:/opt/mav  
en/bin:/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/usr/local/go/bin:/  
usr/local/node_packages/node_modules/.bin:/usr/local/rvm/bin:/home/shumpei_yamakawa/.ge  
ms/bin:/usr/local/rvm/bin:/home/shumpei_yamakawa/gopath/bin:/google/gopath/bin:/google/  
flutter/bin:/usr/local/nvm/versions/node/v22.15.0/bin
```

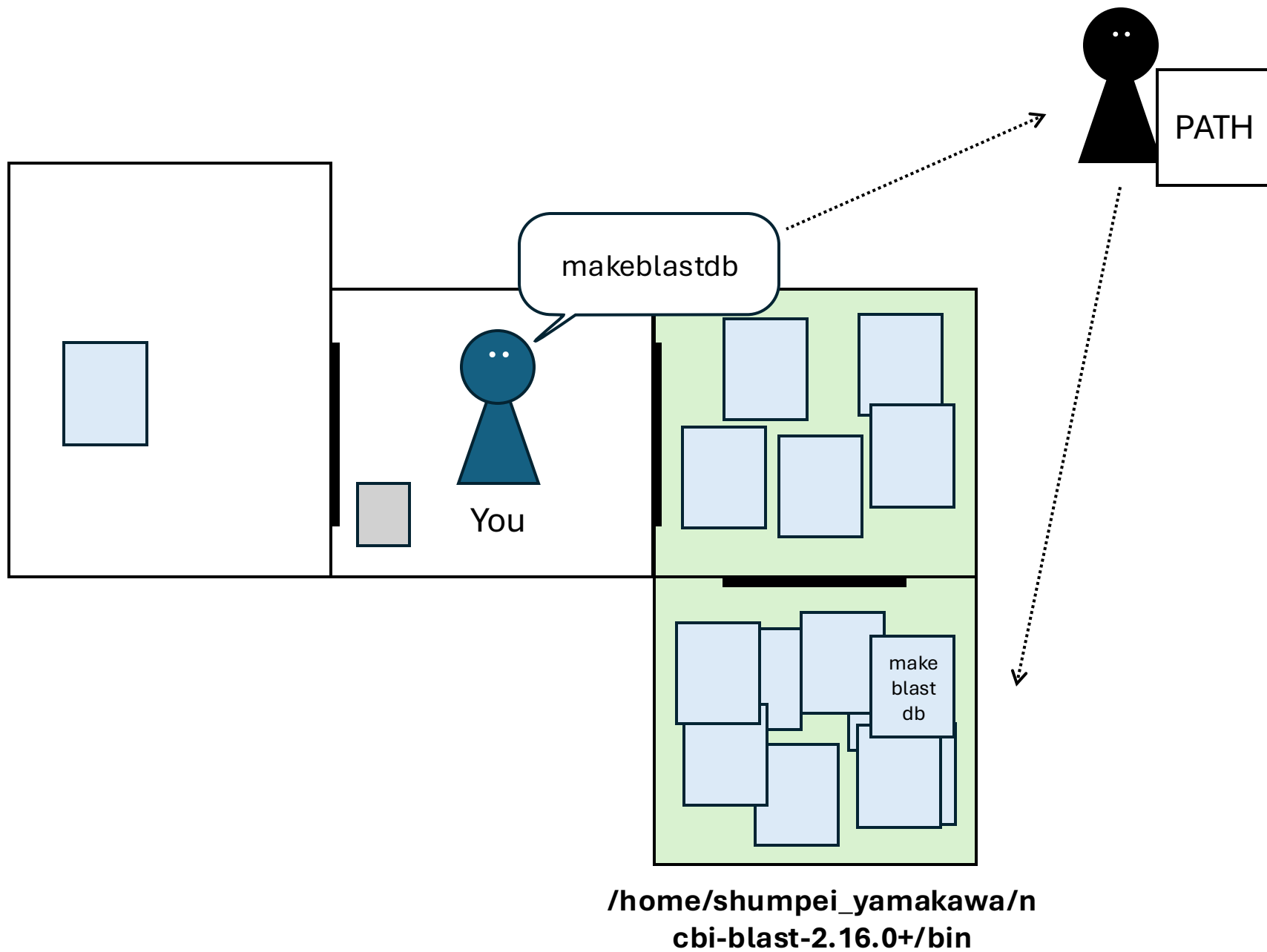
PATH: Search path for executable commands



/home/shumpei_yamakawa/ncbi-blast-2.16.0+/bin

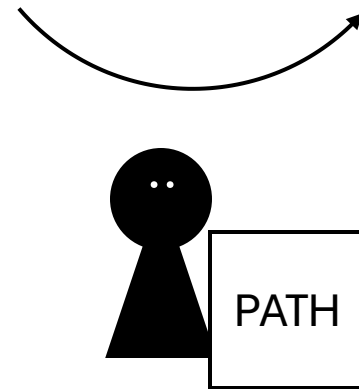
PATH: Search path for executable commands





```
export PATH="/home/shumpei_yamakawa/test/ncbi-blast-2.16.0+/bin:$PATH"
```

Add to PATH!



PC

PATH



```
/home/usr/directoryA:  
/home/usr/direcotryB:  
/home/usr/direcotryC:
```

Set the path



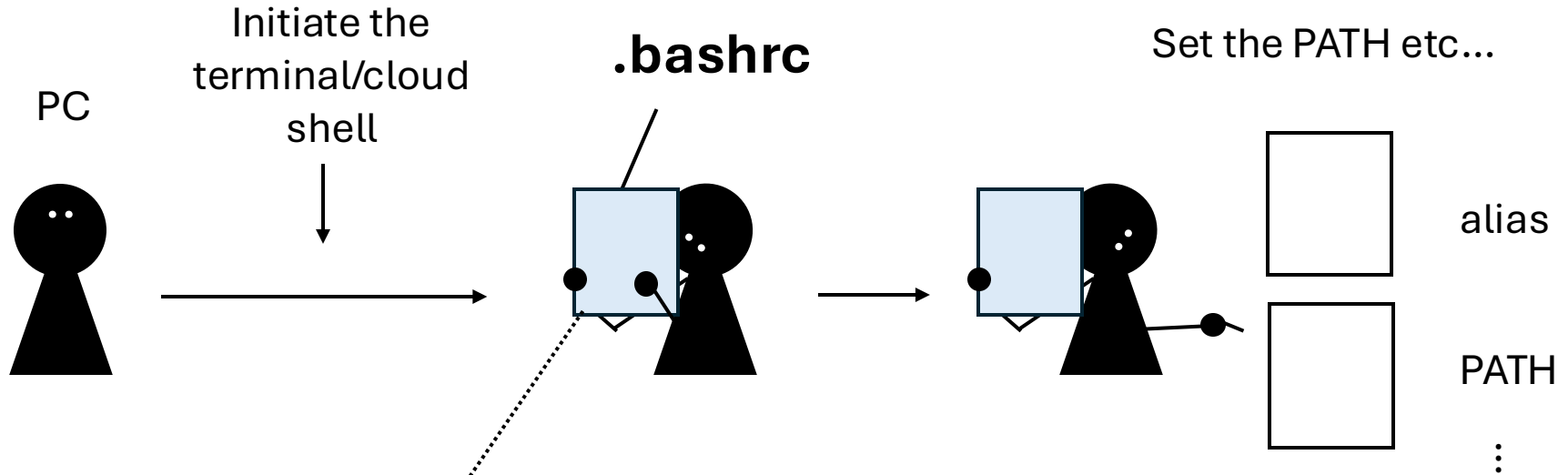
```
/home/usr/directoryA:  
/home/usr/direcotryB:  
/home/usr/direcotryC:  
  
/home/shumpei_yamaka  
wa/ncbi-blast-2.16.0+/bin
```

Terminate
the session



```
/home/usr/directoryA:  
/home/usr/direcotryB:  
/home/usr/direcotryC:
```

**PATH setting is
only temporal
in a session**



```
# ~/.bashrc: executed by bash(1) for non-login shells.
# see /usr/share/doc/bash/examples/startup-files (in the package bash-doc)
# for examples

# If not running interactively, don't do anything
case $- in
  *) ;;
  *) return;;
esac

# don't put duplicate lines or lines starting with space in the history.
# See bash(1) for more options
HISTCONTROL=ignoreboth

# append to the history file, don't overwrite it
shopt -s histappend

# for setting history length see HISTSIZE and HISTFILESIZE in bash(1)
HISTSIZE=1000
HISTFILESIZE=2000

# check the window size after each command and, if necessary,
# update the values of LINES and COLUMNS.
shopt -s checkwinsize

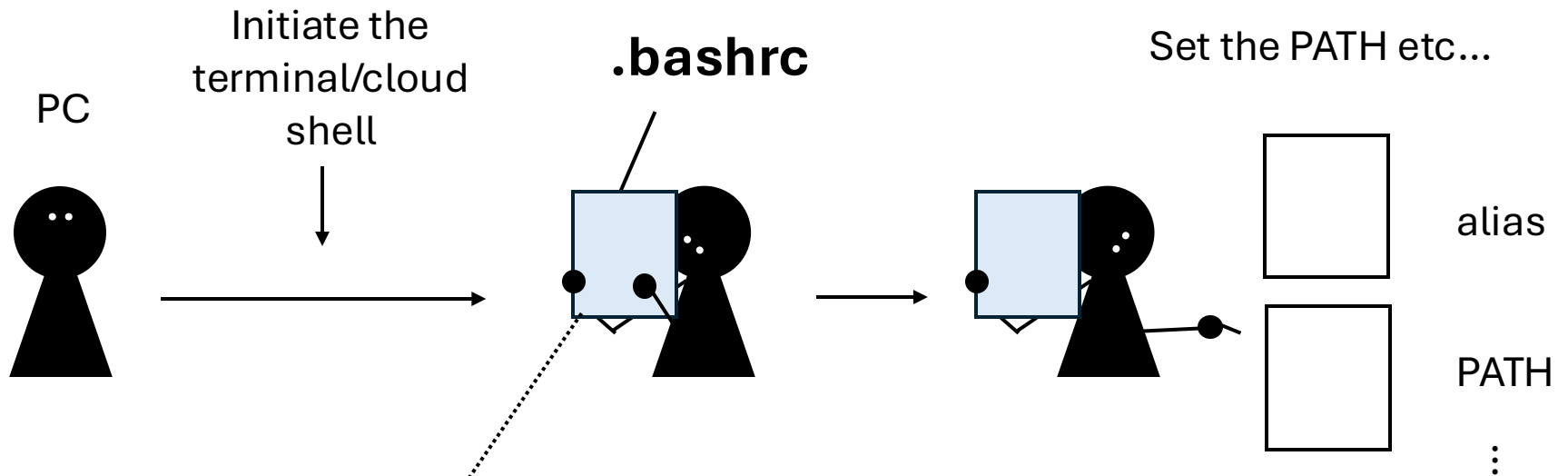
# If set, the pattern "*" used in a pathname expansion context will
# match all files and zero or more directories and subdirectories.
#shopt -s globstar

# make less more friendly for non-text input files, see lesspipe(1)
[ -x /usr/bin/lesspipe ] && eval "$(SHELL=/bin/sh lesspipe)"

# set variable identifying the chroot you work in (used in the prompt below)
if [ -z "${debian_chroot:-}" ] && [ -r /etc/debian_chroot ]; then
  debian_chroot=$(cat /etc/debian_chroot)
fi

# set a fancy prompt (non-color, unless we know we "want" color)
case "$TERM" in
  xterm-color|*-256color) color_prompt=yes;;
esac
```

.bashrc =
A file automatically executed whenever a
Bash shell session starts



```
# ~/.bashrc: executed by bash(1) for non-login shells.
# see /usr/share/doc/bash/examples/startup-files (in the package bash-doc)
# for examples

# If not running interactively, don't do anything
case $- in
  *i*) ;;
  *) return;;
esac

# don't put duplicate lines or lines starting with space in the history.
# See bash(1) for more options
HISTCONTROL=ignoreboth

# append to the history file, don't overwrite it
shopt -s histappend

# for setting history length see HISTSIZE and HISTFILESIZE in bash(1)
HISTSIZE=1000
HISTFILESIZE=2000

# check the window size after each command and, if necessary,
# update the values of LINES and COLUMNS.
shopt -s checkwinsize

# If set, the pattern "*" used in a pathname expansion context will
# match all files and zero or more directories and subdirectories.
#shopt -s globstar

# make less more friendly for non-text input files, see lesspipe(1)
[ -x /usr/bin/lesspipe ] && eval "$(SHELL=/bin/sh lesspipe)"

# set variable identifying the chroot you work in (used in the prompt below)
if [ -z "${debian_chroot:-}" ] && [ -r /etc/debian_chroot ]; then
  debian_chroot=$(cat /etc/debian_chroot)
fi

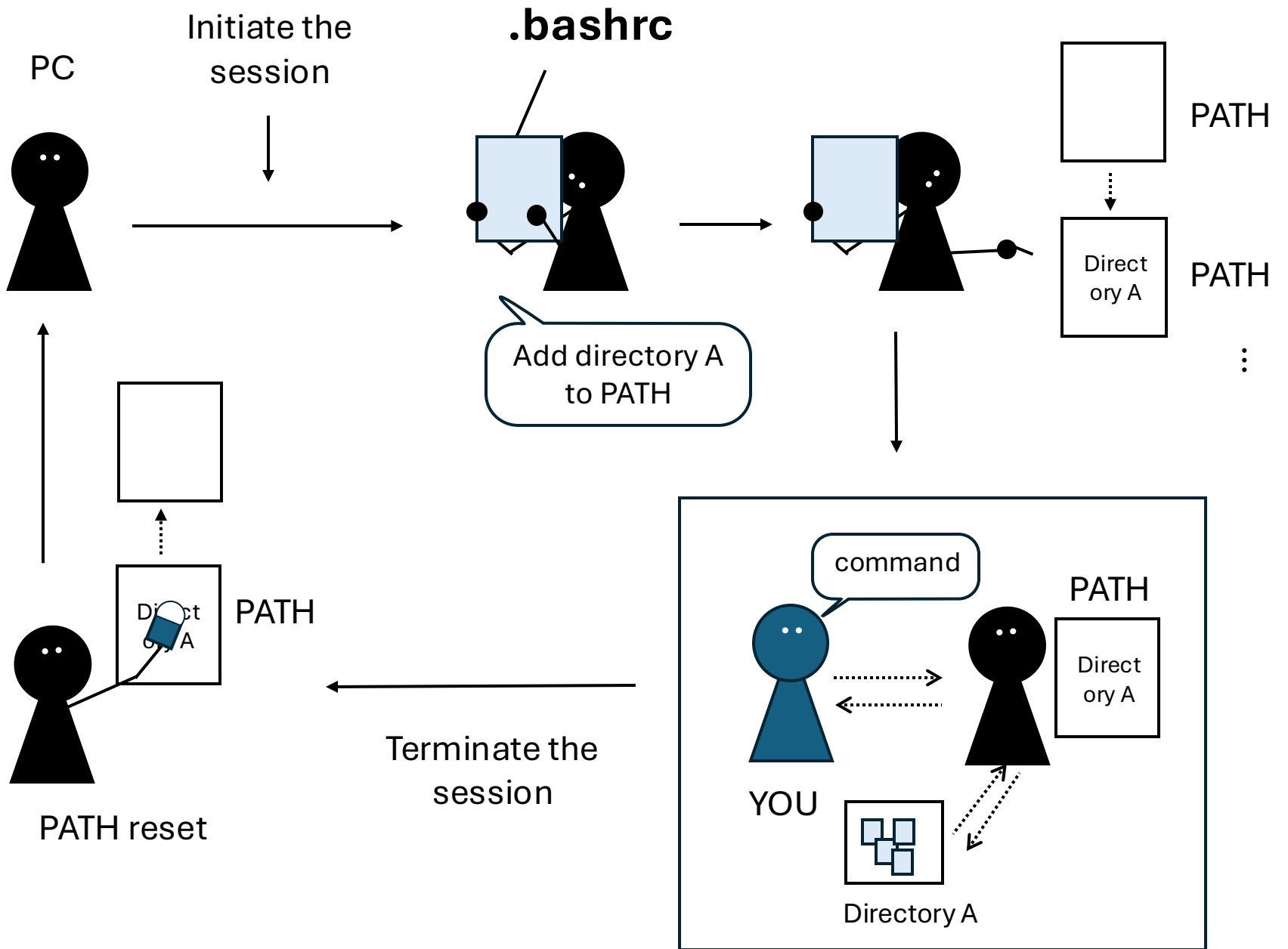
# set a fancy prompt (non-color, unless we know we "want" color)
case "$TERM" in
  xterm-color|*-256color) color_prompt=yes;;
esac
```

Add



export

PATH="/home/shumpei_yamakawa/test/
ncbi-blast-2.16.0+/bin:\$PATH"



```
# ~/.bashrc: executed by bash(1) for non-login shells.
# see /usr/share/doc/bash/examples/startup-files (in the package bash-doc)
# for examples

# If not running interactively, don't do anything
case $- in
    *i*) ;;
    *) return;;
esac

# don't put duplicate lines or lines starting with space in the history.
# See bash(1) for more options
HISTCONTROL=ignoreboth

# append to the history file, don't overwrite it
shopt -s histappend

# for setting history length see HISTSIZE and HISTFILESIZE in bash(1)
HISTSIZE=1000
HISTFILESIZE=2000

# check the window size after each command and, if necessary,
# update the values of LINES and COLUMNS.
shopt -s checkwinsize

# If set, the pattern "*" used in a pathname expansion context will
# match all files and zero or more directories and subdirectories.
#shopt -s globstar

# make less more friendly for non-text input files, see lesspipe(1)
[ -x /usr/bin/lesspipe ] && eval "$(SHELL=/bin/sh lesspipe)"

# set variable identifying the chroot you work in (used in the prompt below)
if [ -z "${debian_chroot:-}" ] && [ -r /etc/debian_chroot ]; then
    debian_chroot=$(cat /etc/debian_chroot)
fi

# set a fancy prompt (non-color, unless we know we "want" color)
case "$TERM" in
    xterm-color|*-256color) color_prompt=yes;;
esac
```

~/.bashrc

⋮

```
alias grep='grep --color=auto'
alias fgrep='fgrep --color=auto'
alias egrep='egrep --color=auto'
fi

# colored GCC warnings and errors
#export GCC_COLORS='error=01;31:warning=01;35:note=01;36:caret=01;32:locus=01'

# some more ls aliases
alias ll='ls -alF'
alias la='ls -A'
alias l='ls -CF'

# Add an "alert" alias for long running commands. Use like so:
#   sleep 10; alert
alias alert='notify-send --urgency=low -i "${[ $? = 0 ]} && echo terminal || echo $?"'

# Alias definitions.
# You may want to put all your additions into a separate file like
# ~/.bash_aliases, instead of adding them here directly.
# See /usr/share/doc/bash-doc/examples in the bash-doc package.

if [ -f ~/.bash_aliases ]; then
    . ~/.bash_aliases
fi

# enable programmable completion features (you don't need to enable
# this, if it's already enabled in /etc/bash.bashrc and /etc/profile
# sources /etc/bash.bashrc).
if ! shopt -oq posix; then
    if [ -f /usr/share/bash-completion/bash_completion ]; then
        . /usr/share/bash-completion/bash_completion
    elif [ -f /etc/bash_completion ]; then
        . /etc/bash_completion
    fi
fi

source /google/devshell/bashrc.google
export PATH="/home/shumpei.yamakawa/test/ncbi-blast-2.16.0+/bin:$PATH"
```