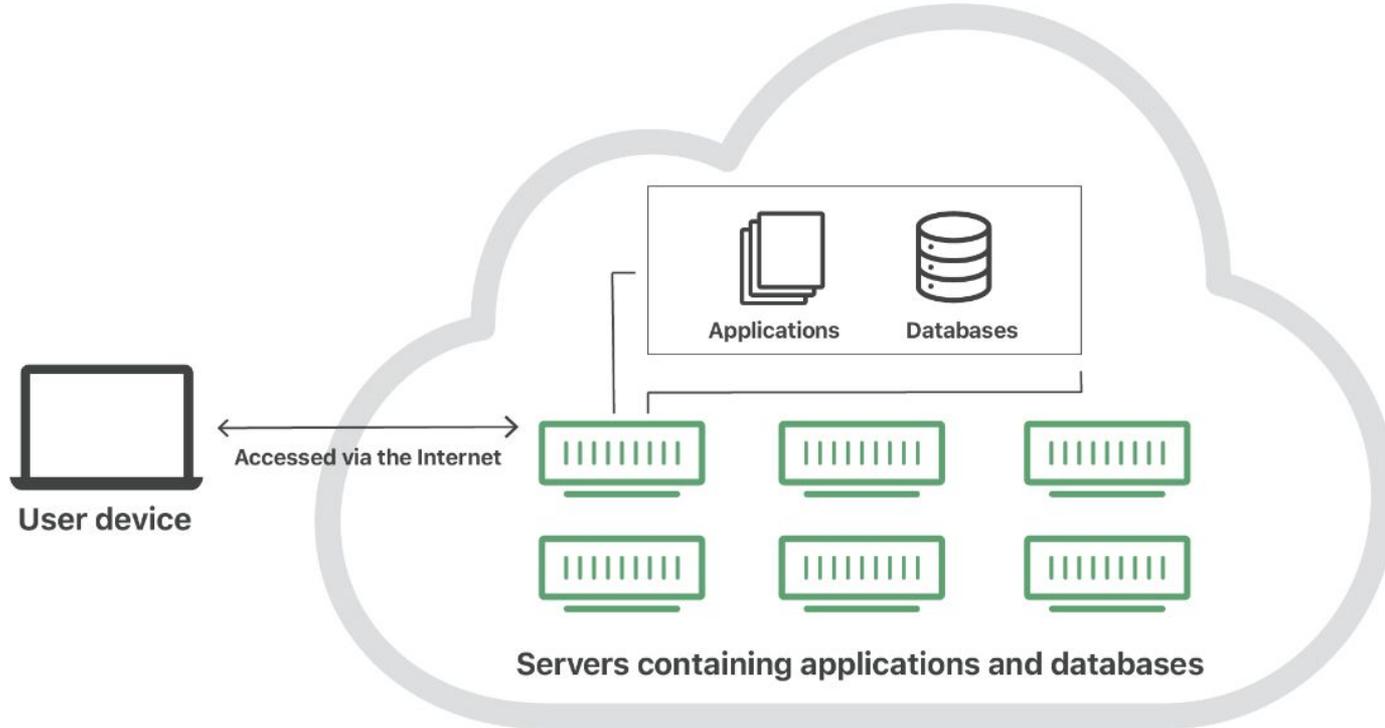


The Cloud, AWS & Guacamole!







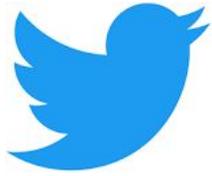






The cloud is everywhere in our lives

Social Media



Cloud Email Providers

Cloud Storage



Cloud Computing



Google Cloud Platform





Data centers

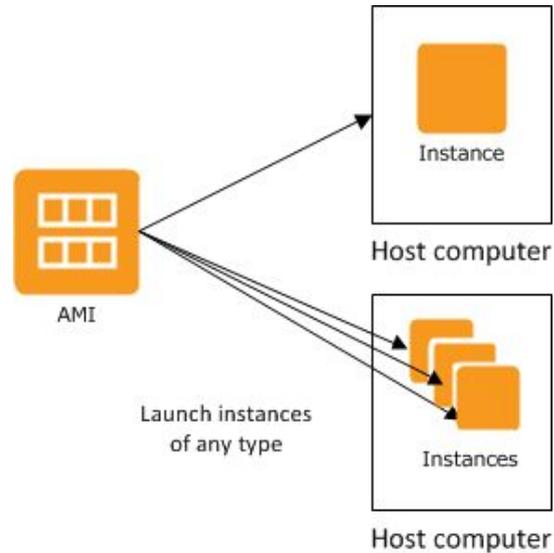


Data centers



How does it work?

AMI: Amazon Machine Image



Base computer with all data and software for the workshop

Terminology

- Creating an instance – buying a brand new computer with software already installed
- Starting an instance – turning that computer on
- Stopping an instance – turning that computer off
- Terminating an instance – setting that computer on fire and throwing it out of the window

Connecting to your Instance



Remote desktop
(Guacamole)



Secure Shell
(ssh)



R Studio
Server



Jupyter
Notebook

Connecting to your Instance

<https://evomics.org/2024-workshop-on-genomics/>

EVOLUTION AND GENOMICS

Intensive and immersive training opportunities

WORKSHOPS

LEARNING

PEOPLE

APPLY

INFORMATION

Get ready for May 2023!

Many important details can be read on our [FAQ](#) page and our [Housing and Transportation](#) page

[Instance addresses](#) (check every day for your new one!)

Check [here](#) to view Faculty / Organiser / Instructor arrival and departure dates. Check out our Faculty for 2023 [here](#) and our Instructors for 2023 [here](#)

As is tradition, we will be having a [T-shirt competition!](#) Best T-shirt design will feature on the Workshop on Genomics 2023 T-shirts – get designing!

Workshop on Genomics 2023 [BINGO!](#)

Faculty lunches sign-up sheet

Our [Code of Conduct](#) contact points are Josie Paris & Joan Ferrer Obiol

Connecting to your instance

	A	B	C	D	E	F	G
1	Instance number	First Name	Last Name	Instance address	Guacamole connection	ssh connection	RStudio server connection
2	1	Joan	Ferrer Obiol	3.238.107.169	3.238.107.169:8080/guacamole	ssh genomics@3.238.107.169	3.238.107.169:8787

Find your name and check your instance address

Check how to connect to your instance using
guacamole, ssh and the RStudio server

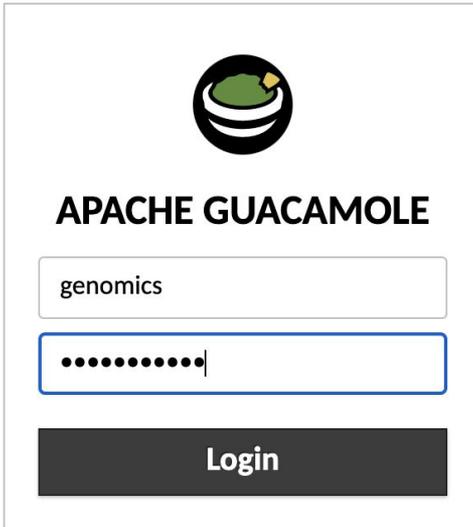
Connecting to guacamole

1. Open your preferred internet browser (i.e. chrome, firefox)
2. Paste your instance address followed by :8080/guacamole



Connecting to guacamole

3. Enter the username "genomics" and password



The image shows a login form for Apache Guacamole. At the top center is the Apache Guacamole logo, which consists of a black circle containing a green bowl with a yellow spoon. Below the logo, the text "APACHE GUACAMOLE" is displayed in a bold, black, sans-serif font. Underneath the text are two input fields: the first is a text box containing the username "genomics", and the second is a password box with ten black dots and a vertical cursor on the right. At the bottom of the form is a dark gray rectangular button with the word "Login" written in white, centered text.

Connecting to guacamole desktop

4. Select Desktop

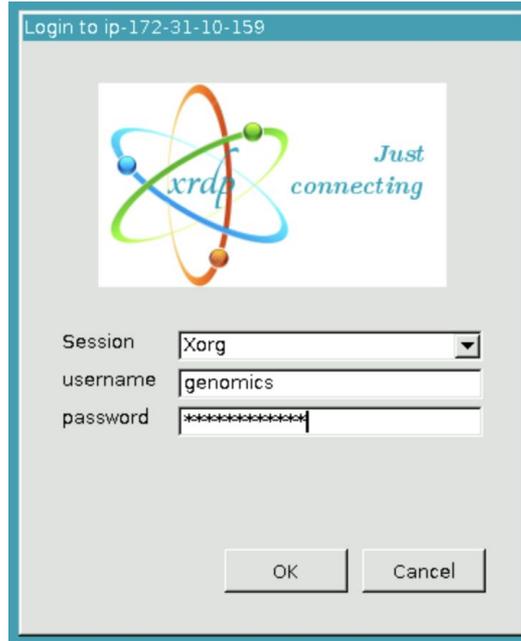
ALL CONNECTIONS

 Desktop

 Terminal

Connecting to guacamole desktop

5. Enter the username "genomics" and password again



The image shows a login dialog box titled "Login to ip-172-31-10-159". The dialog features a logo with the text "xrdp" and "Just connecting" next to a stylized atomic symbol. Below the logo, there are three input fields: "Session" with a dropdown menu showing "Xorg", "username" with the text "genomics", and "password" with masked characters. At the bottom, there are "OK" and "Cancel" buttons.

Login to ip-172-31-10-159

xrdp Just connecting

Session Xorg

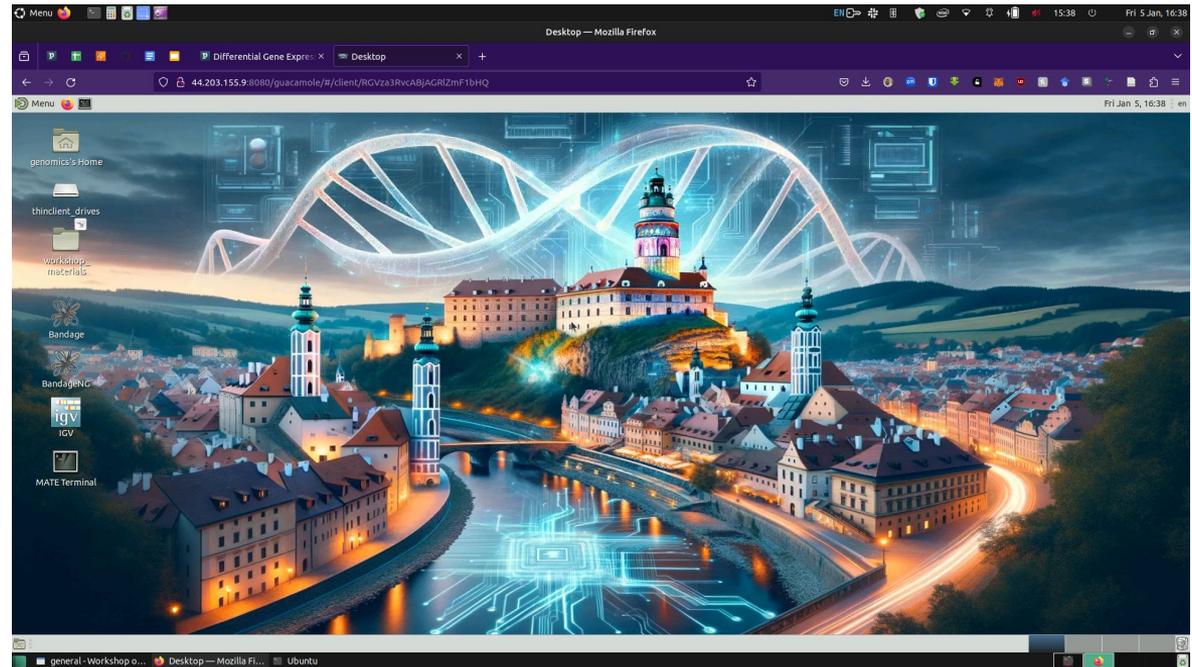
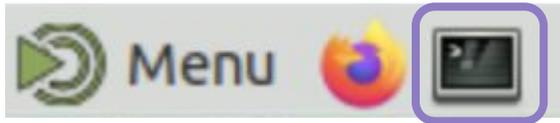
username genomics

password *****

OK Cancel

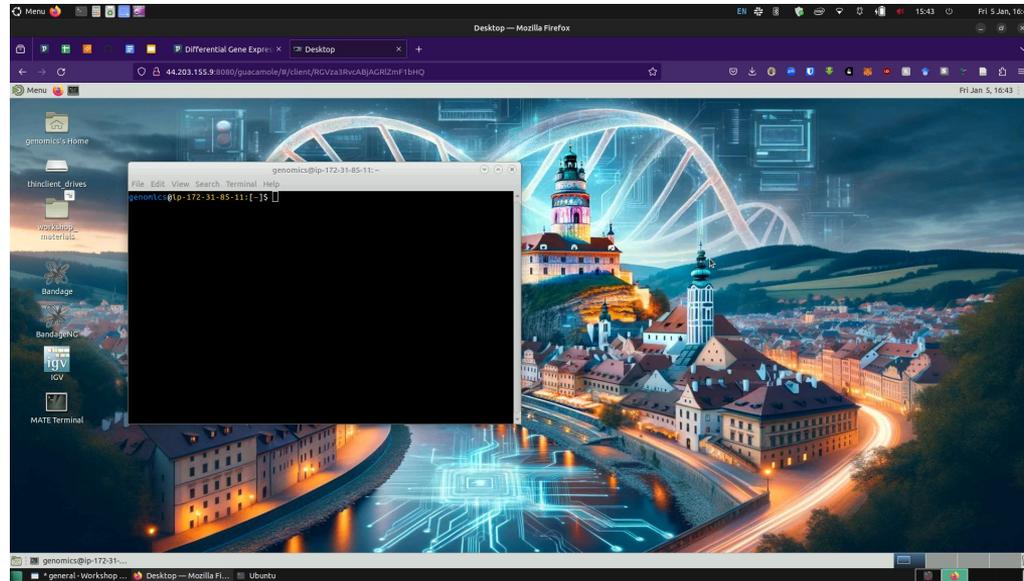
Connecting to guacamole desktop

6. Open a terminal window using the terminal icon



Connecting to guacamole desktop

You are now ready to learn some UNIX!



It's about as powerful as a laptop

Connecting to guacamole terminal

When connecting to guacamole, select Terminal

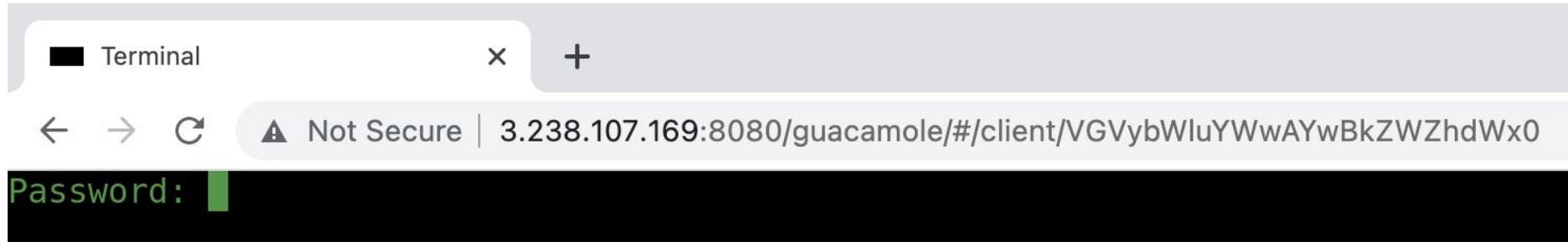
ALL CONNECTIONS

 Desktop

 Terminal

Connecting to guacamole terminal

Enter the password



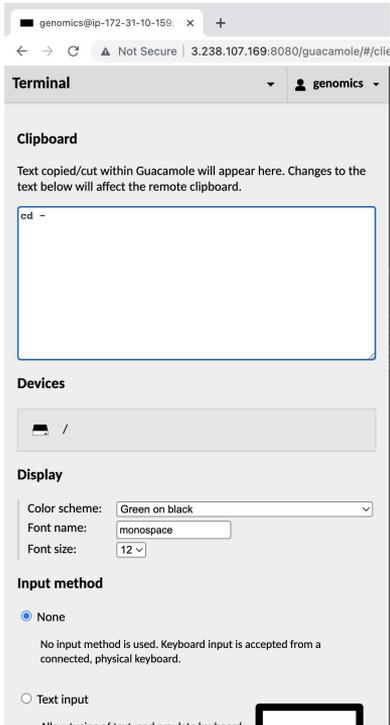
Connecting to guacamole terminal

And you are ready to use the terminal

```
#####  
##          Workshop on Genomics 2023          ##  
##          🌴 🍹 Spring Edition 🍹 🌴          ##  
##          Cesky Krumlov                        ##  
##          @evomics #evomics2023              ##  
#####  
  
Welcome to Ubuntu 22.04.2 LTS (5.19.0-1024-aws).  
  
System information as of Sun May 14 15:35:05 CEST 2023  
  
System load:  0.8310546875      Processes:           222  
Usage of /:   58.1% of 484.63GB  Users logged in:    1  
Memory usage: 29%              IPv4 address for docker0: 172.17.0.1  
Swap usage:   0%               IPv4 address for ens5:   172.31.10.159  
Last login:  Sun May 14 15:33:30 2023 from 194.228.207.170  
genomics@ip-172-31-10-159: [~]$
```

Copying and Pasting

Try to avoid copying and pasting wherever possible



But if you need it:

1. Press Ctrl+Alt+Shift (Mac: Ctrl+Opt+Shift)
2. Paste the text in the pop-up box
3. Press Ctrl+Alt+Shift (Mac: Ctrl+Opt+Shift) again
4. Paste into the instance using right click

Connecting through SSH

1. Open your preferred terminal on your laptop
2. Type `ssh genomics@[instance address]`

```
[apples-MacBook-Pro.local@apple[~]$ ssh genomics@3.238.107.169  
genomics@3.238.107.169's password: 
```

3. Enter the password

Connecting through SSH

And you are ready to use the terminal

```
#####
##          Workshop on Genomics 2023          ##
##      🌴🍹🍷 Spring Edition 🍷🍹🌴          ##
##          Cesky Krumlov                      ##
##          @evomics #evomics2023            ##
#####

Welcome to Ubuntu 22.04.2 LTS (5.19.0-1024-aws).

System information as of Sun May 14 15:33:29 CEST 2023

System load:  0.85107421875      Processes:           220
Usage of /:   58.1% of 484.63GB  Users logged in:    0
Memory usage: 29%                IPv4 address for docker0: 172.17.0.1
Swap usage:   0%                 IPv4 address for ens5:  172.31.10.159
Last login:   Sun May 14 11:08:55 2023 from 194.228.207.170
genomics@ip-172-31-10-159: [~]$
```

Connecting to the RStudio server

1. Open your preferred internet browser (i.e. chrome, firefox)
2. Paste your instance address followed by :8787

Connecting to the RStudio server

3. Enter the username "genomics" and password

RStudio Sign In x +

← → ↻ Not Secure | 3.238.107.169:8787/auth-sign-in?appUri=%2F

RStudio Server

Sign in to RStudio

Username:

Password:

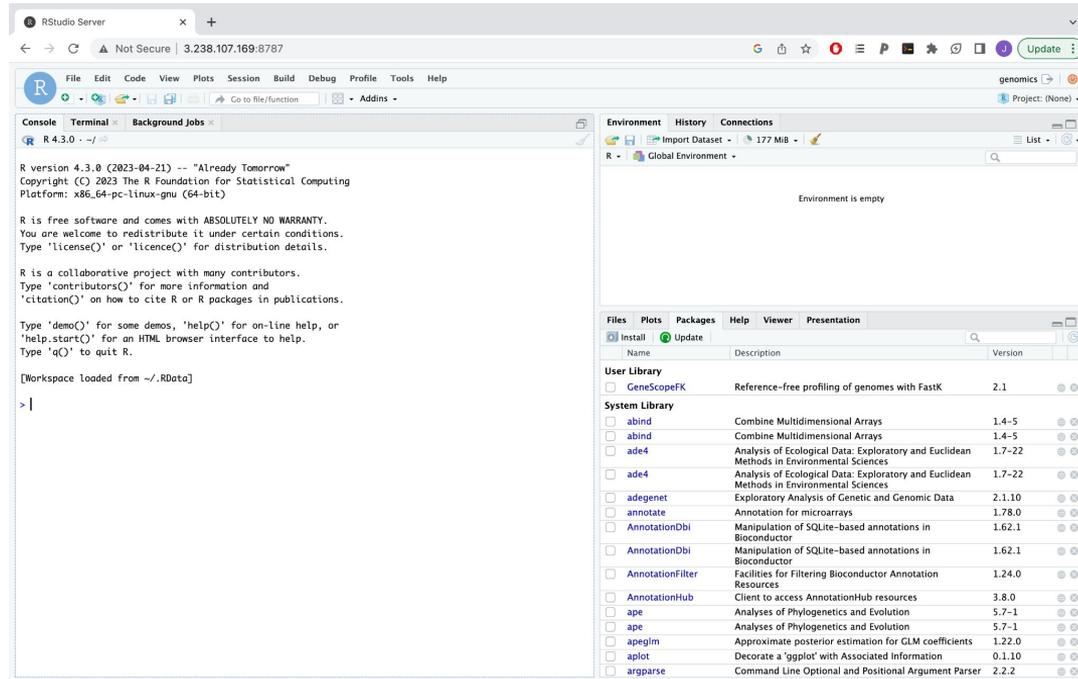
Stay signed in when browser closes

You will automatically be signed out after 60 minutes of inactivity.

Sign in

Connecting to the RStudio server

4. You are now connected to R Studio in your instance



The screenshot displays the RStudio Server interface in a web browser. The browser address bar shows the URL `3.238.107.169:8787`. The RStudio interface includes a menu bar (File, Edit, Code, View, Plots, Session, Build, Debug, Profile, Tools, Help), a toolbar, and a main workspace area. The console window on the left shows the R version 4.3.0 (2023-04-21) and the R logo. The environment window on the right shows the Global Environment with an empty environment. The package list window on the bottom right shows the User Library and System Library, listing various R packages and their versions.

```
R 4.3.0 ->
R version 4.3.0 (2023-04-21) -- "Already Tomorrow"
Copyright (C) 2023 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

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.

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.

[Workspace loaded from ~/._RData]
> |
```

Name	Description	Version
<input type="checkbox"/> GeneScopeK	Reference-free profiling of genomes with FastK	2.1
<input type="checkbox"/> abind	Combine Multidimensional Arrays	1.4-5
<input type="checkbox"/> ade4	Analysis of Ecological Data: Exploratory and Euclidean Methods in Environmental Sciences	1.7-22
<input type="checkbox"/> ade4	Analysis of Ecological Data: Exploratory and Euclidean Methods in Environmental Sciences	1.7-22
<input type="checkbox"/> adegenet	Exploratory Analysis of Genetic and Genomic Data	2.1.10
<input type="checkbox"/> annotate	Annotation for microarrays	1.78.0
<input type="checkbox"/> AnnotationDbi	Manipulation of SQLite-based annotations in Bioconductor	1.62.1
<input type="checkbox"/> AnnotationDbi	Manipulation of SQLite-based annotations in Bioconductor	1.62.1
<input type="checkbox"/> AnnotationFilter	Facilities for Filtering Bioconductor Annotation Resources	1.24.0
<input type="checkbox"/> AnnotationHub	Client to access AnnotationHub resources	3.8.0
<input type="checkbox"/> ape	Analyses of Phylogenetics and Evolution	5.7-1
<input type="checkbox"/> ape	Analyses of Phylogenetics and Evolution	5.7-1
<input type="checkbox"/> apeglm	Approximate posterior estimation for GLM coefficients	1.22.0
<input type="checkbox"/> aplot	Decorate a 'ggplot' with Associated Information	0.1.10
<input type="checkbox"/> argparse	Command Line Optional and Positional Argument Parser	2.2.2

Before starting the UNIX session

The instance address will change every day after we stop and restart the instances.

Each morning, you will need to return to the “Instance address spreadsheet” on the webpage, retrieve your new address and login again using the type of connection you need

	A	B	C	D	E	F	G
	Instance number	First Name	Last Name	Instance address	Guacamole connection	ssh connection	RStudio server connection
1							
2	1	Joan	Ferrer Obiol	3.238.107.169	3.238.107.169:8080/guacamole	ssh genomics@3.238.107.169	3.238.107.169:8787

Before starting the UNIX session

Connect to your instance and open terminal



SSH to your instance



Terminal



Desktop



Terminal

Before starting the UNIX session

Make sure that you can type the following characters:

- tilde (~)
- backslash (\)
- pipe (|)
- carat (^)

If you can't type these characters, get our attention!

Before starting the UNIX session!



tilde

/'tɪldə, 'tɪldi/



Before starting the UNIX session!

backslash
"bakslaf/



Before starting the UNIX session!



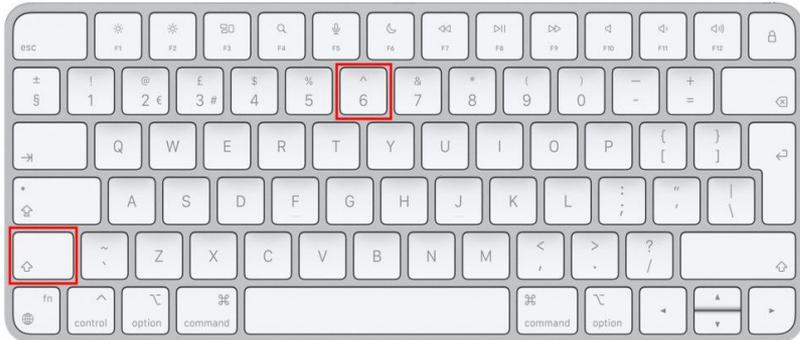
vertical bar
pipe

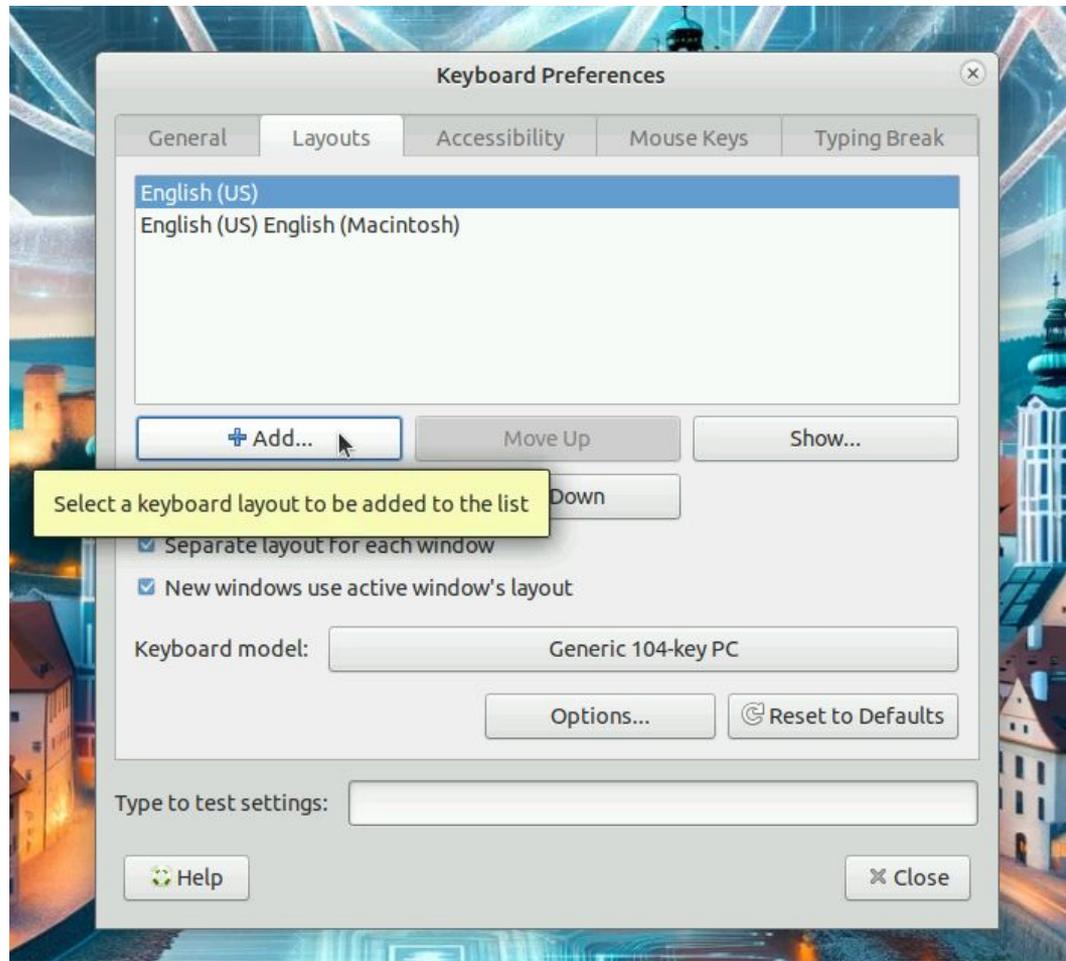
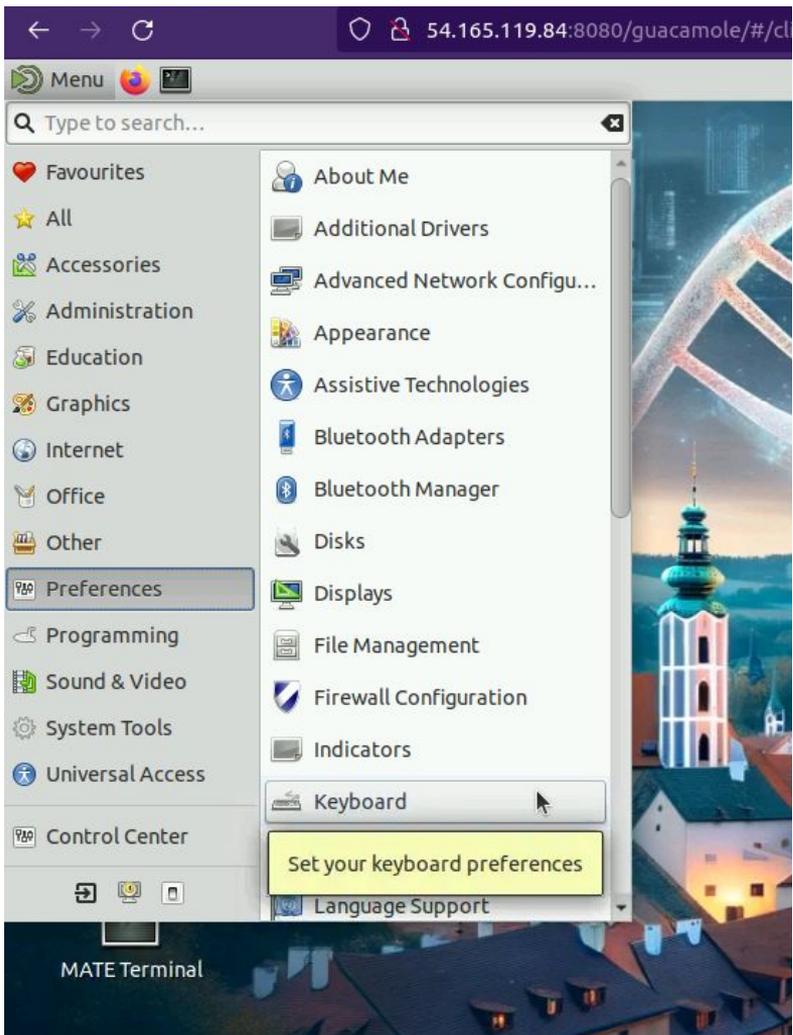


Before starting the UNIX session!



Caret
/kɛrət/





Choose a Layout

By country | **By language**

Country: **Czechia**

Variants: **Czech**

- Preview:
- Czech Czech (QWERTY)
 - Czech Czech (QWERTY, Macintosh)**
 - Czech Czech (QWERTY, extended backslash)
 - Czech Czech (UCW, only accented letters)
 - Czech Czech (US, Dvorak, UCW support)
 - Czech Czech (US, Dvorak, UCW support)
 - Czech Russian (Czech, phonetic)

The image shows a detailed keyboard layout for the Czech language. The main keyboard is a QWERTY layout with the following characters on the keys:

Esc	Q	W	E	R	T	Z	U	I	O	P	/	(BackSpace
	q	w	e	r	t	z	u	i	o	p	/)	BackSpace
Caps Lock	A	S	D	F	G	H	J	K	L	"	!	Return	
	a	s	d	f	g	h	j	k	l	"	!	Return	
Shift	Y	X	C	V	B	N	M	?	:	-	Shift		
	y	x	c	v	b	n	m	?	:	-	Shift		
Control	Super	Meta						ISO_Level...	Super	Menu	Control		

Function keys and other controls are also visible:

- Row 2: F5-F8, F9-F12, Sys Rq (Print), Scroll Lock, Pause
- Row 3: Num Lock, Caps Lock, Scroll Lock
- Row 4: Insert, Home, Page Up, Num Lock, /, *, -, Home, Up, Pg Up, +
- Row 5: Delete, End, Page Down, 7, 8, 9, 4, 5, 6, Left, Begin, Right, +
- Row 6: Up, 1, 2, 3, End, Down, Pg Dn, Enter
- Row 7: Left, Down, Right, 0, ., Del, Enter

Print

Cancel

+ Add

Installation and Software Managers



CONDA

