Part 1.2:
Installing Software and Package Managers

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Computer Programs

- Written in programming languages

- Are not always easily installed

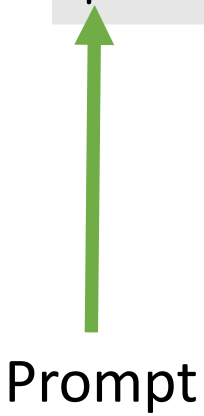
- Scientific programs usually come as source code
  - Contains general information to run on any computer
  - Needs to be compiled and installed

Why compile software?

- Customizes for you system
  - optimized for your computer/cluster
- Can change where things are installed
- Can have multiple versions of a program:
  - In case you are using older software

Important files before you get started

```
$ ls
```



Prompt

Important files before you get started

```
$ ls
```

Prompt

list what is in that folder

Important files before you get started

```
$ ls
README
INSTALL
```

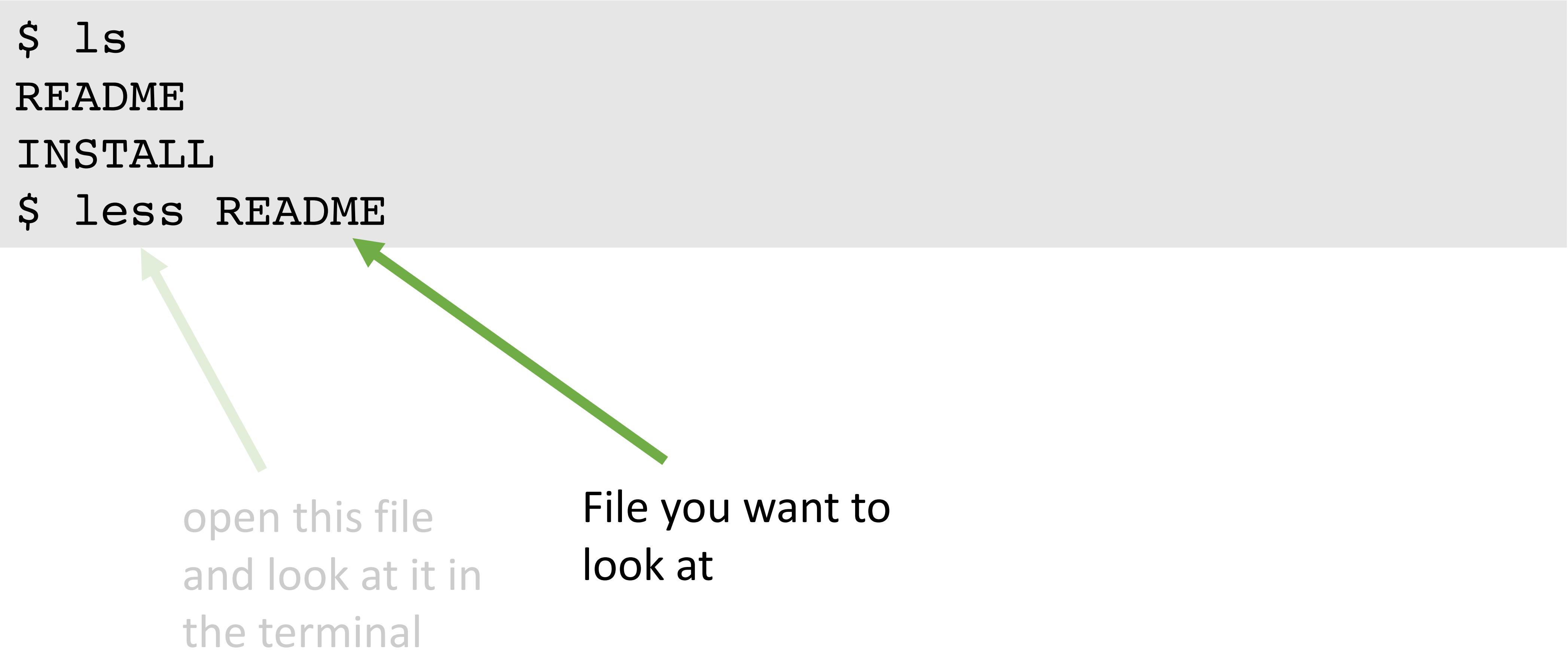
Files that contain information on installing the software

Important files before you get started

```
$ ls
README
INSTALL
$ less README
```

open this file
and look at it in
the terminal

Important files before you get started

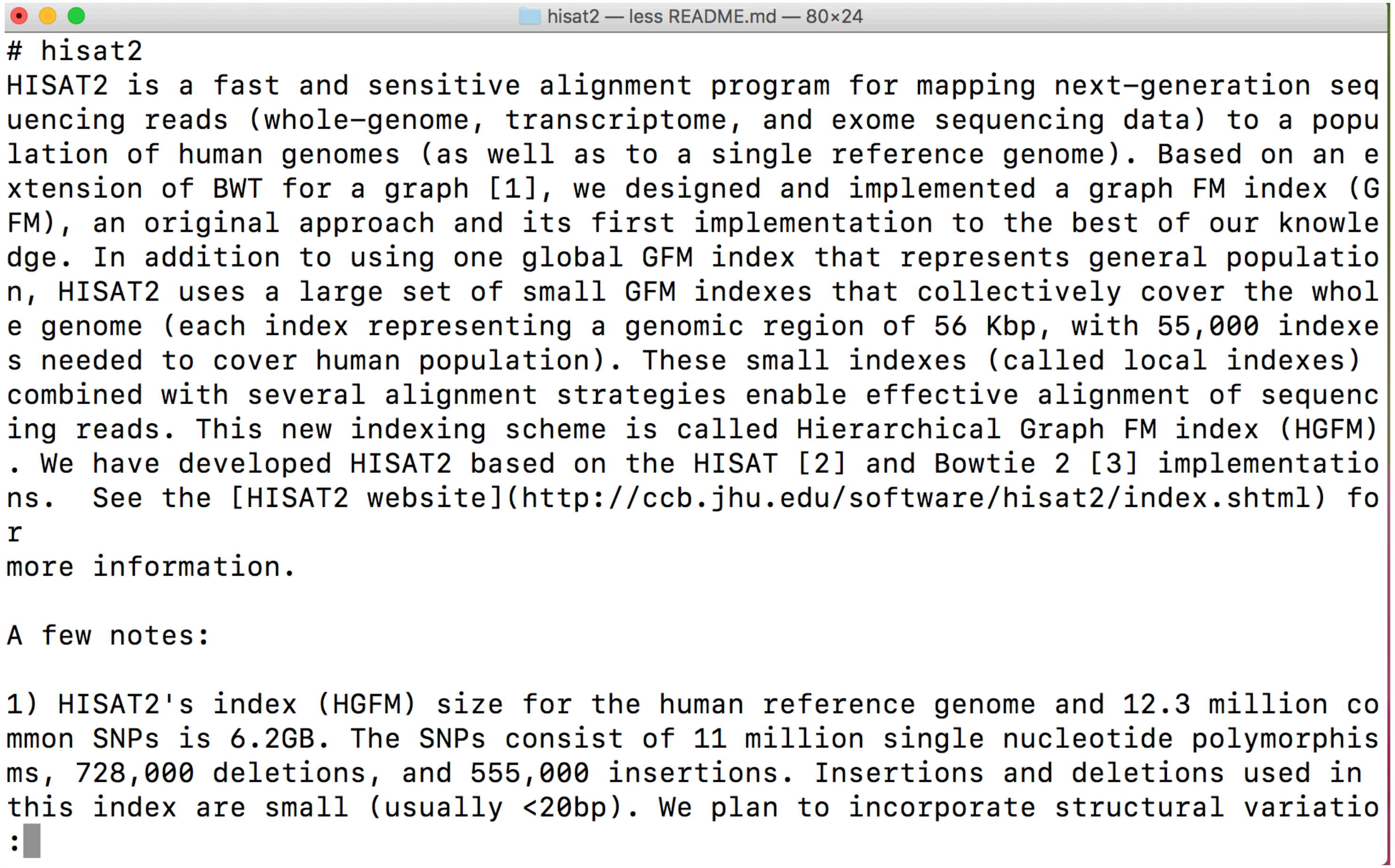


```
$ ls
README
INSTALL
$ less README
```

open this file and look at it in the terminal

File you want to look at

Important files before you get started



```
# hisat2
HISAT2 is a fast and sensitive alignment program for mapping next-generation seq
uencing reads (whole-genome, transcriptome, and exome sequencing data) to a popu
lation of human genomes (as well as to a single reference genome). Based on an e
xtension of BWT for a graph [1], we designed and implemented a graph FM index (G
FM), an original approach and its first implementation to the best of our knowle
dge. In addition to using one global GFM index that represents general populatio
n, HISAT2 uses a large set of small GFM indexes that collectively cover the whol
e genome (each index representing a genomic region of 56 Kbp, with 55,000 indexe
s needed to cover human population). These small indexes (called local indexes)
combined with several alignment strategies enable effective alignment of sequenc
ing reads. This new indexing scheme is called Hierarchical Graph FM index (HGFM)
. We have developed HISAT2 based on the HISAT [2] and Bowtie 2 [3] implementatio
ns.  See the [HISAT2 website](http://ccb.jhu.edu/software/hisat2/index.shtml) fo
r
more information.

A few notes:

1) HISAT2's index (HGFM) size for the human reference genome and 12.3 million co
mmon SNPs is 6.2GB. The SNPs consist of 11 million single nucleotide polymorphis
ms, 728,000 deletions, and 555,000 insertions. Insertions and deletions used in
this index are small (usually <20bp). We plan to incorporate structural variatio
:
```

Compiling and Installing from Source Code

- Once you look at README/INSTALL files

- You install software using three commands (usually):
  - configure
  - make
  - make install

Configure

- Configure sets up the program for your specific system

```
$ ./configure
```

Configure

- Configure sets up the program for your specific system

```
$ ./configure
```

Prompt

Configure

- Configure sets up the program for your specific system

```
$ ./configure
```

Prompt

Means do the command to a file in the folder I am currently in

Configure

- Configure sets up the program for your specific system

```
$ ./configure
```

Prompt

Means do the command to a file in the folder I am currently in

The actual command to configure, will look for a configure script

Configure

- Configure sets up the program for your specific system

```
$ ./configure
$ ls
```

list what is in
that folder

Configure

- Configure sets up the program for your specific system

```
$ ./configure
$ ls
Makefile
```

what is created from the the configure command

Configure

- Configure sets up the program for your specific system

```
$ ./configure
$ ls
Makefile
Makefile.in
```

Some programs
come with a
template file

Configure

- Configure sets up the program for your specific system

```
$ ./configure
$ ls
Makefile
Makefile.in
```

This file is customized to your system

Some programs come with a template file

Make

- Make will finish building the program from source code into a usable form

```
$ ./configure
$ ls
Makefile
```

Uses what is in this file

Make

- Make will finish building the program from source code into a usable form

```
$ ./configure
$ ls
Makefile
$ make
```

Builds the program

Make

- Make will finish building the program from source code into a usable form

```
$ ./configure
$ ls
Makefile
$ make
```

After this you get a useable program in the folder you are currently in

Make install

- Will copy the built program, and its libraries and documentation, to the correct locations (in your $PATH)

```
$ ./configure
$ ls
Makefile
$ make
$ make install
```

After should be able to use the program regardless of where you are in your folders

Not all programs need all three commands

- Commonly you need all three commands:
  - configure
  - make
  - make install
- Some programs come pre-configured:
  - only need to run make and make install
- Some programs you have to do the final install:
  - no make install
  - You have to move programs to your $PATH

What is a package manager?

- A collection of software tools that automates:
  - installing computer programs
  - upgrading computer programs
  - configuring computer programs
  - removing computer programs

- Examples:
  - Homebrew
  - Perlbrew
  - Macports

Using Package Managers

- Example using Homebrew

```
$ brew update
```

Prompt

Using Package Managers

- Example using Homebrew

```
$ brew update
```

Prompt

Telling the computer you want brew (the package manager) to do something

Using Package Managers

- Example using Homebrew

```
$ brew update
```

Prompt

Telling the computer you want brew (the package manager) to do something

Update brew itself to the newest version

Using Package Managers

- Example using Homebrew

```
$ brew update
$ brew upgrade
```

Upgrade any programs to the newest versions

Using Package Managers

- Example using Homebrew

```
$ brew update
$ brew upgrade
$ brew cleanup
```

Uninstall old versions of programs

Using Package Managers

- Example using Homebrew

```
$ brew update
$ brew upgrade
$ brew cleanup
$ brew install git
```

Telling brew you want to install a program and any dependencies

Using Package Managers

- Example using Homebrew

```
$ brew update
$ brew upgrade
$ brew cleanup
$ brew install git
```

Telling brew you want to install a program and any dependencies

Dependencies are any other scripts or programs that are required to run

Using Package Managers

- Example using Homebrew

```
$ brew update
$ brew upgrade
$ brew cleanup
$ brew install git
```

Telling brew you want to install a program and any dependencies

The program you want to install

Using Package Managers

- Example using pip3

```
$ brew install python3
```

installing python3 programming language

Using Package Managers

- Example using pip3

```
$ brew install python3
$ pip3 install biopython
```

package manager specifically for python packages

Using Package Managers

- Example using pip3

```
$ brew install python3
$ pip3 install biopython
```

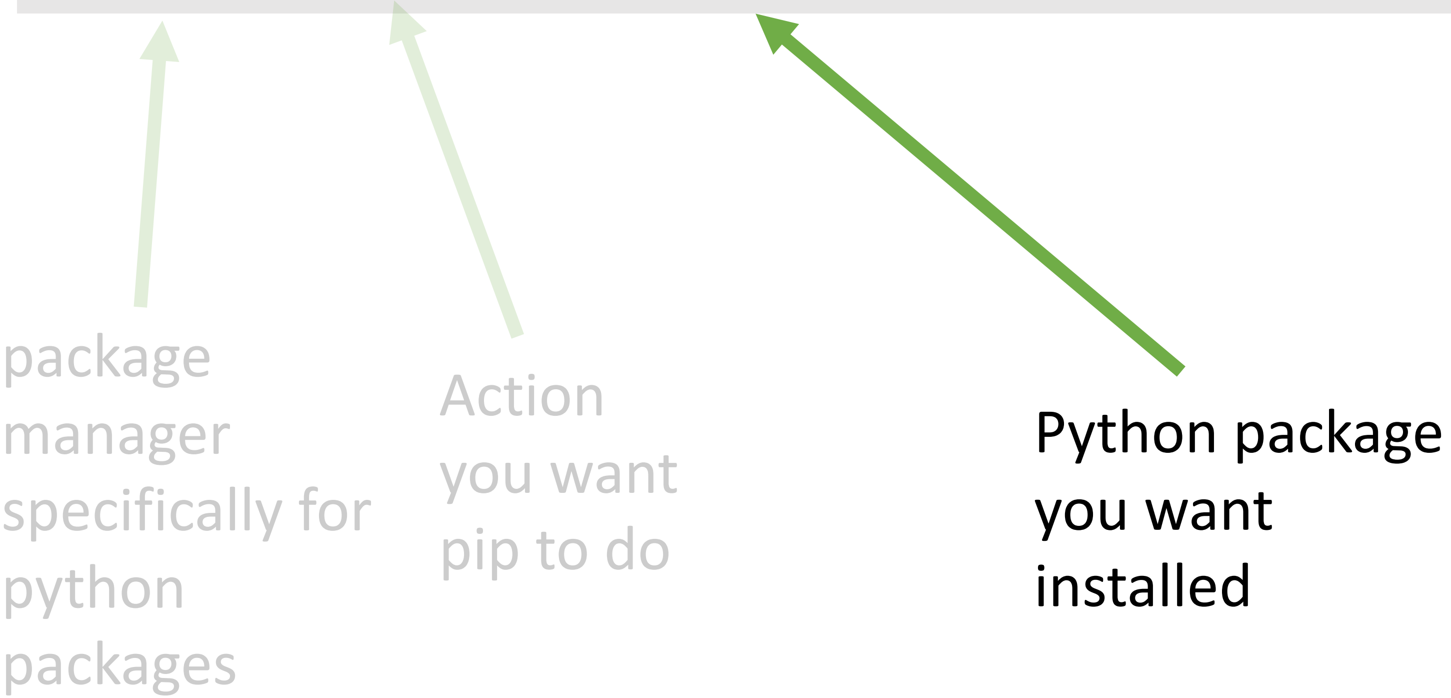
package manager specifically for python packages

Action you want pip to do

Using Package Managers

- Example using pip3

```
$ brew install python3
$ pip3 install biopython
```



package manager specifically for python packages

Action you want pip to do

Python package you want installed

Where are programs stored?

- Programs are usually stored within repositories:
  - cpan: programs written in the programming language perl
  - PyPI : programs written in the programming language python
  - github: generic repository for any program
  - CRAN: programs written in R scripting language

Github

- A web-based repository
- Used for development of programs with many collaborators
- Often has the newest versions of software

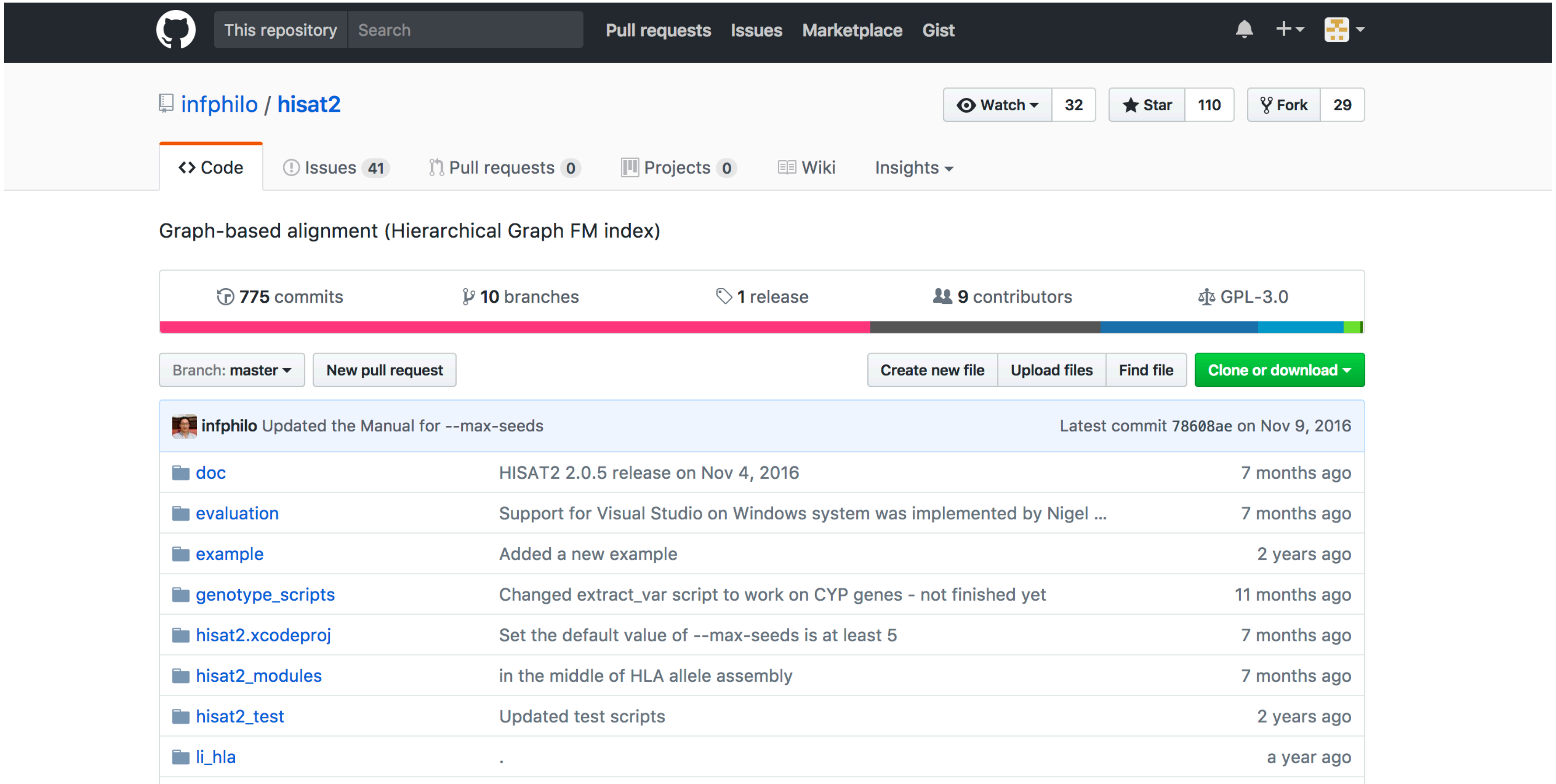
Getting files from git hub

- Requires the program git

```
$ brew install git
```

git can be installed through a package manager

Getting files from git hub



infphilo / hisat2

Graph-based alignment (Hierarchical Graph FM index)

775 commits | 10 branches | 1 release | 9 contributors | GPL-3.0

infphilo Updated the Manual for --max-seeds — Latest commit 78608ae on Nov 9, 2016

doc	HISAT2 2.0.5 release on Nov 4, 2016	7 months ago
evaluation	Support for Visual Studio on Windows system was implemented by Nigel ...	7 months ago
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genotype_scripts	Changed extract_var script to work on CYP genes - not finished yet	11 months ago
hisat2.xcodeproj	Set the default value of --max-seeds is at least 5	7 months ago
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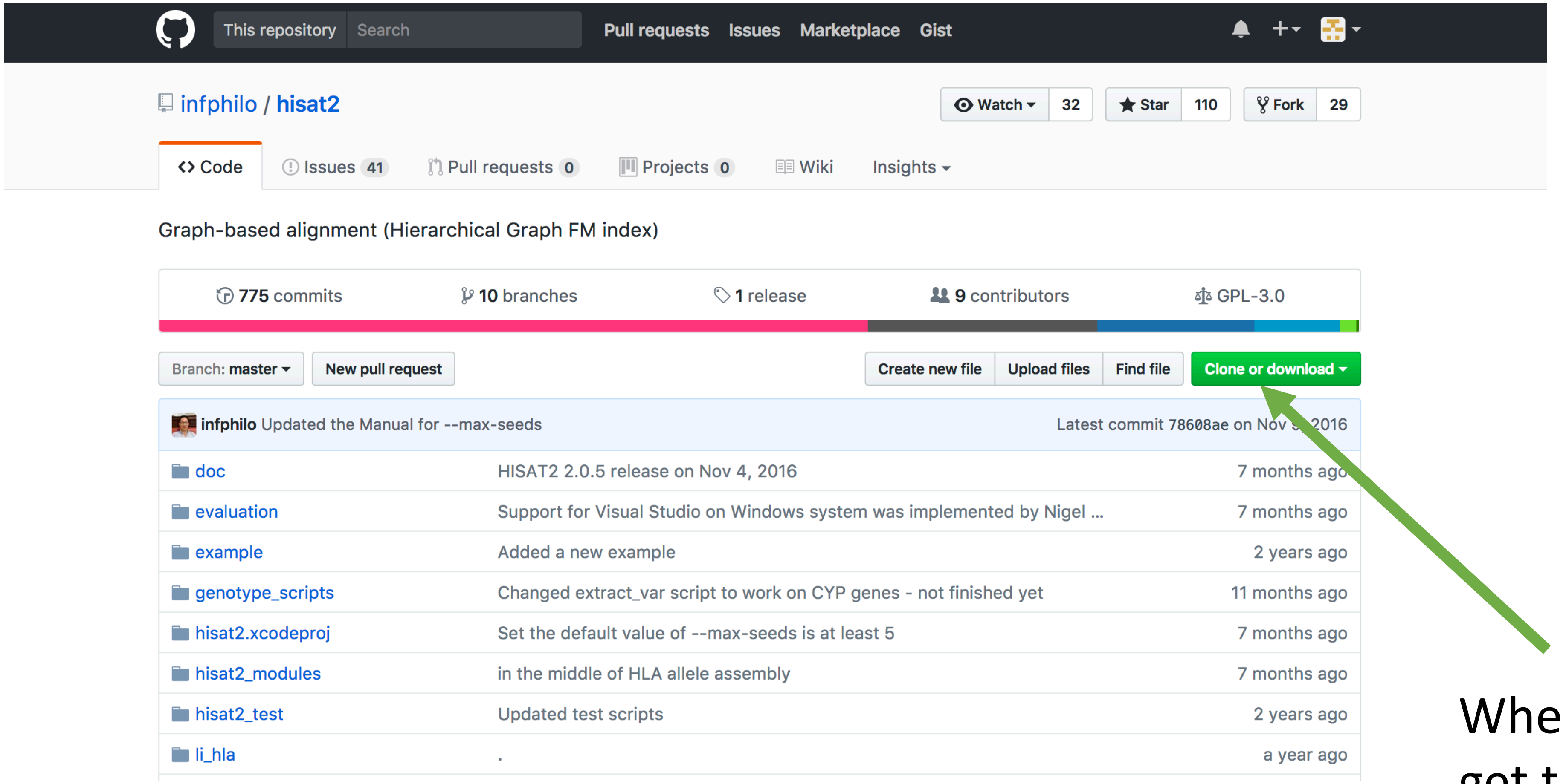
li_hla	.	a year ago

Getting files from git hub



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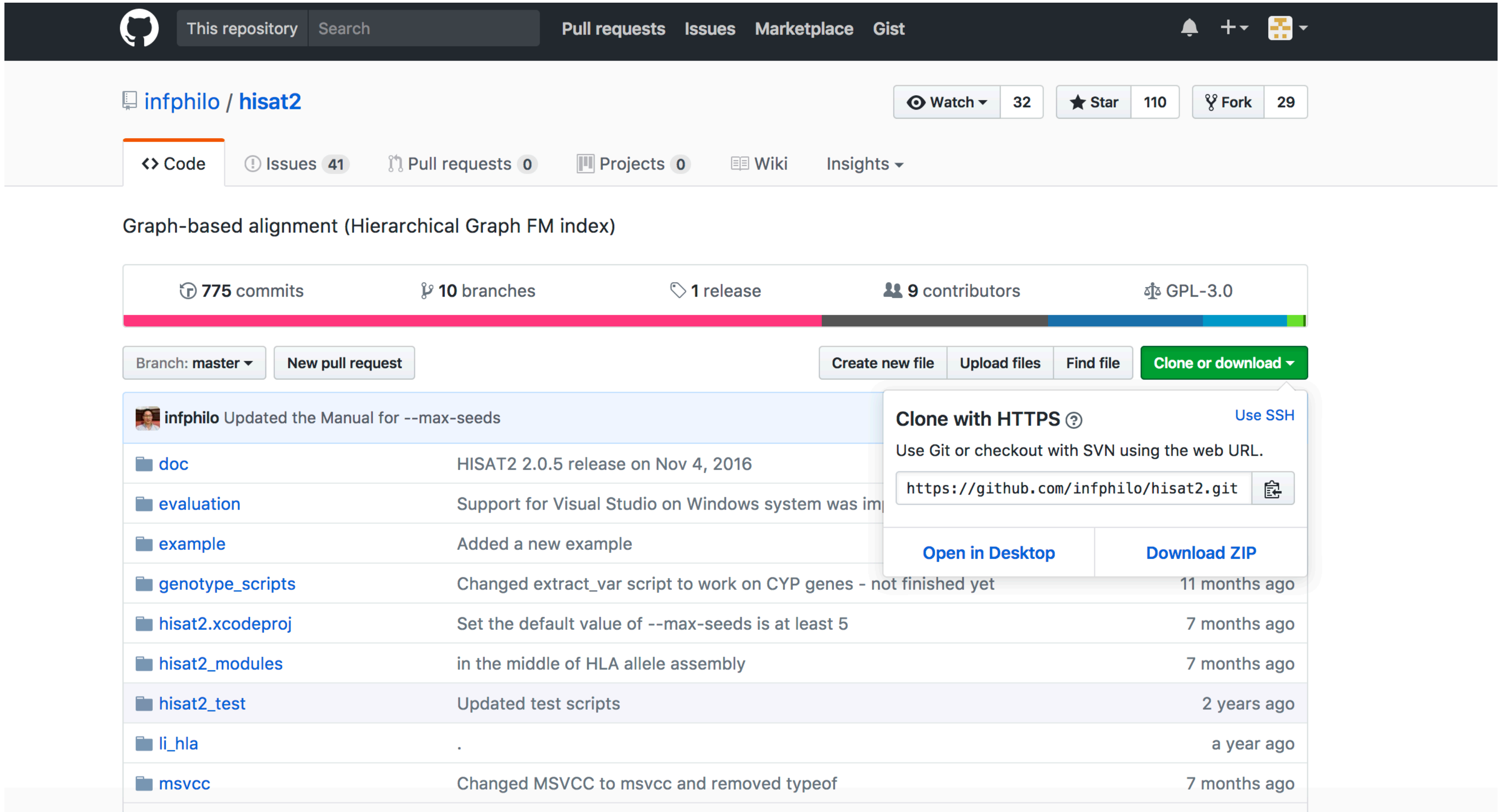
Where you can get the web address

Getting files from git hub



infphilo / hisat2

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Clone with HTTPS

Use Git or checkout with SVN using the web URL.

```
https://github.com/infphilo/hisat2.git
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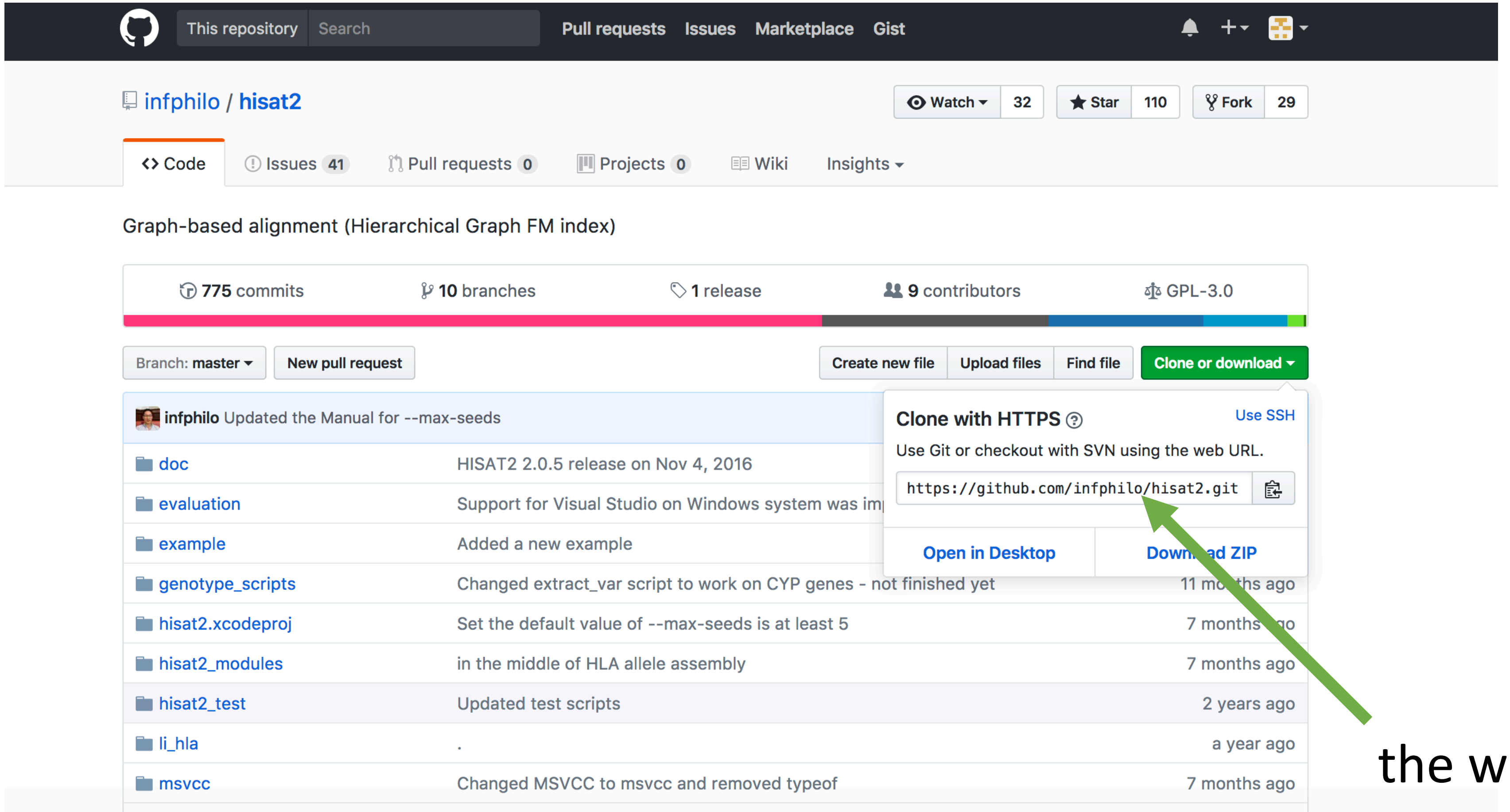

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the web address you need to copy

Getting files from git hub

- Clone repository

```
$ brew install git
$ git clone https://github.com/infphilo/hisat2.git
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Telling the computer you want to use the program git

Getting files from git hub

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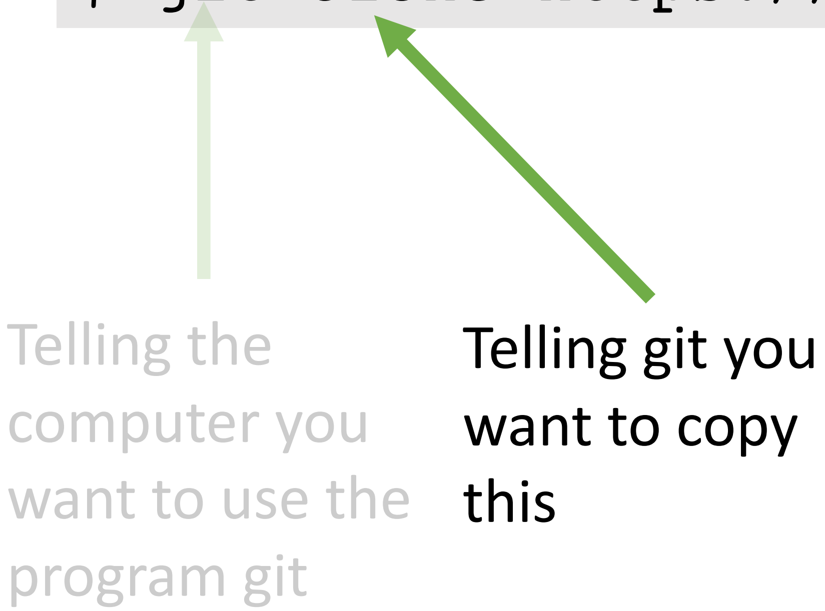

Telling the computer you want to use the program git

Telling git you want to copy this

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The web address of the program you want

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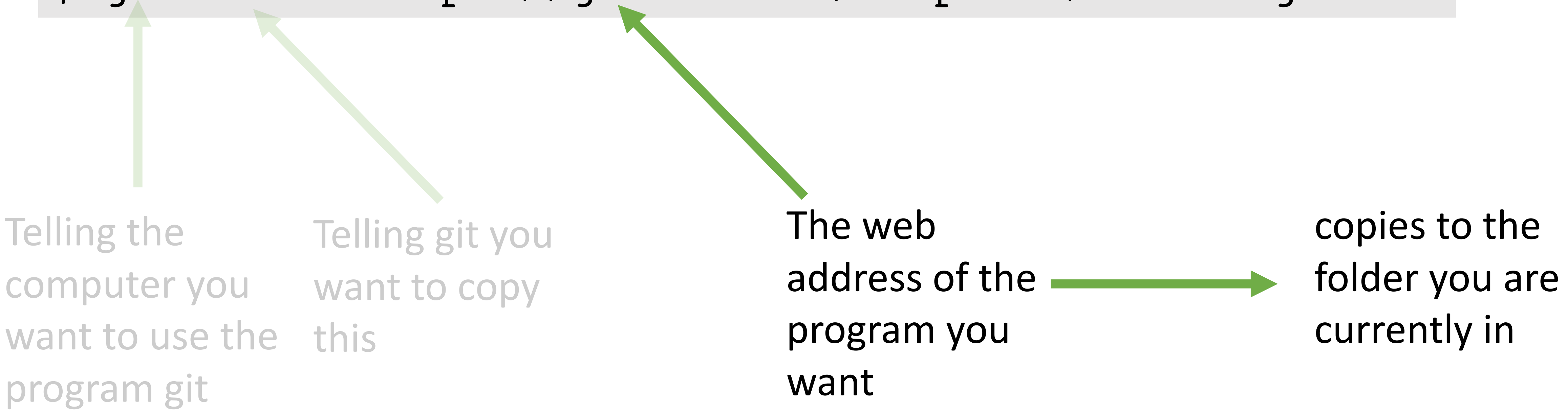

Telling the computer you want to use the program git

Telling git you want to copy this

The web address of the program you want

copies to the folder you are currently in

Getting files from git hub

- Clone repository

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$ brew install git
$ git clone https://github.com/infphilo/hisat2.git
$ ls
```

list what is in that folder

Getting files from git hub

- Clone repository

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$ brew install git
$ git clone https://github.com/infphilo/hisat2.git
$ ls
Applications   Documents Pictures
Bin            Downloads hisat2
```

What you just
copied from github