

Python PROGRAMMING

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Creiamo il nostro profilo su Ubuntu

questo è un commento!

lanciamo il terminale per aggiungere un nuovo profilo

ctrl+alt+t

\$ **sudo adduser nome_battesimo -uid 663**

\$ pw di labx

per eliminare un profilo utente (in caso di errore)

\$ **sudo deluser --remove-home nome_utente**

\$ pw di labx

per recuperare la passwd dimenticata

sostituire <user name> con il proprio nome utente

\$ **sudo passwd user name**

\$ pw di labx

\$ nuova pw

Creiamo il nostro profilo su Ubuntu

acquisiamo i privilegi dell'amministratore di sistema modificando il file di configurazione del Sistema Operativo (SO) /etc/sudoers

\$ **sudo visudo**

questo comando lancia l'editor di testo **nano** per creare ed aprire il file /etc/sudoers.tmp in modalità scrittura (per poterlo modificare); tale file è una copia di backup di /etc/sudoers

GNU nano 7.2 /etc/sudoers.tmp

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```
# This file MUST be edited with the 'visudo' command as root.
#
# Please consider adding local content in /etc/sudoers.d/ instead of
# directly modifying this file.
#
# See the man page for details on how to write a sudoers file.
#
Defaults        env_reset
Defaults        mail_badpass
Defaults        secure_path="/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/snap/bin"

# This fixes CVE-2005-4890 and possibly breaks some versions of kdesu
# (#1011624, https://bugs.kde.org/show_bug.cgi?id=452532)
Defaults        use_pty

# This preserves proxy settings from user environments of root
# equivalent users (group sudo)
#Defaults:%sudo env_keep += "http_proxy https_proxy ftp_proxy all_proxy no_proxy"

# This allows running arbitrary commands, but so does ALL, and it means
# different sudoers have their choice of editor respected.
#Defaults:%sudo env_keep += "EDITOR"

# Completely harmless preservation of a user preference.
#Defaults:%sudo env_keep += "GREP_COLOR"

# While you shouldn't normally run git as root, you need to with etckeeper
#Defaults:%sudo env_keep += "GIT_AUTHOR_* GIT_COMMITTER_"

# Per-user preferences; root won't have sensible values for them.
#Defaults:%sudo env_keep += "EMAIL DEBEMAIL DEBFULLNAME"

# "sudo scp" or "sudo rsync" should be able to use your SSH agent.
#Defaults:%sudo env_keep += "SSH_AGENT_PID SSH_AUTH_SOCK"

# Ditto for GPG agent
#Defaults:%sudo env_keep += "GPG_AGENT_INFO"

# Host alias specification

# User alias specification
```

Creiamo il nostro profilo su Ubuntu

GNU nano 7.2 /etc/sudoers.tmp

```

# This file specifies the proxy settings that is set in environment variables for the
# equivalent users (group sudo)
Defaults:%sudo env_keep += "http_proxy https_proxy ftp_proxy all_proxy no_proxy"

# This allows running arbitrary commands, but so does ALL, and it means
# different sudoers have their choice of editor respected.
Defaults:%sudo env_keep += "EDITOR"

# Completely harmless preservation of a user preference.
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# While you shouldn't normally run git as root, you need to with etckeeper
Defaults:%sudo env_keep += "GIT_AUTHOR_* GIT_COMMITTER_"

# Per-user preferences; root won't have sensible values for them.
Defaults:%sudo env_keep += "EMAIL DEBEMAIL DEBFULLNAME"

# "sudo scp" or "sudo rsync" should be able to use your SSH agent.
Defaults:%sudo env_keep += "SSH_AGENT_PID SSH_AUTH_SOCK"

# Ditto for GPG agent
Defaults:%sudo env_keep += "GPG_AGENT_INFO"

# Host alias specification
# User alias specification
# Cmnd alias specification

# User privilege specification
root    ALL=(ALL:ALL) ALL
piero   ALL=(ALL:ALL) ALL

# Members of the admin group may gain root privileges
%admin  ALL=(ALL) ALL

# Allow members of group sudo to execute any command
%sudo   ALL=(ALL:ALL) ALL

# See sudoers(5) for more information on "@include" directives:

@include /etc/sudoers.d

```

Elenco degli amministratori di sistema

portarsi con il cursore sull'ultima riga della lista

alt-6 # copia

ctrl-u # incolla l'intera riga

inserire il proprio nome utente

ctrl-o # per salvare

cancellare l'estensione .tmp

ctrl-x # per chiudere nano

alt-u # in caso di errore
(per annullare l'ultimo comando inserito)

Elenco degli amministratori di sistema

▲ Guida □ Salva □ Cerca □ Esegui □ Posizione □ Annnulla
■ Esci □ Inserisci □ Sostituisci □ Taolia □ Giustifica □ Vai a riga □ Ripeti □ Contrassegna □ Parentesi
■ Precedente □ Successiva □ Avanti

Per iniziare...

```
piero@piero-XPS-9320:~$ lsb_release -a
No LSB modules are available.
Distributor ID: Ubuntu
Description: Ubuntu 22.04.5 LTS
Release: 22.04
Codename: jammy
piero@piero-XPS-9320:~$
```

```
piero@piero-XPS-9320:~$ python3 --version
Python 3.10.12
piero@piero-XPS-9320:~$
```

Per iniziare...

```
piero@piero-XPS-9320:~$ python3
Python 3.10.12 (main, Nov  6 2024, 20:22:13) [GCC 11.4.0] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>> import dill, os, pickle
>>> import datetime
>>> now = datetime.datetime.now()
>>> now
datetime.datetime(2024, 12, 6, 9, 8, 20, 382891)
>>> day = datetime.datetime.now().strftime("%A")
>>> day
'Friday'
>>> current_time = now.strftime("%H:%M:%S")
>>> current_time
'09:08:20'
>>> user = os.getlogin()
>>> user
'piero'
>>>
```

Creare un archivio

```
piero@piero-XPS-9320:~$ tar -czvf AI.tar.gz COMPUTER_SCIENCE/AI
```

Scaricare un archivio da Github

A screenshot of a GitHub repository page for 'pierorivoira / COMPUTER-SCIENCE'. The page shows a file named 'AI.tar.gz' in the 'main' branch. The file size is 23.6 MB. A 'Download raw file' button is visible, and a red arrow points to the download icon in the toolbar below it. The GitHub interface includes a header with navigation icons, a search bar, and user profile picture. Below the header are tabs for Code, Issues, Pull requests, Actions, Projects, and Wiki. The main content area shows the file details, commit history, and a message indicating the file is too large to view.

https://github.com/pierorivoira/COMPUTER-SCIENCE/blob/main/AI.tar.gz

pierorivoira / COMPUTER-SCIENCE

Code Issues Pull requests Actions Projects Wiki

Files main COMPUTER-SCIENCE / AI.tar.gz

pierorivoira Add files via upload 7f92e45 · 23 minutes ago

23.6 MB

Download raw file

Code Blame Raw

View raw

(Sorry about that, but we can't show files that are this big right now.)

Estrarre il contenuto dell'archivio

```
piero@piero-XPS-9320:~$ cd Scaricati/  
piero@piero-XPS-9320:~/Scaricati$ file AI.tar.gz  
AI.tar.gz: gzip compressed data, from Unix, original size modulo 2^32 29859840
```

```
piero@piero-XPS-9320:~/Scaricati$ tar -xvzf AI.tar.gz  
COMPUTER_SCIENCE/AI/  
COMPUTER_SCIENCE/AI/unpacker.py  
COMPUTER_SCIENCE/AI/Leguminosa.py  
COMPUTER_SCIENCE/AI/Foraggio.py  
COMPUTER_SCIENCE/AI/trova_massimo.py  
COMPUTER_SCIENCE/AI/blocco_di_testo_last_rows.py  
COMPUTER_SCIENCE/AI/tartaglia_modulo.py  
COMPUTER_SCIENCE/AI/triangolo_di_Tartaglia.ods  
COMPUTER_SCIENCE/AI/blocco_di_testo_mod.py  
COMPUTER_SCIENCE/AI/metabolismo_basale.xlsx  
COMPUTER_SCIENCE/AI/initdata_mod.py  
COMPUTER_SCIENCE/AI/script5.py  
COMPUTER_SCIENCE/AI/rubrica.txt  
COMPUTER_SCIENCE/AI/Sottoprodotto.py  
COMPUTER_SCIENCE/AI/leggi_dati_e_trova_massimo.py  
...
```

Estrarre il contenuto dell'archivio

```
piero@piero-XPS-9320:~/Scaricati$ ls
AI.tar.gz                                eap1499-sup-0004-appendixs4.txt
ALIMENTI.tar.gz                            infoalunno_prospettoassenzeorarie.xlsx
COMPUTER_SCIENCE                           vettori.txt
eap1499-sup-0002-appendixs2.pdf           wolves.csv
eap1499-sup-0002-appendixs2.txt          wolves.xlsx
eap1499-sup-0004-appendixs4.pdf
piero@piero-XPS-9320:~/Scaricati$ cd COMPUTER_SCIENCE/
piero@piero-XPS-9320:~/Scaricati/COMPUTER_SCIENCE$ ls
AI
piero@piero-XPS-9320:~/Scaricati/COMPUTER_SCIENCE$ cd AI
piero@piero-XPS-9320:~/Scaricati/COMPUTER_SCIENCE/AI$
```

Per iniziare...

```
piero@piero-XPS-9320:~/Scaricati/COMPUTER_SCIENCE/AI$ ls
alimenti_26_febbraio_25.py
alimenti.ods
alimenti.py
blocco_di_testo_last_rows.py
blocco_di_testo_mod.py
blocco_di_testo.py
CARTELLA
Cereale.py
DATA
dati_istogramma.txt
docs-pdf
eleva_a_potenza.py
Farina_di_estrazione.py
Fonte_di_fibra.py
Foraggio.py
GRAFICI
importa_fieno_prato_stabile_primo_taglio.py
initdata_mod.py
...
```

Per iniziare...

```
piero@piero-XPS-9320:~/Scaricati/COMPUTER_SCIENCE/AI$ ls *.py
alimenti_26_febbraio_25.py
alimenti.py
blocco_di_testo_last_rows.py
blocco_di_testo_mod.py
blocco_di_testo.py
Cereale.py
eleva_a_potenza.py
Farina_di_estrazione.py
Fonte_di_fibra.py
Foraggio.py
importa_fieno_prato_stabile_primo_taglio.py
initdata_mod.py
initdata.py
inserisci_gruppo.py
leggi_dati_e_trova_massimo.py
Leguminosa.py
maxarray.py
more.py
packdlg.py
packer.py
parmfile.py
```

Per iniziare...

```
piero@piero-XPS-9320:~$ pwd
/home/piero
piero@piero-XPS-9320:~$ mkdir COMPUTER_SCIENCE
piero@piero-XPS-9320:~$ cd COMPUTER_SCIENCE/
piero@piero-XPS-9320:~/COMPUTER_SCIENCE$ pwd
/home/piero/COMPUTER_SCIENCE
piero@piero-XPS-9320:~/COMPUTER_SCIENCE$ mkdir AI
piero@piero-XPS-9320:~/COMPUTER_SCIENCE$ cd AI
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ pwd
/home/piero/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$
```

Per iniziare...

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ cd
piero@piero-XPS-9320:~$ pwd
/home/piero
piero@piero-XPS-9320:~$ python3
Python 3.10.12 (main, Feb 4 2025, 14:57:36) [GCC 11.4.0] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>> import os
>>> os.getcwd()
'/home/piero'
>>> os.getlogin()
'piero'
>>> user = os.getlogin()
>>> user
'piero'
>>> os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
>>> cartella = os.getcwd()
>>> cartella
'/home/piero/COMPUTER_SCIENCE/AI'
>>> os.chdir('/home/%s' % user)
>>> os.getcwd()
'/home/piero'
```

Elencare i file in una dir: the hard way

```
>>> os.chdir('/home/%s/Scaricati/COMPUTER_SCIENCE/AI' % user)
>>> os.getcwd()
'/home/piero/Scaricati/COMPUTER_SCIENCE/AI'
>>> for line in os.popen('ls *.py'): print(line, end=' ')
...
alimenti_26_febbraio_25.py
alimenti.py
blocco_di_testo_last_rows.py
blocco_di_testo_mod.py
blocco_di_testo.py
Cereale.py
eleva_a_potenza.py
Farina_di_estrazione.py
Fonte_di_fibra.py
Foraggio.py
importa_fieno_prato_stabile_primo_taglio.py
initdata_mod.py
initdata.py
inserisci_gruppo.py
leggi_dati_e_trova_massimo.py
Leguminosa.py
...
>>>
```

Salvare un oggetto in un file esterno

```
piero@piero-XPS-9320:~$ sudo apt install python3-dill
piero@piero-XPS-9320:~$ python3
>>> import dill, os, pickle
>>> species_1 = ['Tachyglossus aculeatus', 'Monotremata', 2.404, 2725, 30.7, 19.7]
>>> species_2 = ['Plecotus auritus', 'Chiroptera', 0.082, 10.25, 35.5, 4.4]
>>> taxa = (species_1, species_2)
>>> file_name = 'piero.pkl'
>>> with open(file_name, 'wb') as file:
...     dill.dump(taxa, file)
...
>>> exit()
```

Salvare un oggetto in un file esterno

```
>>> import dill, os, pickle
>>> os.getcwd()
'/home/piero'
>>> user = os.getlogin()
>>> os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
>>> os.getcwd()
'/home/piero/COMPUTER_SCIENCE/AI'
>>> with open("piero.pkl", "rb") as file:
...     taxa = pickle.load(file)
...
>>> taxa
(['Tachyglossus aculeatus', 'Monotremata', 2.404, 2725, 30.7, 19.7], ['Plecotus
auritus', 'Chiroptera', 0.082, 10.25, 35.5, 4.4])
>>> taxa[0]
['Tachyglossus aculeatus', 'Monotremata', 2.404, 2725, 30.7, 19.7]
>>> taxa[1]
['Plecotus auritus', 'Chiroptera', 0.082, 10.25, 35.5, 4.4]
>>>
```

Salvare un oggetto in un file esterno

```
>>> NAME, ORDER, METABOLIC_RATE, BODY_MASS, BODY_TEMP, AMBIENT_TEMP = range(6)
>>> taxa[0][NAME]
'Tachyglossus aculeatus'
>>> taxa[0][ORDER]
'Monotremata'
>>>
```

Il ciclo for

```
>>> for i in taxa:  
...     print(i)  
...  
['Tachyglossus aculeatus', 'Monotremata', 2.404, 2725, 30.7, 19.7]  
['Plecotus auritus', 'Chiroptera', 0.082, 10.25, 35.5, 4.4]  
>>>
```

La gerarchia concettuale di Python

1. I programmi sono composti da moduli
2. I moduli contengono affermazioni ("statements")
3. Le affermazioni contengono espressioni
4. Le espressioni creano e modificano gli oggetti

Il nostro primo programma in Python: script1.py

```
# A first Python script
# script1.py

import os, sys
# Importa due diversi moduli di Python (os e sys) per identificare il nome dell'utente e del sistema operativo

print(os.getlogin())
print(sys.platform)
print(2**100)
x = 'Python è una figata!'
# Crea la variabile x e le assegna una stringa di caratteri
print(x * 8)
# Esegue la chiamata della funzione print per 4 volte, per inviare i risultati all'output standard (lo schermo)
```

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 script1.py
```

piero

linux

1267650600228229401496703205376

Python è una figata!Python è una figata!Python è una figata!Python è una figata!Python è una figata!

Stream redirection

```
$ python3 script1.py > script1_out.txt
```

- L'output viene scritto nel file di testo <`script1_out.txt`>

The screenshot shows a code editor interface with two tabs open. The left tab is titled "script1.py" and contains the following Python code:

```
1 piero
2 linux
3 1267650600228229401496703205376
4 Python è una figata!Python è una figata!
```

The right tab is titled "script1_out.txt" and contains the same text as the output of the script, repeated multiple times. The tabs are separated by a red horizontal line.

Importare i moduli

Ogni file di codice sorgente scritto in linguaggio Python, il cui nome abbia l'estensione `.py`, è un **modulo** e può essere importato

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3
Python 3.10.12 (main, Nov  6 2024, 20:22:13) [GCC 11.4.0] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>> import script1
piero
linux
1267650600228229401496703205376
Python è una figata!Python è una figata!Python è una figata!Python è una
figata!Python è una figata!Python è una figata!Python è una figata!Python è
una figata!
```

Importare i moduli

- I moduli vengono utilizzati come *librerie* di strumenti
- Un modulo è un pacchetto (*package*) di nomi di variabili, noto come *namespace*
- I nomi (attributi) designano un oggetto specifico
- Importando un modulo si ottiene accesso a tutti i nomi assegnati all'inizio del file del modulo stesso

Da dove vengono importati i moduli?

```
>>> import sys  
>>> sys.path  
['', '/usr/lib/python310.zip', '/usr/lib/python3.10', '/usr/lib/python3.10/lib-  
dynload', '/usr/local/lib/python3.10/dist-packages', '/usr/lib/python3/dist-packages']  
>>>
```

Scaricare un file da internet usando il terminale

```
piero@piero-XPS-9320:~/Scaricati$ wget https://github.com/pierorivoira/COMPUTER-SCIENCE/raw/refs/heads/main/taxa.py
--2025-03-27 08:34:49--
https://github.com/pierorivoira/COMPUTER-SCIENCE/raw/refs/heads/main/taxa.py
Risoluzione di github.com (github.com) ... 140.82.121.4
Connessione a github.com (github.com) |140.82.121.4|:443... connesso.
Richiesta HTTP inviata, in attesa di risposta... 302 Found
Posizione: https://raw.githubusercontent.com/pierorivoira/COMPUTER-SCIENCE/refs/heads/main/taxa.py [segue]
--2025-03-27 08:34:50-- https://raw.githubusercontent.com/pierorivoira/COMPUTER-SCIENCE/refs/heads/main/taxa.py
Risoluzione di raw.githubusercontent.com (raw.githubusercontent.com) ...
185.199.111.133, 185.199.108.133, 185.199.109.133, ...
Connessione a raw.githubusercontent.com (raw.githubusercontent.com) | 185.199.111.133|:443... connesso.
Richiesta HTTP inviata, in attesa di risposta... 200 OK
Lunghezza: 35851 (35K) [text/plain]
Salvataggio in: 'taxa.py'

taxa.py          100% [=====>]  35,01K  --.-KB/s    in 0,08s

2025-03-27 08:34:50 (460 KB/s) - 'taxa.py' salvato [35851/35851]

piero@piero-XPS-9320:~/Scaricati$
```

Importare i moduli: il file taxa.py

Ogni file di codice sorgente scritto in linguaggio Python, il cui nome abbia l'estensione `<.py>`, è un **modulo** e può essere importato

```
NA = 'Not Available'  
species_1 = ['Tachyglossus aculeatus', 2.404, 2725, 30.7, 19.7]  
species_2 = ['Zaglossus bruijni', 6.778, 10300, 30.8, 16.2]  
species_3 = ['Ornithorhynchus anatinus', 1.082, 693, 32.1, 12.9]  
species_4 = ['Caluromys derbianus', 1.255, 329, 35, 19.3]  
species_5 = ['Chironectes minimus', 2.549, 935, 35, 21.5]  
species_6 = ['Didelphis marsupialis', 3.185, 1165, 35, 23.5]  
species_7 = ['Didelphis virginiana', 4.641, 2488, 35, 15.4]  
species_8 = ['Gracilinanus microtarsus', 0.106, 13, 35, 16.8]  
species_9 = ['Lutreolina crassicaudata', 2.265, 812, 35.8, 19.1]  
species_10 = ['Marmosa robinsoni', 0.547, 122, 34, 19.3]  
...
```

Importare i moduli: il file taxa.py

```
import, from, reload
```

```
>>> import os
>>> user = os.getlogin()
>>> os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
>>> os.getcwd()
'/home/piero/COMPUTER_SCIENCE/AI'
>>> import taxa
>>> taxa.species_1
['Tachyglossus aculeatus', 2.404, 2725, 30.7, 19.7]
>>> taxa.species_2
['Zaglossus bruijni', 6.778, 10300, 30.8, 16.2]
>>> taxa.species_3
['Ornithorhynchus anatinus', 1.082, 693, 32.1, 12.9]
>>> taxa.species_3[1]
1.082
>>>
```

Importare i moduli: il file taxa.py

```
import, from, reload

>>> NAME, METABOLIC_RATE, BODY_MASS, BODY_TEMP, AMBIENT_TEMP = range(5)
>>> taxa.species_3[NAME]
'Ornithorhynchus anatinus'
>>> taxa.species_3[BODY_MASS]
693
>>>
```

Importare i moduli: il file taxa.py

Quali sono la temperatura corporea ed il tasso metabolico basale del coyote?

```
>>> from taxa import species_582
>>> species_582
['Canis latrans', 14.99, 10000, 37, 5.5]
>>> species_582[3]
37
>>> print('The body temperature of %s is %f' % (species_582[0],
species_582[3]))
The body temperature of Canis latrans is 37.000000
>>> print('The body temperature of %s is %f°C' % (species_582[0],
species_582[3]))
The body temperature of Canis latrans is 37.000000°C
>>> print('The coyote (%s) has a basal metabolic rate of %f watt' %
(species_582[0], species_582[1]))
The coyote (Canis latrans) has a basal metabolic rate of 14.990000 watt
>>>
```

Il programma initdata.py

```
# initialize data to be stored in files, pickles, shelves
import os
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
# records
species_1 = {'NAME': 'Tachyglossus aculeatus', 'ORDER': 'Monotremata', 'METABOLIC RATE (Watt)': 2.404, 'BODY MASS': 2725, 'BODY TEMPERATURE': 30.7, 'AMBIENT TEMPERATURE': 19.7}
species_2 = {'NAME': 'Plecotus auritus', 'ORDER': 'Chiroptera', 'METABOLIC RATE (Watt)': 0.082, 'BODY MASS': 10.25, 'BODY TEMPERATURE': 35.5, 'AMBIENT TEMPERATURE': 4.4}
# database
db = {}
db['species_1'] = species_1
db['species_2'] = species_2

if __name__ == '__main__':
# se questo modulo è il programma principale, ossia viene eseguito e non importato da un altro
# programma o dall'interprete dei comandi di python
    for key in db:
        print(key, '=>\n      ', db[key])
```

Il programma initdata.py

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 initdata.py
species_1 =>
    {'NAME': 'Tachyglossus aculeatus', 'ORDER': 'Monotremata', 'METABOLIC RATE (Watt)': 2.404, 'BODY MASS': 2725, 'BODY TEMPERATURE': 30.7, 'AMBIENT TEMPERATURE': 19.7}
species_2 =>
    {'NAME': 'Plecotus auritus', 'ORDER': 'Chiroptera', 'METABOLIC RATE (Watt)': 0.082, 'BODY MASS': 10.25, 'BODY TEMPERATURE': 35.5, 'AMBIENT TEMPERATURE': 4.4}

>>> exec(open('initdata.py').read())
species_1 =>
    {'NAME': 'Tachyglossus aculeatus', 'ORDER': 'Monotremata', 'METABOLIC RATE (Watt)': 2.404, 'BODY MASS': 2725, 'BODY TEMPERATURE': 30.7, 'AMBIENT TEMPERATURE': 19.7}
species_2 =>
    {'NAME': 'Plecotus auritus', 'ORDER': 'Chiroptera', 'METABOLIC RATE (Watt)': 0.082, 'BODY MASS': 10.25, 'BODY TEMPERATURE': 35.5, 'AMBIENT TEMPERATURE': 4.4}
>>>
```

Il programma initdata.py

```
>>> from initdata import db
>>> db
{'species_1': {'NAME': 'Tachyglossus aculeatus', 'ORDER': 'Monotremata', 'METABOLIC RATE (Watt)': 2.404, 'BODY MASS': 2725, 'BODY TEMPERATURE': 30.7, 'AMBIENT TEMPERATURE': 19.7}, 'species_2': {'NAME': 'Plecotus auritus', 'ORDER': 'Chiroptera', 'METABOLIC RATE (Watt)': 0.082, 'BODY MASS': 10.25, 'BODY TEMPERATURE': 35.5, 'AMBIENT TEMPERATURE': 4.4}}}
>>>
```

Il programma initdata_mod.py

```
# initialize data to be stored in files, pickles, shelves
import os
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
# records
species_1 = {'NAME': 'Tachyglossus aculeatus', 'ORDER': 'Monotremata', 'METABOLIC RATE
(Watt)': 2.404, 'BODY MASS': 2725, 'BODY TEMPERATURE': 30.7, 'AMBIENT TEMPERATURE':
19.7}
species_2 = {'NAME': 'Plecotus auritus', 'ORDER': 'Chiroptera', 'METABOLIC RATE
(Watt)': 0.082, 'BODY MASS': 10.25, 'BODY TEMPERATURE': 35.5, 'AMBIENT TEMPERATURE':
4.4}
# database
db = {}
db['species_1'] = species_1
db['species_2'] = species_2

# if __name__ == '__main__':
# questa riga verrà ignorata, quindi il successivo ciclo for sarà eseguito anche in caso di importazione del
# modulo initdata_mod
for key in db:
    print(key, '=>\n      ', db[key])
```

Il programma initdata_mod.py

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 initdata_mod.py
species_1 =>
    {'NAME': 'Tachyglossus aculeatus', 'ORDER': 'Monotremata', 'METABOLIC RATE (Watt)': 2.404, 'BODY MASS': 2725, 'BODY TEMPERATURE': 30.7, 'AMBIENT TEMPERATURE': 19.7}
species_2 =>
    {'NAME': 'Plecotus auritus', 'ORDER': 'Chiroptera', 'METABOLIC RATE (Watt)': 0.082, 'BODY MASS': 10.25, 'BODY TEMPERATURE': 35.5, 'AMBIENT TEMPERATURE': 4.4}
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$
```

Il funzionamento del programma, quando viene eseguito come programma principale (main) non cambia ma...

```
>>> from initdata_mod import db
species_1 =>
    {'NAME': 'Tachyglossus aculeatus', 'ORDER': 'Monotremata', 'METABOLIC RATE (Watt)': 2.404, 'BODY MASS': 2725, 'BODY TEMPERATURE': 30.7, 'AMBIENT TEMPERATURE': 19.7}
species_2 =>
    {'NAME': 'Plecotus auritus', 'ORDER': 'Chiroptera', 'METABOLIC RATE (Watt)': 0.082, 'BODY MASS': 10.25, 'BODY TEMPERATURE': 35.5, 'AMBIENT TEMPERATURE': 4.4}
>>>
```

Importare i moduli: il file `parmfile.py`

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ wget  
https://github.com/pierorivoira/COMPUTER-SCIENCE/blob/main/parmfile.py  
...  
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ gedit parmfile.py
```

Apri



Salva



```
1 #####  
2 #_Parmfile_for_Migrate_5.0.4(git:distribution_version)_May_09_2022  
3 #_DO_NOT_REMOVE_THE_FIRST_TWO_LINES!  
4 #  
5 #_generated Automatically_on  
6 #_Thu_Apr_6_08:44:47_2023  
7 #  
8 #_please_report_problems_to_Peter_Beerli  
9 #_email:beerli@fsu.edu  
10 #_http://popgen.sc.fsu.edu/migrate.html  
11 #####  
12 #  
13 #####  
14 #_General_options  
15 #####  
16 #  
17 #_Interactive_or_batch_job_usage  
18 #__Syntax:_menu=<YES_|_NO>  
19 #_For_batch_runs_it_needs_to_be_set_to_NO  
20 #_menu='YES'  
21 #  
22 #_Specification_of_length_of_names_of_individuals_(default=10)  
23 #__Syntax:_nmLength=<INTEGER_between_0..._30>  
24 nmLength=12  
25 #  
26 #  
27 #_If you long_runs_fails because_of_timelimits  
28 #_AND you have specified bayes_allfile='YES'....  
29 #_then you can recover_and_continue  
30 #_by_setting_recover_to_yes,_default_is_NO  
31 #_This_option_fails_if_your_bayesallfile_is_complete!  
32 #_At the moment,_I have no experience about_failure_rate_etc._[March_30_2015]  
33 #_____recover=<YES_|_NO>  
34 #  
35 #####  
36 #_Data_options  
37 #####  
38 #  
39 #_Several different_main_datatypes_are_possible:  
40 #_INFINITE_ALLELE:_usable_for_electrophoretic_markers,  
41 #_____other_markers_with_unknown_mutation_model  
42 #_STEPWISE_MUTATION:_usable_for_microsatellite_data_or  
43 #_____other_markers_with_stepwise_change
```

Importare i moduli: il file `parmfile.py`

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ gedit parmfile.py
#####
# Parmfile_for_Migrate_5.0.4 (git:distribution_version) May_09_2022
# DO_NOT_REMOVE_THE_FIRST_TWO_LINES!
#
#_generated Automatically_on
#_Thu_Apr_6_08:44:47_2023
#
#_please_report_problems_to_Peter_Beerli
#_email: beerli@fsu.edu
#_http://popgen.sc.fsu.edu/migrate.html
#####
#
#####
# General_options
#####
#
#_Interactive_or_batch_job_usage
#_Syntax: _menu=<_YES_|_NO_>
#_For_batch_runs_it_needs_to_be_set_to_NO
menu='YES'
#
#_Specification_of_length_of_names_of_individuals_(default=10)
#_Syntax: nmlength=<INTEGER_between_0.._30>
nmlength=12
```

```
datatype='BrownianMicrosatelliteData'
#include_unknown='NO'
datamodel='BM (BROWNIAN_MOTION)'
#
...
inheritance_scalars='NO'
#
...
haplotyping='NO'
#
#
# population_relabel=={assignment_for_each_location_in_the_infile}
# example_is_population_relabel=={1_2_2}
population_relabel='{1,_2,_2,_2,_2,_2,_2,_2,_2,_3,_3,_3}'
#
# __#random_subset=number:#random_numberseed
# allows_to_subset_the_dataset_randomly,_if_number>sample_in_population
# all_samples_are_taken,_if_number_is_smaller_then_the_pop_sample_is_shuffled_and
# and_the_first_number_samples_are_taken
random_subset=10:3176820
#
#####
# Input options
#####
#
# _input_file_location
# Syntax_infile=FILEPATH
infile='infile.msat.Myotis.myotis_13_pop'
...
```

Importare i moduli: il file `parmfile.py`

```
import, from, reload

>>> import parmfile
>>> parmfile.nmlength
12
>>> parmfile.datamodel
'BM (BROWNIAN_MOTION)'
>>> parmfile.infile
'infile.msat.Myotis.myotis_13_pop'
>>> parmfile.burn_in
100
>>> parmfile.outfile
'outfile_msat_13_pop_27_mag'
>>> parmfile.datatype
'BrownianMicrosatelliteData'
>>> from parmfile import datatype
>>> datatype
'BrownianMicrosatelliteData'
>>> print('My data model is %s' % parmfile.datamodel)
My data model is BM (BROWNIAN_MOTION)
>>>
```

Oggetti “built-in”: lists

L’oggetto `<list>` è il tipo di sequenza più generale in Python. È una collezione di oggetti di tipo arbitrario, ordinati in base alla loro posizione.

A differenza delle stringhe, le lists sono mutabili: ogni elemento di una list può essere modificato conoscendone la posizione.

Oggetti “built-in”: lists

```
>>> address_1 = ['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it']
>>> address_1
['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it']
>>> len(address_1)
5
>>> for x in address_1: print(x)
...
piero
rivoira
istitutopennaasti
edu
it
>>>
>>> address_1[0]
'piero'
>>> address_1[0][0]
'p'
>>> school_name = address_1[2][8:13]
>>> school_name
'penna'
```

Oggetti “built-in”: lists

```
>>> 'the name of my school is ' + school_name
'the name of my school is penna'
>>> address_1.append('Via della Resistenza, 18/D')
>>> len(address_1)
6
>>> address_1
['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it', 'Via della Resistenza,
18/D']
>>> address_1.append('Saluzzo')
>>> len(address_1)
7
>>> address_1
['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it', 'Via della Resistenza,
18/D', 'Saluzzo']
>>> address_1.append('CN')
>>> len(address_1)
8
>>> address_1
['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it', 'Via della Resistenza,
18/D', 'Saluzzo', 'CN']
>>>
```

Oggetti “built-in”: lists

```
>>> address_1.remove('CN')
>>> address_1
['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it', 'Via della Resistenza,
18/D', 'Saluzzo']
>>> address_1.remove('edu')
>>> address_1
['piero', 'rivoira', 'istitutopennaasti', 'it', 'Via della Resistenza, 18/D',
'Saluzzo']
>>> address_1 = ['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it', 'Via
della Resistenza, 18/D', 'Saluzzo']
>>> address_1[0] + '.' + address_1[1] + '@' + address_1[2] + '.' +
address_1[3] + '.' + address_1[4]
'piero.rivoira@istitutopennaasti.edu.it'
>>>
```

Oggetti “built-in”: lists

```
>>> address_1 = ['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it', 'Via  
della Resistenza, 18/D', 'Saluzzo']  
>>> address_1[2]  
'istitutopennaasti'  
>>> address_1[2] = 'yahoo'  
>>> address_1[2]  
'yahoo'  
>>> address_1  
['piero', 'rivoira', 'yahoo', 'edu', 'it', 'via della Resistenza, 18/D',  
'Saluzzo']  
>>> address_1.remove('edu')  
>>> address_1  
['piero', 'rivoira', 'yahoo', 'it', 'via della Resistenza, 18/D', 'Saluzzo']  
>>>
```

Oggetti “built-in”: comprehensions

When applied to strings, the % operator provides a simple way to format values as strings according to a format definition, coding multiple substitutions all at once, instead of building and concatenating parts individually.

```
>>>
```

Oggetti “built-in”: tuples

When applied to strings, the % operator provides a simple way to format values as strings according to a format definition, coding multiple substitutions all at once, instead of building and concatenating parts individually.

```
>>>
```

Oggetti “built-in”: stringhe

Strings can be indexed (subscripted), with the first character having index 0. There is no separate character type; a character is simply a string of size one:

```
>>> word = 'Python'  
>>> word[0] # character in position 0  
'P'  
>>> word[5] # character in position 5  
'n'  
>>> word[-1] # last character  
'n'  
>>> word[-6] # first character  
'P'  
>>>
```

Oggetti “built-in”: stringhe

```
>>> s = 'Migrate-n'  
>>> s  
'Migrate-n'  
>>>  
>>> s[-1]  
'n'  
>>> s[-2]  
'-'  
>>> s[-9]  
'M'  
>>> s[len(s)-1]  
'n'  
>>> s[0:7]  
'Migrate'  
>>> s[1:]  
'igrate-n'  
>>> s[:-2]  
'Migrate'
```

Oggetti “built-in”: stringhe

```
>>> S + ' is a great program!'
'Migrate-n is a great program!'
>>> L = list(S)
>>> L
['M', 'i', 'g', 'r', 'a', 't', 'e', '-', 'n']
>>> ''.join(L)
'Migrate-n'
```

Oggetti “built-in”: stringhe

```
>>> S = S.replace('Migrate-n', 'Lamarc')
>>> S
'Lamarc'
>>> S = ('Migrate-n')
>>> L = S.replace('Migrate-n', 'lamarc')
>>> L
'lamarc'
>>> L.capitalize()
'Lamarc'
>>> L
'lamarc'
>>> L = L.capitalize()
>>> L
'Lamarc'
>>> L.upper()
'LAMARC'
>>> L.isalpha()
True
>>>
```

Oggetti “built-in”: stringhe

```
>>> S1 = 'Migrate-n '
>>> S1
'Migrate-n '
>>> S2 = 'uses genetic data (microsatellite data, sequences) to infer
populaiton genetic parameters'
>>> S12 = S1 + S2
>>> S12
'Migrate-n uses genetic data (microsatellite data, sequences) to infer
populaiton genetic parameters'
>>> S12 * 2
'Migrate-n uses genetic data (microsatellite data, sequences) to infer
populaiton genetic parametersMigrate-n uses genetic data (microsatellite data,
sequences) to infer populaiton genetic parameters'
>>> S1[1]
'i'
>>>
```

Oggetti “built-in”: stringhe

```
>>> S3 = 'MIGRATE uses genetic data (microsatellite data ,sequences) to infer  
populaiton genetic parameters, such a population size, immigration rates, and  
population divergence times.\n This is our flagship product! There is also a  
google-support group (migrate-support@google.com)'  
>>> S3  
'MIGRATE uses genetic data (microsatellite data ,sequences) to infer  
populaiton genetic parameters, such a population size, immigration rates, and  
population divergence times.\n This is our flagship product! There is also a  
google-support group (migrate-support@google.com)'  
>>> print(S3)  
MIGRATE uses genetic data (microsatellite data ,sequences) to infer populaiton  
genetic parameters, such a population size, immigration rates, and population  
divergence times.  
This is our flagship product! There is also a google-support group (migrate-  
support@google.com)  
>>>
```

Oggetti “built-in”: stringhe

```
>>> 'Py' 'thon'  
'Python'  
text = ('Put several strings within parentheses '  
... 'to have them joined together.')  
>>> text  
'Put several strings within parentheses to have them joined together.'  
>>> prefix = 'Py'  
>>> prefix + 'thon'  
'Python'
```

Oggetti “built-in”: stringhe

```
>>> address_1 = ['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it']
>>> address_1
['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it']
>>> address_2 = ['piero', 'rivoira', 'yahoo', '', 'it']
>>> address_2
['piero', 'rivoira', 'yahoo', '', 'it']
>>> address_book = (address_1, address_2)
>>> address_book
([['piero', 'rivoira', 'istitutopennaasti', 'edu', 'it'], ['piero', 'rivoira',
'yahoo', '', 'it']])
>>> NAME, SURNAME, INSTITUTION, DOMAIN, EXTENSION = range(5)
>>> address_book[0][NAME]
'piero'
>>> whole_address_1 = address_book[0][NAME] + '.' + address_book[0][SURNAME] +
'@' + address_book[0][INSTITUTION] + '.' + address_book[0][DOMAIN] + '.' +
address_book[0][EXTENSION]
>>> whole_address_1
'piero.rivoira@istitutopennaasti.edu.it'
>>>
```

Oggetti “built-in”: stringhe

```
>>> address_1 = ['piero', '.', 'rivoira', '@', 'istitutopennaasti', '.',  
'edu', '.', 'it']  
>>> type(address_1)  
<class 'list'>  
>>> import string  
>>> ''.join(address_1)  
'piero.rivoira@istitutopennaasti.edu.it'  
>>>
```

Scriviamo il nostro indirizzo e-mail istituzionale

```
# $ sudo apt install python3-tk
# script5.py

import os, sys
from tkinter.simpledialog import askstring

NOME = askstring('Entry', 'inserisci il tuo nome')
print(NOME)
COGNOME = askstring('Entry', 'inserisci il tuo cognome')
print(COGNOME)
ISTITUZIONE = askstring('Entry', 'inserisci il nome della tua istituzione')
print(ISTITUZIONE)
DOMINIO = askstring('Entry', "inserisci il dominio della tua istituzione, es. 'edu'")
print(DOMINIO)
ESTENSIONE = askstring('Entry', "inserisci l'estensione, es. 'it'")
print(ESTENSIONE)
indirizzo_1 = [NOME, COGNOME, ISTITUZIONE, DOMINIO, ESTENSIONE]
print(indirizzo_1)
NOME, COGNOME, ISTITUZIONE, DOMINIO, ESTENSIONE = range(5)
RUBRICA = (indirizzo_1)
indirizzo_completo_1 = RUBRICA[NOME] + '.' + RUBRICA[COGNOME] + '@' + RUBRICA[ISTITUZIONE] + '.' +
RUBRICA[DOMINIO] + '.' + RUBRICA[ESTENSIONE]
print(indirizzo_completo_1)
print(os.getlogin())
print(sys.platform)
```

Scaricare un file da internet

```
piero@piero-XPS-9320:~$ wget
https://github.com/pierorivoira/COMPUTER-SCIENCE/raw/refs/heads/main/parmfile.txt
--2025-04-01 18:35:34--
https://github.com/pierorivoira/COMPUTER-SCIENCE/raw/refs/heads/main/parmfile.txt
Risoluzione di github.com (github.com) ... 140.82.121.4
Connessione a github.com (github.com) |140.82.121.4|:443... connesso.
Richiesta HTTP inviata, in attesa di risposta... 302 Found
Posizione: https://raw.githubusercontent.com/pierorivoira/COMPUTER-SCIENCE/refs/heads/
main/parmfile.txt [segue]
--2025-04-01 18:35:34-- https://raw.githubusercontent.com/pierorivoira/COMPUTER-
SCIENCE/refs/heads/main/parmfile.txt
Risoluzione di raw.githubusercontent.com (raw.githubusercontent.com) ...
185.199.110.133, 185.199.108.133, 185.199.109.133, ...
Connessione a raw.githubusercontent.com (raw.githubusercontent.com) |
185.199.110.133|:443... connesso.
Richiesta HTTP inviata, in attesa di risposta... 200 OK
Lunghezza: 25960 (25K) [text/plain]
Salvataggio in: 'parmfile.txt'

parmfile.txt      100% [=====>]  25,35K  --.-KB/s    in 0,05s

2025-04-01 18:35:34 (495 KB/s) - 'parmfile.txt' salvato [25960/25960]

piero@piero-XPS-9320:~$
```

Scaricare un file da internet

```
>>> import os
>>> os.system('wget
https://github.com/pierorivoira/COMPUTER-SCIENCE/raw/refs/heads/main/parmfile.txt')
--2025-04-01 18:41:17--
https://github.com/pierorivoira/COMPUTER-SCIENCE/raw/refs/heads/main/parmfile.txt
Risoluzione di github.com (github.com) ... 140.82.121.4
Connessione a github.com (github.com) |140.82.121.4|:443... connesso.
Richiesta HTTP inviata, in attesa di risposta... 302 Found
...
>>>
```

Files di testo

Contengono stringhe di caratteri (tipo `str`), codificati secondo il sistema **Unicode** (<https://www.unicode.org/charts/>)

	000	001	002	003	004	005	006	007
0	[NUL] 000	[DLE] 0010	[SP] 0020	0	@	P	`	p
1	[SOH] 0001	[DC1] 0011	!	1	A	Q	a	q
2	[STX] 0002	[DC2] 0012	"	2	B	R	b	r
3	[ETX] 0003	[DC3] 0013	#	3	C	S	c	s
4	[EOT] 0004	[DC4] 0014	\$	4	D	T	d	t
5	[ENQ] 0005	[NAK] 0015	%	5	E	U	e	u
6	[ACK] 0006	[SYN] 0016	&	6	F	V	f	v
7	[BEL] 0007	[ETB] 0017	'	7	G	W	g	w
8	[BS] 0008	[CAN] 0018	(8	H	X	h	x
9	[HT] 0009	[EM] 0019)	9	I	Y	i	y
A	[LF] 000A	[SUB] 001A	*	:	J	Z	j	z
B	[VT] 000B	[ESC] 001B	+	;	K	[k	{
C	[FF] 000C	[FS] 001C	,	<	L	\	l	
D	[CR] 000D	[GS] 001D	-	=	M]	m	}
E	[SO] 000E	[RS] 001E	.	>	N	^	n	~
F	[SI] 000F	[US] 001F	/	?	O	_	o	[DEL] 007F

Leggere un file di testo

```
>>> for line in open('parmfile.txt'): print(line)
...
#####
# Parmfile for Migrate 5.0.4(git:distribution-version)-May-09-2022
# DO NOT REMOVE THE FIRST TWO LINES!
#
# generated automatically on
# Thu Apr  6 08:44:47 2023
```

Leggere un testo in un oggetto di tipo stringa

```
>>> import os
>>> user = os.getlogin()
>>> os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
>>> with open('parmfile.txt', 'r') as file:
...     text = file.read()
...
>>> text
"#####\n# Parmfile for Migrate 5.0.4 (git:distribution-version) -May-09-2022\n# DO NOT REMOVE THE
FIRST TWO LINES!\n#\n# generated automatically on\n# Thu Apr  6 08:44:47 2023\n#\n#
please report problems to Peter Beerli\n#   email: beerli@fsu.edu\n#
http://popgen.sc.fsu.edu/migrate.html\n"
...
>>> type(text)
<class 'str'>
>>> text.find('ALLEL')
1439
>>>
```

Leggere un testo in un oggetto di tipo stringa

```
>>> text.find('RANDOM')
12443
>>> text = text.replace('RANDOM', 'CASUALE')
>>> text.find('RANDOM')
-1
>>> text.find('CASUALE')
12443
>>> 'RANDOM' in text
False
>>> 'CASUALE' in text
True
>>> string = '# DO NOT REMOVE THE FIRST TWO LINES!\n'
>>> string
'# DO NOT REMOVE THE FIRST TWO LINES!\n'
>>> string.strip()
'# DO NOT REMOVE THE FIRST TWO LINES!'
>>>
```

```
ctrl-maiusc-c piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI x piero@piero-XPS-9320: ~ x
Syntax: heating=< NO | <YES | ADAPTIVE>:SKIP:TEMPERATURES\n#
NO      No heating\n#          YES    heating using TEMPERATURES\n#          ADAPT
IVE adaptive heating using start TEMPERATURES [fails sometimes!!]\n#
SKIP skip that many comparisons, this lengthens the run by SKIP\n#
TEMPERATURES { 1.0, templ, temp2, temp3 .. tempn}\n# Example: heati
ng=YES:1:{1.0, 1.2, 3.0,1000000.0}\n# Heating: swapping chains\n# Syntax: heated-swap=< YES | NO >\n#           YES swapping of chains enabled [DEFA
ULT]\n#           NO    swapping of chains disabled\n# Example: heated-swa
p=YES\nheating=YES:1:{1.0,1.071,1.154,1.25,1.364,1.5,1.667,1.875,2.143,2.5,3
.0,3.75,5.0,7.5,15.0,1000000.0}\nheated-swap=YES\n#\n# Lengthening chain sch
emes\n# Syntax: moving-steps=< NO | YES:VALUE>\n#           VALUE frequency
is between 0..1\nmoving-steps=NO\n#\n#\n# Convergence statistic [Gelman
and Rubin]\n# Syntax: gelman-convergence=< YES:Pairs|Summary | NO >\n#
NO      do not use Gelman's convergence criterium\n#           YES      use G
elman's convergence criteria between chain i, and i-1\n#           PAIRS
reports all replicate pairs\n#           SUM    reports only mean and ma
xima\ngelman-convergence=No\n#\n# REPLICATON:\n# Syntax: replicate=< N
0 | YES:<VALUE> >\n#           NO      no replication of run\n#           YES    repl
icate run\n#           VALUE    number between 2 and many, complete replica
tes\nreplicate=YES:10\n#\n#-----\n-----\n#\nend\n"
>>>
```

ctrl-alt-t

piero@piero-XPS-9320:~\$ gedit

ctrl-v

```

*Documento 1 senza nome
#####
## Parmfile for Migrate 5.0.4(git:distribution-version)-May-09-2022## DO NOT
## tically on## Thu Apr 6 08:44:47 2023## please report problems to Peter Beerli## email: beerli@fsu.edu##
#####
## Interactive or batch job usage## Syntax: menu= < YES | NO
u=YES## Specification of length of names of individuals (default=10)## Syntax: nmlength=<INTEGER between
0 .. 30>nmlength=12## If you long runs fails because of timelimits## AND you have specified bayes-allfile=YES....## then you can recover and continue## [March
by setting recover to yes, default is NO## This option fails if your bayesallfile is complete!## At the moment, I have no experience about failure rate etc. [March
30 2015]## recover=<YES | NO> \n## Several different main datatypes are possible:## INFINITE ALLELE:
options## usable for electrophoretic markers,## other markers with unknown mutation model## STEPWISE MUTATION: usable for microsatellite data
or## other markers with stepwise change## from one allele to another## [singlestep versus multistep model, see
micro-submodel option]## FINITE SITES MUTATION: standard DNA/RNA sequence mutation## model, usable for DNA or RNA contiguous## INFINITE ALLELE## Syntax:
sequences or variable sites only (SNP)##-----datatype=ALLELICDATA \n## include-unknown=<YES | NO> with YES unknown alleles## are included into analysis, NO is the
default##-----## STEPWISE MUTATION## Syntax: datatype=<MICROSATELLITEDATA | BROWNIANDATA##-----MICRO specifies the standard stepwise mutation## model, the BROWNIAN is an approximation to this## FOR 99%
of all cases BROWNIAN WILL BE FASTEST AND 'BEST'## for MICRO several suboptions are available, again use BROWNIAN! \n## micro-submodel=<1|2:
{tune,pinc}>\n## 1 means singlestep mutation model (this is the default and the standard## 2 is the Multistep model (see Watkins 2007
TPB, section 4.2) it needs## two parameters: tune specifies how close the model is to a singlestep model## so tune=0 -->
singlestep, tune=1 --> infinite allele model;\n## the second parameter defines the probability that the repeat number## is
increasing, this value cannot be larger than 0.666, I suggest 0.5.\n## Example: micro-submodel=2:{0.5,0.5}\n## micro-threshold=<INTEGER>
Default is 10 [MICRO only, NEEDS TO BE EVEN!],\n## smaller values speed up analysis, but might also\n## crash, large values slow down
analysis considerably.\n## Change this value only when you suspect that your## data has huge gaps in repeat length.\n## include-unknown=<YES | NO> with YES unknown alleles## are included into analysis, NO is the
default##-----## FINITE SITES MUTATION## Syntax: datatype=<SEQUENCEDATA | NUCLEOTIDE##-----SEQNUCLEOTIDE: typical linked stretches of DNA, for example mtDNA## NUCLEOTIDE: linked DNA stretches, all invariant sites
removed##-----freqs-from-data=<YES | NO: freq(A), freq(C), freq(G), freq(T)>\n## calculate the prior base frequencies from the data,
##-----or specify the frequencies## ttratio=<RATIO1 RATIO2 ....> Default is 2.0,\n## ratio between transitions and transversions.
##-----seqerror-rate=<{VALUE,VALUE,VALUE,VALUE}|Estimate:1|4> Default is 0.0, typical values for ABI 3700 \n## sequencers after base calling are
around 0.001 (1/650)\n## categories=<VALUE:CATFILE> The categories are integers or letters## specified in file called CATFILE, this assumes
that all## sites belong to known categories, this can be used to## weight third positions etc.\n## rates=<VALUE1 VALUE2 ...>
the rates are specified arbitrarily or## then are from a Gamma distribution with alpha=x, currently\n## the alpha value gets lost and
is not recorded in the parmfile## prob-rates=<RATE2 RATE1 ... > These rates can be arbitrary or## generated with gamma-deviated rates and
then are derived## using Laguerre's quadrature, this should get better## results than equal probability methods.\n## autocorrelation=<NO | YES:VALUE> Default is NO\n## autocorrelation makes only sense with rates,\n## VALUE should be >1.0\n## weights=<NO | YES:WEIGHTFILE> The weights are specified## in file called WEIGHTFILE, this assumes that all sites## belong to known
weights, this can be used to weight## portions of the sequence etc.\n## fast-likelihood=<YES | NO> Default is
NO##-----## population-relabel={assignment for each location in the infile}
##-----example is population-relabel={1 2 2}\n## random-subset=number:<:seed>\n## allows to subset the dataset randomly, if number >
sample in population##-----all samples are taken, if number is smaller then the pop sample is shuffled and##-----and the first number samples
are taken.\n##-----the random number seed guarantees that the## same subset is chosen in different
runs\n##-----datatype=BrownianMicrosatelliteData\n##-----include-unknown=NO\n##-----datatype=BM (BROWNIAN MOTION)\n##-----inheritance-scalars=<NO|YES:{values for each locus}>\n##-----these values are multiplied with Theta, for example having##-----two autosomal and a locus on X- and one on Y-chromosome we would give
inheritance-scalars=YES:{1 1 1.33 4.0}\n##-----# this will scale Theta = 4*N*mu\n##-----# We can scale differently:\n##-----inheritance-scalars=YES:{0.25 0.25 0.33
1.00}\n##-----# this will scale Theta = N*mu all is in scale for Y or mtDNA\n##-----the first locus is the reference and the combined estimate has its
inheritance-scalar\n##-----if loci are {mtDNA,nucDNA} then {1.0 0.25} --> Theta=N*mu for all\n##-----inheritance-scalars=NO\n##-----Haplotyping: \n##-----Syntax:
haplotyping=<YES:<report|no-report> | NO >\n##-----If you have diplotype data input two lines per individual marking\n##-----individual names name:other where name must
be on both lines, it will##-----will be used to build the individual database for the haplotyping.\n##-----If you are not interested in the haplotypes, refrain from

```

Perché gedit trova un solo <\n>?

***Documento 1 senza nome**

Salva ≡ - □ ×

VALUE is a ratio between 0 and 1\n# If the value is 0.4 in a 2-population scenario and with 1000000 steps\n# will be each evaluated 125000 times. The second value is the ratio for parameter\n# frequency of haplotype updates.\n# the fourth values is for assignment of individual updates\n# recalculated to do so\n# For example: 1.0 2.0 0.1 0.0 results in 0.32 treeupdates 0.65 parameter\n# bayes-posteriorbins=VALUE VALUE is the number of bins in the posterior distribution histogram for Theta or -posteriormaxtype=< ALL | P99 | MAXP99 | TOTAL >\n# ALL plots the WHOLE prior-parameter range\n# MAXP99 sets all axes from minimum to the range value to\n# the 99% percentile value of EACH parameter\n# TOTAL plots from the minimum prior range value to\n# .le value of EACH parameter\n# bayes-file=<YES:FILENAME|NO>\n# FILENAME is the name of the file that will contain the results for the posterior distribution\n# bayes-allfile=<>YES|TEMP>:INTERVAL:FILENAME|NO>\n# INTERVAL is the interval at which all parameters of the posterior distribution [HUGE]\n# written to file\n# PROPOSAL:\n# bayes-proposals= THETA < SLICE | METROPOLIS >\n# bayes-proposals= MIG < SLICE | METROPOLIS SLICE uses the slice sampler to propose new parameter values\n# METROPOLIS uses the Metropolis-Hastings sampler\n# each parameter group: THETA or MIGration)\n# PRIORS:\n# Priors can be set for each parameter\n# There are several ways to set: a. format for all, c. individual\n# bayes-priors= FORCE <PRIORdistribution priorvalues> # a. all in FORCE\n# bayes-priors= FORCE * *\n# priorvalues> # b. all in FORCE\n# bayes-priors= FORCE from to <PRIORdistribution priorvalues> # c. individual, from and to are population numbers\n# FORCE is one of THETA, MIG, RATE, SPLIT, or SPLITSTD\n# THETA is on size parameters\n# MIG is used for migration rate parameters\n# RATE is used for evolutionary rate differences (use imple)\n# SPLIT is used for mean of the normal distributed population divergence\n# SPLITSTD is used for the standard population divergence\n# PRIORdistribution is one of UNIFORMPRIOR, EXPPRIOR, WEXPRIOR, GAMMAPRIOR, NORMALPRIOR\n# min max delta\n# exppriorvalues: min mean max\n# wexpriorvalues: min mean max delta\n# normalpriorvalues: min mean max std\n# Search OPTIONS\n# long-inc=VALUE\n# VALUE is the number of not recorded\n# long-sample=VALUE\n# VALUE is the number of sampled updates\n# burn-in=VALUE\n# VALUE is the number of updates to beginning\n# auto-tune=<NO | YES>\n# VALUE the target acceptance ratio\n# if value is missing, it is set to :sign=<YES:<FREQ|UNIFORM<:{pop1,pop2,...}>> | NO>\n# YES will assign individuals to populations\n# with '?' as first [FREQ uses past assignment during the MCMC\n# optional list if populations to assign to\n# UNFORM picks a random can be supplied using :{pop1,pop2,...}\n# parameter haplotype timeparam assignment seqerror, ml-alpha\n# nupdatefreq=0.200000 0.200000 0.200000 0.200000 0.100000 0.000000 \nbayes- 0 1500 1500 1500 \nbayes-posteriorbins=TOTAL \nbayes-file=YES:bayesfile_msat_13_pop_27_mag\n\tnbayes-allfile=NO\n\tnbayes-all-postriors=NO\n\tnbayes-SLICE Sampler\n\tnbayes-proposals= MIG SLICE Sampler\n\tnbayes-proposals= DIVERGENCE METROPOLIS-HASTINGS Sampler\n\tnbayes-proposals= DIVERGENCESTD IGS Sampler\n\tnbayes-proposals= GROWTH METROPOLIS-HASTINGS Sampler\n\tnbayes-priors= THETA * * UNIFORMPRIOR: 0.000000 1.00000 0.10000 \nbayes-priors= MIG 0.000000 1000.000000 100.000000 \nbayes-priors= RATE * * UNIFORMPRIOR: 0.000000 1000000000.000000 1000000000.000000 \n#\n# Hyper-prior for all ie parameter of the prior is drawn from a Gamma distribution with mean and alpha\n# for example:\n# bayes-hyperprior=YES:10000:1.0:5.0\n# uses a the mean of the specified prior\n# and and alpha so that this specifies ~Normal\n# \nbayes-hyperpriors=NO\n# nlong-chains=1\n# long-inc=100\n# nlong-n-in=100\n# nauto-tune=YES:0.440000\n# nassign=NO\n# ----- Schemes to ching and/or thermodynamic integration\n# Heating schemes {MCMCMC = MC cubed}\n# Syntax: heating=< NO | <YES | TEMPERATURES\n# NO No heating\n# YES heating using TEMPERATURES\n# ADAPTIVE adaptive heating using start TEMPERATURES [fails SKIP skip that many comparisons, this lengthens the run by SKIP\n# TEMPERATURES { 1.0, temp1, temp2, temp3 .. tempn}\n# YES:1:{1.0, 1.2, 3.0,1000000.0}\n# Heating: swapping chains\n# Syntax: heated-swap=< YES | NO >\n# YES swapping of chains enabled NO swapping of chains disabled\n# Example: heated-swap=YES\n# nheating=YES:1:1.25,1.364,1.5,1.667,1.875,2.143,2.5,3.0,3.75,5.0,7.5,15.0,1000000.0\n# nheated-swap=YES\n# Lengthening chain schemes\n# Syntax: moving-steps=< VALUE frequency is between 0..1\n# moving-steps=NO\n# Convergence statistic [Gelman and Rubin]\n# Syntax: gelman-convergence=< i | NO >\n# NO do not use Gelman's convergence criterium\n# YES use Gelman's convergence criteria between chain i, and PAIRS reports all replicate pairs\n# SUM reports only mean and maxima\n# gelman-convergence=No\n# REPLICATON:\n# Syntax: YES:<VALUE> >\n# NO no replication of run\n# YES replicate run\n# VALUE number between 2 and many, complete .cate=YES:10\n# -----

piero@piero-XPS-9320:~\$ gedit

~/COMPUTER_SCIENCE/AI/parmfile.txt

Perché gedit trova 526 <\n>?

```
0 # Thu Apr 0 08:44:47 2023
1 #
2 # please report problems to Peter Beerli
3 # email: beerli@fsu.edu
4 # http://popgen.sc.fsu.edu/migrate.html
5 #####
6 #
7 #####
8 # General options
9 #####
10 #
11 #####
12 #
13 #####
14 # Interactive or batch job usage
15 #####
16 #
17 # Syntax: menu= < YES | NO >
18 # For batch runs it needs to be set to NO
19 menu=YES
20 #
21 #
22 # Specification of length of names of individuals (default=10)
23 # Syntax: nmlength=<INTEGER between 0 .. 30>
24 nmlength=12
25 #
26 #
27 # If you long runs fails because of timelimits
28 # AND you have specified bayes-allfile=YES....
29 # then you can recover and continue
30 # by setting recover to yes, default is NO
31 # This option fails if your bayesallfile is complete!
32 # At the moment, I have no experience about failure rate etc. [March 30 2015]
33 # recover=<YES | NO>
34 #
35 #####
36 # Data options
37 #####
38 #
39 # Several different main datatypes are possible:
40 # INFINITE ALLELE: usable for electrophoretic markers,
41 # other markers with unknown mutation model
42 # STEPWISE MUTATION: usable for microsatellite data or
43 # other markers with stepwise change
44 # from one allele to another
45 # [singlestep versus multistep model, see micro-submodel option]
46 # FINITE SITES MUTATION: standard DNA/RNA sequence mutation
47 # model, usable for DNA or RNA contiguous
48 # sequences or variable sites only (SNP)
49 #-----
```

parmfile.txt
~/COMPUTER_SCIENCE/AI

Salva - x

Search: \n 1 di 526

The screenshot shows a terminal window on the left and a file editor window on the right. The terminal window displays a command to open a file named 'parmfile.txt' with the gedit text editor. The file editor window shows the contents of 'parmfile.txt'. The search bar at the top of the editor has the regular expression '\n' entered, and the status bar indicates '1 di 526', which means '1 of 526' in Italian. The file contains several lines of configuration options for a software, including settings for names, data types, and mutation models.

Apri



Salva



-

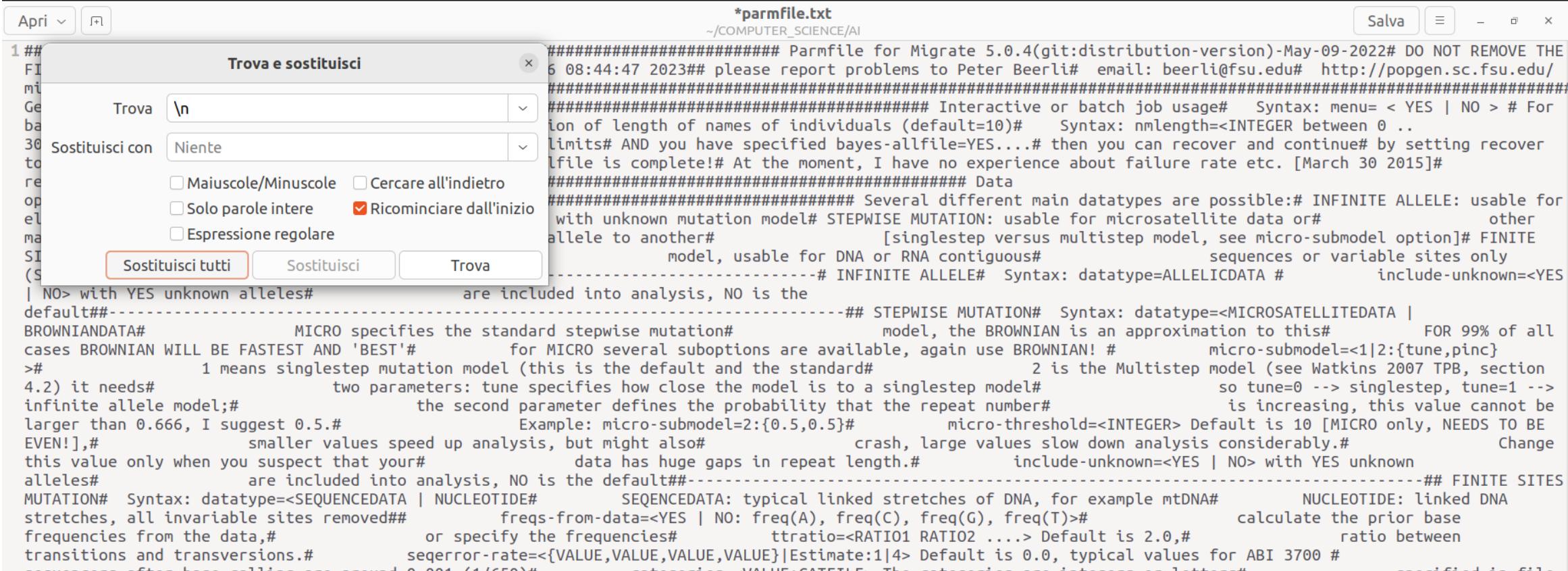


x

parmfile.txt

~/COMPUTER_SCIENCE/AI

```
1#                                         #####
2#                                         Trova e sostituisci
3#                                         May-09-2022
4#     Trova: \n
5#     Sostituisco con: Niente
6#          Maiuscole/Minuscole  Cercare all'indietro
7#          Solo parole intere  Ricominciare dall'inizio
8#          Espressione regolare
9#                                         #####
10#                                         #####
11#                                         #####
12#     Sostituisci tutti  
13#                                         #####
14# General options
15#####
16#
17# Interactive or batch job usage
18# Syntax: menu= < YES | NO >
19# For batch runs it needs to be set to NO
20menu=YES
21#
22# Specification of length of names of individuals (default=10)
23# Syntax: nmlength=<INTEGER between 0 .. 30>
24nmlength=12
25#
26#
27# If you long runs fails because of timelimits
28# AND you have specified bayes-allfile=YES....
29# then you can recover and continue
30# by setting recover to yes, default is NO
31# This option fails if your bayesallfile is complete!
32# At the moment, I have no experience about failure rate etc. [March 30 2015]
33#         recover=<YES | NO>
34#
35#####
36# Data options
37#####
38#
39# Several different main datatypes are possible:
40# INFINITE ALLELE: usable for electrophoretic markers,
41#                     other markers with unknown mutation model
42# STEPWISE MUTATION: usable for microsatellite data or
43#                     other markers with stepwise change
44#                     from one allele to another
45#                     [singlestep versus multistep model, see micro-submodel option]
46# FINITE SITES MUTATION: standard DNA/RNA sequence mutation
47#                     model, usable for DNA or RNA contiguous
48#                     sequences or variable sites only (SNP)
49#-----
```



Da quante righe risulta formato il file di testo `parmfile.txt` dopo l'ultima modifica?

```
1.0# weights=<NO | YES:WEIGHTFILE> The weights are specified#           in file called WEIGHTFILE, this assumes that all sites#   belong
to known weights, this can be used to weight#           portions of the sequence etc.#           fast-likelihood=<YES | NO> Default is
NO#-----#           population-relabel={assignment for each location in the infile}
#           example is population-relabel={1 2 2}#           random-subset=number:<seed>#           allows to subset the dataset randomly, if number >
sample in population#           all samples are taken, if number is smaller then the pop sample is shuffled and#           and the first number samples are
taken.#           the random number seed guarantees that the#           same subset is chosen in different runsdatatype=BrownianMicrosatelliteDatainclude-
unknown=NODatamodel=BM (BROWNIAN MOTION)## inheritance-scalars=<NO|YES:{values for each locus}>#           these values are multiplied with Theta, for example
having#           two autosomal and a locus on X- and one on Y-chromosome we would give #           inheritance-scalars=YES:{1 1 1.33 4.0}#           # this will scale Theta
= 4*N*mu#           # We can scale differently:#           inheritance-scalars=YES:{0.25 0.25 0.33 1.00}#           # this will scale Theta = N*mu all is in scale for Y or
mtDNA#           the first locus is the reference and the combined estimate has its inheritance-scalar#           if loci are {mtDNA,nucDNA} then {1.0 0.25} --> Theta=N*mu
for allinheritance-scalars=NOD## Haplotyping: #           Syntax: haplotyping=<YES:<report|no-report> | NO > #           If you have diplotype data input two lines per
individual marking#           individual names name:other where name must be on both lines, it will#           will be used to build the individual database for the
haplotyping.#           If you are not interested in the haplotypes, refrain from reporting the#           the haplotypes because this will be very time consuming and slows the
programhaplotyping=NOD##           population-relabel={assignment for each location in the infile}#           example is population-relabel={1 2 2}population-
relabel={1, 2, 2, 2, 2, 2, 2, 2, 2, 3, 3, 3}##           random-subset=number:random_numberseed#           allows to subset the dataset randomly, if number > sample in
```

Trova le differenze

Trova le differenze

```
>>> lines = text.splitlines()  
  
>>> lines  
[ '# #####', '# Parmfile for Migrate 5.0.4(git:distribution-version)-May-09-2022', '# DO NOT REMOVE THE  
FIRST TWO LINES!', '#', '# generated automatically on', '# Thu Apr 6 08:44:47 2023',  
'#', '# please report problems to Peter Beerli', '# email: beerli@fsu.edu', '#  
http://popgen.sc.fsu.edu/migrate.html',  
' #####', '#',  
' #####', '# General options',  
' #####', '# Interactive or batch job usage', '# Syntax:
```

<lines> è una list!

```
>>> type(lines)
<class 'list'>
>>> lines[0]
'#####
>>> lines[1]
'# Parmfile for Migrate 5.0.4 (git:distribution-version) -May-09-2022'
>>> lines[2]
'# DO NOT REMOVE THE FIRST TWO LINES!'
>>> lines[3]
'#'
>>> lines[4]
'# generated automatically on'
>>> lines[5]
'# Thu Apr  6 08:44:47 2023'
>>> lines[500]
'heating=YES:1:
{1.0,1.071,1.154,1.25,1.364,1.5,1.667,1.875,2.143,2.5,3.0,3.75,5.0,7.5,15.0,1000000.0}'
>>>
```

Leggere un testo in un oggetto di tipo stringa

```
>>> numlines = 19
>>> chunk = lines[:numlines]
>>> chunk
[ '# #####', '# Parmfile for Migrate 5.0.4(git:distribution-version)-May-09-2022', '# DO NOT REMOVE THE',
FIRST TWO LINES!', '#', '# generated automatically on', '# Thu Apr 6 08:44:47 2023',
 '#', '# please report problems to Peter Beerli', '# email: beerli@fsu.edu', '#
http://popgen.sc.fsu.edu/migrate.html',
 '# #####', '#',
 '# #####', '# General options',
 '# #####', '# Interactive or batch job usage', '# Syntax: menu= < YES | NO >', '# For
batch runs it needs to be set to NO']
>>>
```

parmfile.txt

*Documento 1 senza nome

```
1 ['#' #####', '# Parmfile for Migrate 5.0.4(git:distribution-version)-May-09-2022', '# DO NOT
REMOVE THE FIRST TWO LINES!', '#', '# generated automatically on', '# Thu Apr  6 08:44:47 2023', '#', '# please report problems to Peter Beerli', '# email:
beerli@fsu.edu', '# http://popgen.sc.fsu.edu/migrate.html', '#' #####', '# General options',
'#####', '# Interactive or batch job usage', '# Syntax: menu= < YES | NO > ', '#
For batch runs it needs to be set to NO']
```



parmfile.txt

```
1 ['#' #####', '#'
2 # Parmfile for Migrate 5.0.4(git:distribution-version)-May-09-2022', '#'
3 # DO NOT REMOVE THE FIRST TWO LINES!', '#', '
4 # generated automatically on', '
5 # Thu Apr  6 08:44:47 2023', '#', '
6 # please report problems to Peter Beerli', '
7 # email: beerli@fsu.edu', '
8 # http://popgen.sc.fsu.edu/migrate.html', '#', '
9 # General options', '#', '#', '#', '
10 # Interactive or batch job usage', '
11 # Syntax: menu= < YES | NO > ', '
12 # For batch runs it needs to be set to NO']
```



Leggere un testo in un oggetto di tipo stringa

```
>>> text = open('parmfile.txt').read()
>>> type(text)
<class 'str'>
>>> lines = open('parmfile.txt').readlines()
>>> type(lines)
<class 'list'>
>>> lines[0]
'#####\n'
>>> lines[7]
'# please report problems to Peter Beerli\n'
>>> lines[500]
'heating=YES:1:
{1.0,1.071,1.154,1.25,1.364,1.5,1.667,1.875,2.143,2.5,3.0,3.75,5.0,7.5,15.0,1000000.0}\n'
>>>
```

Common os.path Tools

```
piero@piero-XPS-9320:~$ python3
Python 3.10.12 (main, Feb 4 2025, 14:57:36) [GCC 11.4.0] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>> import os
>>> os.getcwd()
'/home/piero'
>>> os.path.isdir('COMPUTER_SCIENCE')
True
>>> os.path.isdir('COMPUTER_SCIENCE/AI')
True
>>> os.path.isdir('COMPUTER_SCIENCE/AI/PARMFILE')
False
>>>
```

'PARMFILE' è un file o una directory?

```
>>> import dill, os, pickle
>>> name = 'PARMFILE'
>>> def apri(name):
...     if os.path.isdir('COMPUTER_SCIENCE/AI/%s' % name):
...         print('The object %s is a directory' % name)
...
...     else:
...         print('The object %s is not a directory' % name)
...
>>> apri(name)
The object PARMFILE is not a directory
>>> name = 'CARTELLA'
>>> apri(name)
The object CARTELLA is a directory
>>>
```

Cos'è la shell?

Shell: system that reads and runs command-line strings on your computer

Shell command: command-line string that you would normally enter at your computer's shell prompt

Eseguire un comando della shell

```
>>> os.getcwd()
'/home/piero/COMPUTER_SCIENCE/AI'
>>> os.system('ls')
1_Python_PROGRAMMING_01.03.2025_non_eliminare.odp
1_Python_PROGRAMMING_09.03.2025.odp
ALGORITMO_18.01.2022.odt
alimenti_26_febbraio_25.py
alimenti.ods
alimenti.py
blocco_di_testo_last_rows.py
blocco_di_testo_mod.py
blocco_di_testo.py
CARTELLA
Cereale.py
DATA
dati_istogramma.txt
docs-pdf
eleva_a_potenza.py
Farina_di_estrazione.py
Fonte_di_fibra.py
Foraggio.py
...
>>>
```

Home / COMPUTER_SCIENCE / AI				
	Nome	Dimensione	Modifica	
Recenti	CARTELLA	0 oggetti	ieri	★
Preferiti	DATA	5 oggetti	9 feb	★
Home	docs-pdf	35 oggetti	23 gen	★
Documenti	GRAFICI	1 oggetto	11 feb	★
Immagini	_pycache_	32 oggetti	lun	★
Musica	1_Python_PROGRAMMING_01.03.2025_non_eliminare.odp	1,8 MB	1 mar	★
Scaricati	1_Python_PROGRAMMING_09.03.2025.odp	4,8 MB	08:24	★
Video	ALGORITMO_18.01.2022.odt	31,1 kB	27 gen	★
Cestino	alimenti.ods	2,7 MB	1 feb	★
+ Altre posizioni	alimenti.py	72,7 kB	26 feb	★
	alimenti_26_febbraio_25.py	72,7 kB	26 feb	★
	blocco_di_testo.py	592 byte	lun	★
	blocco_di_testo_last_rows.py	673 byte	mer	★
	blocco_di_testo_mod.py	592 byte	lun	★
	Cereale.py	790 byte	2 feb	★
	dati_istogramma.txt	3,1 MB	1 mar	★
	eleva_a_potenza.py	632 byte	14 feb	★
	Farina_di_estrazione.py	1,2 kB	2 feb	★
	Fonte_di_fibra.py	2,7 kB	3 feb	★
	Foraggio.py	2,4 kB	1 feb	★

Eseguire un comando della shell

```
>>> os.system('lsb_release -a')
No LSB modules are available.
Distributor ID: Ubuntu
Description: Ubuntu 22.04.5 LTS
Release: 22.04
Codename: jammy
0
>>>
```

Formatting Expression Basics

```
>>> 'These are %d %s bones' % (2, 'animal')
```

```
'These are 2 animal bones'
```

```
>>>
```

When applied to strings, the `%` operator provides a simple way to format values as strings according to a format definition, coding multiple substitutions all at once, instead of building and concatenating parts individually.

To format strings:

- To the left `%` operator, provide one or more conversion targets, each of which starts with a `%` (e.g., `%d`)
- To the right `%` operator, provide the object (or objects, embedded in a **tuple**) that you want Python to insert into the format string on the left in place of the conversion target (or targets)

Formatting Expression Basics

```
>>> import math  
>>> 'The base of the natural logarithms is %f' % math.e  
'The base of the natural logarithms is 2.718281828459045'  
>>>
```

Il programma blocco_di_testo.py

```
"""
print a chunk of text
"""

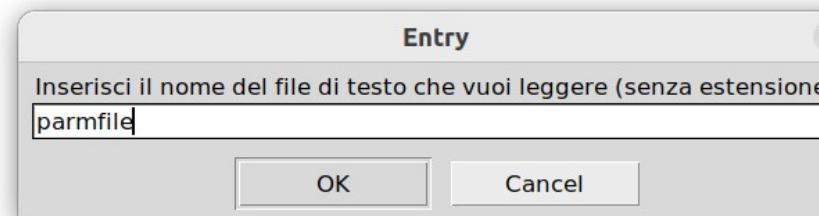
import os
from tkinter.simpledialog import askstring
from tkinter.simpledialog import askinteger
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
filename = askstring('Entry', 'Inserisci il nome del file di testo che vuoi leggere (senza estensione)')
numlines = askinteger('Entry', 'Inserisci il numero di righe del blocco')
with open('%s.txt' % filename, 'r') as file:
    text = file.read()

def more(text, numlines):
    lines = text.splitlines()
    chunk = lines[:numlines]
    print(chunk)

blocco = more(text, numlines)
print(blocco)
```

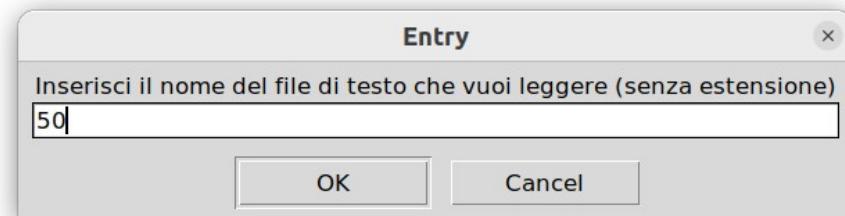
Il programma blocco_di_testo.py

```
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI$ python3 blocco_di_testo.py
```



Il programma blocco_di_testo.py

```
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 blocco_di_testo.py
```



Il programma blocco_di_testo.py

Il programma blocco_di_testo.py

ESERCIZIO: modificare il codice sorgente <blocco_di_testo.py> affinchè il programma visualizzi in output tutto il testo del file **tranne le prime <numlines> righe**

Il programma blocco_di_testo_mod.py

```
"""
print a chunk of text
"""

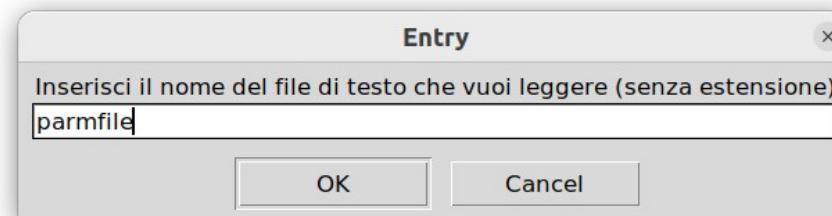
import os
from tkinter.simpledialog import askstring
from tkinter.simpledialog import askinteger
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
filename = askstring('Entry', 'Inserisci il nome del file di testo che vuoi leggere (senza estensione)')
numlines = askinteger('Entry', 'Inserisci il numero di righe del blocco')
with open('%s.txt' % filename, 'r') as file:
    text = file.read()

def more(text, numlines):
    lines = text.splitlines()
    chunk = lines[numlines:]
    print(chunk)

blocco = more(text, numlines)
print(blocco)
```

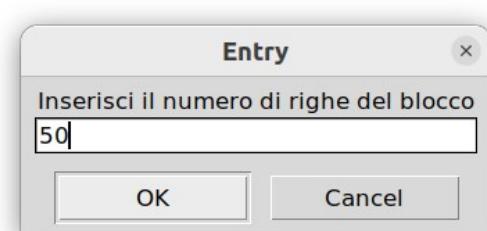
Il programma blocco_di_testo_mod.py

```
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 blocco_di_testo_mod.py
```



Il programma blocco_di_testo_mod.py

```
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI$ python3 blocco_di_testo_mod.py
```



Il programma blocco_di_testo_mod.py

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 blocco_di_testo_mod.py
['# Syntax: datatype=ALLELICDATA ', '#           include-unknown=<YES | NO> with YES unknown
alleles', '#           are included into analysis, NO is the default', '#',
'#-----
...
tive heating using start TEMPERATURES [fails sometimes!!]', '#           SKIP skip that many
comparisons, this lengthens the run by SKIP', '#           TEMPERATURES { 1.0, templ, temp2,
temp3 .. tempn}', '#           Example: heating=YES:1:{1.0, 1.2, 3.0,1000000.0}', '# Heating: swapping
chains', '#           Syntax: heated-swap=< YES | NO >', '#           YES swapping of chains enabled
[DEFAULT]', '#           NO swapping of chains disabled', '#           Example: heated-swap=YES',
'heating=YES:1:
{1.0,1.071,1.154,1.25,1.364,1.5,1.667,1.875,2.143,2.5,3.0,3.75,5.0,7.5,15.0,1000000.0}', 'heated-
swap=YES', '#', '# Lengthening chain schemes', '#           Syntax: moving-steps=< NO | YES:VALUE>', '#
VALUE frequency is between 0..1', 'moving-steps=NO', '#', '#', '#           Convergence statistic
[Gelman and Rubin]', '#           Syntax: gelman-convergence=< YES:Pairs|Summary | NO >', '#           NO
do not use Gelman's convergence criterium", "#           YES use Gelman's convergence criteria
between chain i, and i-1", '#           PAIRS reports all replicate pairs', '#
SUM reports only mean and maxima', 'gelman-convergence=No', '#', '#           REPLICATON:', '#
Syntax: replicate=< NO | YES:<VALUE> >', '#           NO no replication of run', '#           YES
replicate run', '#           VALUE number between 2 and many, complete replicates',
'replicate=YES:10', '#',
'#-----', '#', 'end']
None
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$
```

Leggere un testo in un oggetto di tipo stringa

```
>>> lines[1:19]
['# Parmfile for Migrate 5.0.4(git:distribution-version)-May-09-2022', '# DO NOT REMOVE
THE FIRST TWO LINES!', '#', '# generated automatically on', '# Thu Apr 6 08:44:47
2023', '#', '# please report problems to Peter Beerli', '# email: beerli@fsu.edu', '#
http://popgen.sc.fsu.edu/migrate.html',
'#####', '#',
'#####', '# General options',
'#####', '#',
'#', '# Interactive or batch job usage', '# Syntax: menu= < YES | NO >', '# For
batch runs it needs to be set to NO']
>>>
```

Leggere un testo in un oggetto di tipo stringa

```
>>> righe_successive = lines[numlines:]
>>> righe_successive
YES  heating using TEMPERATURES', '#          ADAPTIVE adaptive heating using start
TEMPERATURES [fails sometimes!!]', '#'          SKIP skip that many comparisons, this
lengthens the run by SKIP', '#'          TEMPERATURES { 1.0, templ, temp2, temp3 ..
tempn}', '#'          Example: heating=YES:1:{1.0, 1.2, 3.0,1000000.0}', '#' Heating:
swapping chains', '#'          Syntax: heated-swap=< YES | NO >', '#'          YES swapping of
chains enabled [DEFAULT]', '#'          NO swapping of chains disabled', '#'
Example: heated-swap=YES', 'heating=YES:1:
{1.0,1.071,1.154,1.25,1.364,1.5,1.667,1.875,2.143,2.5,3.0,3.75,5.0,7.5,15.0,1000000.0}'
, 'heated-swap=YES', '#', '# Lengthening chain schemes', '#'          Syntax: moving-steps=<
NO | YES:VALUE>', '#'          VALUE frequency is between 0..1', 'moving-steps=NO', '#',
'#', '# Convergence statistic [Gelman and Rubin]', '#'          Syntax: gelman-
convergence=< YES:Pairs|Summary | NO >', "#          NO          do not use Gelman's
convergence criterium", "#"          YES          use Gelman's convergence criteria between
chain i, and i-1", '#'          PAIRS reports all replicate pairs', '#'
SUM          reports only mean and maxima', 'gelman-convergence=No', '#', '#          REPLICATON:',
'#          Syntax: replicate=< NO | YES:<VALUE> >', '#'          NO          no replication of run',
'#          YES          replicate run', '#'          VALUE          number between 2 and many,
complete replicates', 'replicate=YES:10', '#',
'-----',
'##', 'end']
>>>
```

Il programma blocco_di_testo.py

ESERCIZIO: modificare il codice sorgente <blocco_di_testo.py> affinchè il programma visualizzi in output **le ultime <numlines> righe**

SUGGERIMENTO:

```
>>> nrows = len(list(open("parmfile.txt")))
>>> nrows
527
>>>
```

```
470 long-chains=1
479 long-inc=100
480 long-sample=10000
481 burn-in=100
482 auto-tune=YES:0.440000
483 assign=NO
484 #
485 #-----
486 # Schemes to improve MCMC searching and/or thermodynamic integration
487 #
488 # Heating schemes {MCMCMC = MC cubed}
489 #   Syntax: heating=< NO | <YES | ADAPTIVE>:SKIP:TEMPERATURES
490 #     NO      No heating
491 #     YES     heating using TEMPERATURES
492 #     ADAPTIVE adaptive heating using start TEMPERATURES [fails sometimes!!]
493 #     SKIP    skip that many comparisons, this lengthens the run by SKIP
494 #           TEMPERATURES { 1.0, temp1, temp2, temp3 .. tempn}
495 #   Example: heating=YES:1:{1.0, 1.2, 3.0,1000000.0}
496 # Heating: swapping chains
497 #   Syntax: heated-swap=< YES | NO >
498 #     YES    swapping of chains enabled [DEFAULT]
499 #     NO     swapping of chains disabled
500 #   Example: heated-swap=YES
501 heating=YES:1:{1.0,1.071,1.154,1.25,1.364,1.5,1.667,1.875,2.143,2.5,3.0,3.75,5.0,7.5,15.0,1000000.0}
502 heated-swap=YES
503 #
504 # Lengthening chain schemes
505 #   Syntax: moving-steps=< NO | YES:VALUE>
506 #     VALUE   frequency is between 0..1
507 moving-steps=NO
508 #
509 #
510 # Convergence statistic [Gelman and Rubin]
511 #   Syntax: gelman-convergence=< YES:Pairs|Summary | NO >
512 #     NO      do not use Gelman's convergence criterium
513 #     YES     use Gelman's convergence criteria between chain i, and i-1
514 #           PAIRS reports all replicate pairs
515 #           SUM    reports only mean and maxima
516 gelman-convergence=No
517 #
518 # REPLICATON:
519 #   Syntax: replicate=< NO | YES:<VALUE> >
520 #     NO      no replication of run
521 #     YES     replicate run
522 #           VALUE   number between 2 and many, complete replicates
523 replicate=YES:10
524 #
525 #-----
526 #
527 end
```

Il programma blocco_di_testo_last_rows.py

```
"""
print a chunk of text
"""

import os
from tkinter.simpledialog import askstring
from tkinter.simpledialog import askinteger
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
filename = askstring('Entry', 'Inserisci il nome del file di testo che vuoi leggere (senza estensione)')
numlines = askinteger('Entry', 'Inserisci il numero di righe del blocco')
nrows = len(list(open('%s.txt' % filename)))
lines_2_skip = nrows - numlines
with open('%s.txt' % filename, 'r') as file:
    text = file.read()

def more(text, numlines):
    lines = text.splitlines()
    chunk = lines[lines_2_skip:]
    print(chunk)

blocco = more(text, numlines)
print(blocco)
```

Il programma blocco_di_testo_last_rows.py

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 blocco_di_testo_last_rows.py
['#      REPLICATON:', '#      Syntax: replicate=< NO | YES:<VALUE> >', '#      NO      no
replication of run', '#      YES      replicate run', '#      VALUE      number
between 2 and many, complete replicates', 'replicate=YES:10', '#',
'-----',
'#', 'end']
None
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$
```

Il programma more.py

```
"""
split and interactively page a string or file of text
"""

import os
from tkinter.simpledialog import askinteger, askstring
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
filename = askstring('Entry', 'Inserisci il nome del file di testo che vuoi leggere (senza estensione)')
numlines = askinteger('Entry', 'Inserisci il numero di righe del blocco')
with open('%s.txt' % filename, 'r') as file:
    text = file.read()

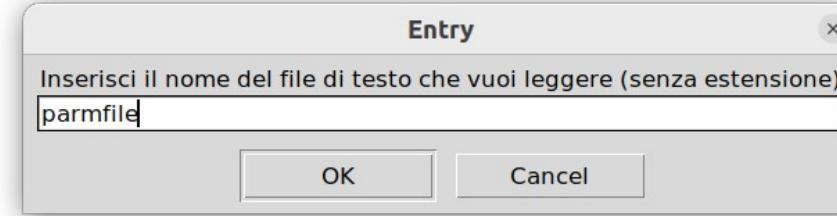
def more(text, numlines):
    lines = text.splitlines()
    while lines:
        chunk = lines[:numlines]
        lines = lines[numlines:]
        for line in chunk: print(line)
        if lines and input('More?') not in ['y', 'Y']: break

more(text, numlines)
```

Il programma more.py

```
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~
piero@piero-XPS-9320: ~
piero@piero-XPS-9320: ~

piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 more.py
```

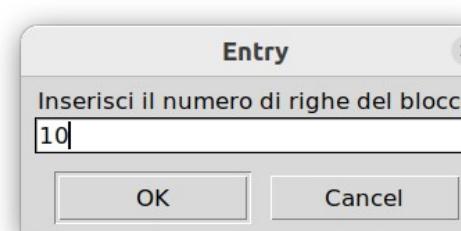


The terminal window shows the command `python3 more.py` being run. A modal dialog box titled "Entry" is displayed, prompting the user to enter the name of the text file to read (without extension). The input field contains "parmfile".

Il programma more.py

```
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI
piero@piero-XPS-9320: ~
piero@piero-XPS-9320: ~
piero@piero-XPS-9320: ~
```

piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI\$ python3 more.py



The terminal window has three tabs open, all showing the same path: piero@piero-XPS-9320: ~/COMPUTER_SCIENCE/AI. The third tab is active and shows the command being run. A modal dialog box titled "Entry" is overlaid on the terminal, prompting the user to enter the number of lines to block. The input field contains "10".

Il programma more.py

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 more.py
#####
# Parmfile for Migrate 5.0.4 (git:distribution-version) -May-09-2022
# DO NOT REMOVE THE FIRST TWO LINES!
#
# generated automatically on
# Thu Apr  6 08:44:47 2023
#
# please report problems to Peter Beerli
# email: beerli@fsu.edu
# http://popgen.sc.fsu.edu/migrate.html
More?
```

Il programma more.py step by step

```
"""
split and interactively page a string or file of text
"""
```

```
# un altro modo per inserire un commento, anche su più righe
```

Il programma more.py step by step

```
"""
split and interactively page a string or file of text
"""

import os
from tkinter.simpledialog import askinteger, askstring

# importiamo il modulo os (operating system) e le funzioni necessarie per creare una
# finestra di dialogo che chieda all'utente di inserire un numero intero, ossia da quante
# righe ogni blocco debba essere formato (askinteger ) ed una finestra di dialogo che
# consenta all'utente di inserire il nome del file (askstring); quest'ultimo, infatti, è una
# stringa di caratteri
```

Il programma more.py step by step

```
"""
split and interactively page a string or file of text
"""

import os
from tkinter.simpledialog import askinteger, askstring
user = os.getlogin()

# usiamo l'attributo getlogin() del modulo os per ottenere il nome dell'utente e lo
# salviamo nella variabile user
```

```
>>> dir(os)
['CLD_CONTINUED', 'CLD_DUMPED', 'CLD_EXITED', 'CLD_KILLED', 'CLD_STOPPED', 'CLD_TRAPPED', 'DirEntry', 'EFD_CLOEXEC', 'EFD_NONBLOCK',
'EFD_SEMAPHORE', 'EX_CANTCREAT', 'EX_CONFIG', 'EX_DATAERR', 'EX_IOERR', 'EX_NOHOST', 'EX_NOINPUT', 'EX_NOPERM', 'EX_NOUSER', 'EX_OK',
'EX_OSERR', 'EX_OFILE', 'EX_PROTOCOL', 'EX_SOFTWARE', 'EX_TEMPFAIL', 'EX_UNAVAILABLE', 'EX_USAGE', 'F_LOCK', 'F_OK', 'F_TEST',
'F_TLOCK', 'F_ULOCK', 'GRND_NONBLOCK', 'GRND_RANDOM', 'GenericAlias', 'MFD_ALLOW_SEALING', 'MFD_CLOEXEC', 'MFD_HUGETLB',
'MFD_HUGE_16GB', 'MFD_HUGE_16MB', 'MFD_HUGE_1GB', 'MFD_HUGE_1MB', 'MFD_HUGE_256MB', 'MFD_HUGE_2GB', 'MFD_HUGE_2MB', 'MFD_HUGE_32MB',
'MFD_HUGE_512KB', 'MFD_HUGE_512MB', 'MFD_HUGE_64KB', 'MFD_HUGE_8MB', 'MFD_HUGE_MASK', 'MFD_HUGE_SHIFT', 'Mapping', 'MutableMapping',
'NGROUPS_MAX', 'O_ACCMODE', 'O_APPEND', 'O_ASYNC', 'O_CLOEXEC', 'O_CREAT', 'O_DIRECT', 'O_DIRECTORY', 'O_DSYNC', 'O_EXCL', 'O_FSYNC',
'O_LARGEFILE', 'O_NDELAY', 'O_NOATIME', 'O_NOCTTY', 'O_NOFOLLOW', 'O_NONBLOCK', 'O_PATH', 'O_RDONLY', 'O_RDWR', 'O_RSYNC', 'O_SYNC',
'O_TMPFILE', 'O_TRUNC', 'O_WRONLY', 'POSIX_FADV_DONTNEED', 'POSIX_FADV_NOREUSE', 'POSIX_FADV_NORMAL', 'POSIX_FADV_RANDOM',
'POSIX_FADV_SEQUENTIAL', 'POSIX_FADV_WILLNEED', 'POSIX_SPAWN_CLOSE', 'POSIX_SPAWN_DUP2', 'POSIX_SPAWN_OPEN', 'PRIO_PGRP',
'PRIO_PROCESS', 'PRIO_USER', 'P_ALL', 'P_NOWAIT', 'P_NOWAITO', 'P_PGID', 'P_PID', 'P_PIDFD', 'P_WAIT', 'PathLike', 'RTLD_DEEPBIND',
'RTLD_GLOBAL', 'RTLD_LAZY', 'RTLD_LOCAL', 'RTLD_NODELETE', 'RTLD_NOLOAD', 'RTLD_NOW', 'RWF_APPEND', 'RWF_DSYNC', 'RWF_HIPRI',
'RWF_NOWAIT', 'RWF_SYNC', 'R_OK', 'SCHED_BATCH', 'SCHED_FIFO', 'SCHED_IDLE', 'SCHED_OTHER', 'SCHED_RESET_ON_FORK', 'SCHED_RR',
'SEEK_CUR', 'SEEK_DATA', 'SEEK_END', 'SEEK_HOLE', 'SEEK_SET', 'SPICE_F_MORE', 'SPICE_F_MOVE', 'SPICE_F_NONBLOCK', 'ST_APPEND',
'ST_MANDLOCK', 'ST_NOATIME', 'ST_NODEV', 'ST_NODIRATIME', 'ST_NOEXEC', 'ST_NOSUID', 'ST_RDONLY', 'ST_RELATIME', 'ST_SYNCHRONOUS',
'ST_WRITE', 'TMP_MAX', 'WCONTINUED', 'WCOREDUMP', 'WEXITED', 'WEXITSTATUS', 'WIFCONTINUED', 'WIFEXITED', 'WIFSIGNALED', 'WIFSTOPPED',
'WNOHANG', 'WNOWAIT', 'WSTOPPED', 'WTERMSIG', 'WUNTRACED', 'W_OK', 'XATTR_CREATE', 'XATTR_REPLACE', 'XATTR_SIZE_MAX',
'X_OK', '__Environ', '__all__', '__builtins__', '__cached__', '__doc__', '__file__', '__loader__', '__name__', '__package__',
['__spec__', '__check_methods__', '__execvpe__', '__exists__', '__exit__', '__fspath__', '__fwalk__', '__get_exports_list__', '__spawnvef__', '__walk__',
 '__wrap_close__', 'abc', 'abort', 'access', 'altsep', 'chdir', 'chmod', 'chown', 'chroot', 'close', 'closerange', 'confstr',
 'confstr_names', 'copy_file_range', 'cpu_count', 'ctermid', 'curdir', 'defpath', 'device_encoding', 'devnull', 'dup', 'dup2',
 'environ', 'environb', 'error', 'eventfd', 'eventfd_read', 'eventfd_write', 'execl', 'execl', 'execlp', 'execle', 'execv', 'execve',
 'execvp', 'execvpe', 'extsep', 'fchdir', 'fchmod', 'fchown', 'fdatasync', 'fdopen', 'fork', 'forkpty', 'fpathconf', 'fsdecode',
 'fsencode', 'fspath', 'fstat', 'fstatvfs', 'fsync', 'ftruncate', 'fwalk', 'get_blocking', 'get_exec_path', 'get_inheritable',
 'get_terminal_size', 'getcwd', 'getcwdb', 'getegid', 'getenv', 'getenvb', 'geteuid', 'getgid', 'getgroupplist', 'getgroups',
 'getloadavg', 'getlogin', 'getpgid', 'getpgrp', 'getpid', 'getppid', 'getpriority', 'getrandom', 'getresgid', 'getresuid', 'getsid',
 'getuid', 'getxattr', 'initgroups', 'isatty', 'kill', 'killpg', 'lchown', 'linesep', 'link', 'listdir', 'listxattr', 'lockf', 'lseek',
 'lstat', 'major', 'makedev', 'makedirs', 'memfd_create', 'minor', 'mkdir', 'mkfifo', 'mknod', 'name', 'nice', 'open', 'openpty',
 'pardir', 'path', 'pathconf', 'pathconf_names', 'pathsep', 'pidfd_open', 'pipe', 'pipe2', 'popen', 'posix_fadvise', 'posix_fallocate',
 'posix_spawn', 'posix_spawnnp', 'pread', 'preadv', 'putenv', 'pwrite', 'pwritev', 'read', 'readlink', 'readv', 'register_at_fork',
 'remove', 'removedirs', 'removexattr', 'rename', 'renames', 'replace', 'rmdir', 'scandir', 'sched_get_priority_max',
 'sched_get_priority_min', 'sched_getaffinity', 'sched_getparam', 'sched_getscheduler', 'sched_param', 'sched_rr_get_interval',
 'sched_setaffinity', 'sched_setparam', 'sched_setscheduler', 'sched_yield', 'sendfile', 'sep', 'set_blocking', 'set_inheritable',
 'setegid', 'seteuid', 'setgid', 'setgroups', 'setpgid', 'setpgrp', 'setpriority', 'setregid', 'setresgid', 'setresuid', 'setreuid',
 'setsid', 'setuid', 'setxattr', 'spawnl', 'spawnle', 'spawnlp', 'spawnlpe', 'spawnnv', 'spawnve', 'spawnvp', 'spawnvpe', 'splice', 'st',
 'stat', 'stat_result', 'statvfs', 'statvfs_result', 'strerror', 'supports_bytes_environ', 'supports_dir_fd', 'supports_effective_ids',
 'supports_fd', 'supports_follow_symlinks', 'symlink', 'sync', 'sys', 'sysconf', 'sysconf_names', 'system', 'tcgetpgrp', 'tcsetpgrp',
 'terminal_size', 'times', 'times_result', 'truncate', 'ttynname', 'umask', 'uname', 'uname_result', 'unlink', 'unsetenv', 'urandom',
 'utime', 'wait', 'wait3', 'wait4', 'waitid', 'waitid_result', 'waitpid', 'waitstatus_to_exitcode', 'walk', 'write', 'writev']
>>>
```

Il modulo os di Python

Contiene funzioni utili ad interagire con il sistema operativo. Qualche esempio:

```
>>> import os
>>> info = os.uname()
>>> type(info)
<class 'posix.uname_result'>
>>> info
posix.uname_result(sysname='Linux', nodename='piero-XPS-9320', release='6.8.0-52-
generic', version='#53~22.04.1-Ubuntu SMP PREEMPT_DYNAMIC Wed Jan 15 19:18:46 UTC 2',
machine='x86_64')
>>> info = "{0}".format(info)
>>> type(info)
<class 'str'>
>>> info
"posix.uname_result(sysname='Linux', nodename='piero-XPS-9320', release='6.8.0-52-
generic', version='#53~22.04.1-Ubuntu SMP PREEMPT_DYNAMIC Wed Jan 15 19:18:46 UTC 2',
machine='x86_64')"
>>> with open("uname.txt", "w") as text_file:
...     text_file.write("%s" % info)
...
184
>>>
```

Il programma more.py step by step

```
"""
split and interactively page a string or file of text
"""

import os
from tkinter.simpledialog import askinteger, askstring
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
# impostiamo la dir di lavoro usando l'operatore di formattazione %s
```

Il programma more.py step by step

```
"""
split and interactively page a string or file of text
"""

import os
from tkinter.simpledialog import askinteger, askstring
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
filename = askstring('Entry', 'Inserisci il nome del file di testo che vuoi leggere  
(senza estensione)')
# creiamo una finestra di dialogo per chiedere all'utente il nome del file di testo da
# leggere
# il nome del file viene salvato nella variabile, di tipo stringa, <filename>
```

Il programma more.py step by step

```
"""
split and interactively page a string or file of text
"""

import os
from tkinter.simpledialog import askinteger, askstring
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
filename = askstring('Entry', 'Inserisci il nome del file di testo che vuoi leggere  
(senza estensione)')
numlines = askinteger('Entry', 'Inserisci il numero di righe del blocco')
# creiamo una finestra di dialogo per chiedere all'utente da quante righe dev'essere
# formato ogni blocco di testo
# tale numero viene salvato nella variabile numerica (di tipo intero) <numlines>
```

Il programma more.py step by step

```
with open('%s.txt' % filename, 'r') as file:  
    text = file.read()
```

leggiamo il file di testo, usando l'operatore di formattazione <%s>, a cui viene sostituito
il nome del file, memorizzato nella variabile di tipo stringa <filename>
il contenuto testuale del file viene letto nella variabile di tipo stringa <text>

Il programma more.py step by step

```
with open('%s.txt' % filename, 'r') as file:  
    text = file.read()  
  
def more(text, numlines):  
# definiamo la funzione <more>, che ha come argomenti:  
# 1) la stringa <text>, che rappresenta il testo del file  
# 2) la variabile numerica <numlines>, il cui valore è il numero di righe di ogni blocco di  
#   testo
```

Il programma more.py step by step

```
with open('%s.txt' % filename, 'r') as file:  
    text = file.read()  
  
def more(text, numlines):  
    lines = text.splitlines()  
# suddividiamo il testo nelle singole righe, creando la list di righe <lines>
```

Il programma more.py step by step

```
with open('%s.txt' % filename, 'r') as file:  
    text = file.read()  
  
def more(text, numlines):  
    lines = text.splitlines()  
    while lines:  
        chunk = lines[:numlines]  
        lines = lines[numlines:]  
        # finché non si sia arrivati alla fine della list di righe <lines>, prendi le prime <numlines>  
        # righe e memorizzale nella nuova list <chunk>  
        # <:numlines> significa "le prime numlines righe", per es. le prime 50 righe del file  
        # (dalla riga 0 alla riga 49)  
        # la list <lines> viene aggiornata: le vengono assegnate le righe dalla 50 all'ultima  
  
        # nel ciclo successivo, a <chunk> vengono assegnate le righe dalla 50 alla 99  
        # la list <lines> viene nuovamente aggiornata: le vengono assegnate le righe dalla 100  
        # all'ultima
```

Il programma more.py step by step

```
with open('%s.txt' % filename, 'r') as file:  
    text = file.read()  
  
def more(text, numlines):  
    lines = text.splitlines()  
    while lines:  
        chunk = lines[:numlines]  
        lines = lines[numlines:]  
        for line in chunk: print(line)  
# stampa (invia all'output standard, lo schermo) le righe del blocco
```

Il programma more.py step by step

```
with open('%s.txt' % filename, 'r') as file:  
    text = file.read()  
  
def more(text, numlines):  
    lines = text.splitlines()  
    while lines:  
        chunk = lines[:numlines]  
        lines = lines[numlines:]  
        for line in chunk: print(line)  
        if lines and input('More?') not in ['y', 'Y']: break  
# se ci sono ancora righe ma alla domanda <More?> l'utente non risponde sì, interrompi  
# l'esecuzione del programma
```

Il programma more.py step by step

```
with open('%s.txt' % filename, 'r') as file:  
    text = file.read()  
  
def more(text, numlines):  
    lines = text.splitlines()  
    while lines:  
        chunk = lines[:numlines]  
        lines = lines[numlines:]  
        for line in chunk: print(line)  
        if lines and input('More?') not in ['y', 'Y']: break  
  
more(text, numlines)  
# chiamata della funzione <more>
```

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[nascondi]



☰ Successione di Fibonacci

文 39 lingue ▾

Voce Discussione

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**Questa voce o sezione sull'argomento matematica è ritenuta da controllare.****Motivo:** È stato inserito parecchio materiale mal formattato, con notazioni diverse rispetto al resto della voce, alcuni passi sono poco contestualizzati e di altri non si coglie la rilevanzaPartecipa alla [discussione](#) e/o [correggi](#) la voce. Segui i suggerimenti del progetto di riferimento.

In [matematica](#), la **successione di Fibonacci** (detta anche **successione aurea**) è una successione di numeri interi in cui ciascun numero è la somma dei due precedenti, eccetto i primi due che sono, per definizione, 0 e 1.^[1] Questa successione, indicata con F_n o con $\text{Fib}(n)$, è [definita ricorsivamente](#): partendo dai primi due elementi, $F_0 = 0$ e $F_1 = 1$, ogni altro elemento della successione sarà dato dalla relazione:

$$F_n = F_{n-1} + F_{n-2}.$$

Gli elementi F_n sono anche detti *numeri di Fibonacci*. I primi termini della successione di Fibonacci, che prende il nome dal matematico pisano del XIII secolo [Leonardo Fibonacci](#), sono: 0, 1, 1, 2, 3, 5, 8, 13, 21, 34, 55, 89, 144, 233, 377, 610, 987, ...

The while statement

```
>>> # Fibonacci series:  
>>> # the sum of two elements defines the next  
>>> a, b = 0, 1
```

- The first line contains a multiple assignment: the variables a and b simultaneously get the new values 0 and 1

```
>>> a  
0  
>>> b  
1  
>>> while a < 10:  
...     print(a)  
...     a, b = b, a+b  
...  
0  
1  
1  
2  
3  
5  
8  
>>>
```

The **while** loop executes as long as the condition (here: $a < 10$) remains true. In Python, like in C, any non-zero integer value is true; zero is false. The condition may also be a string or list value, in fact any sequence; anything with a non-zero length is true, empty sequences are false. The test used in the example is a simple comparison. The standard comparison operators are written the same as in C: $<$ (less than), $>$ (greater than), $==$ (equal to), \leq (less than or equal to), \geq (greater than or equal to) and \neq (not equal to).

Fibonacci series

```
>>> a, b = 0, 1
>>> a
0
>>> b
1
>>> a, b = b, a+b
>>> a
1
>>> b
1
>>> a, b = b, a+b
>>> a
1
>>> b
2
>>> a, b = b, a+b
>>> a
2
>>> b
3
>>>
```

Fibonacci series

```
>>> a, b = b, a+b  
>>> a  
3  
>>> b  
5  
>>> a, b = b, a+b  
>>> a  
5  
>>> b  
8  
>>> a, b = b, a+b  
>>> a  
8  
>>> b  
13  
>>> a, b = b, a+b  
>>> a  
13  
>>> b  
21  
>>>
```

```
>>> a, b = 0, 1  
>>> while a < 22:  
...     print(a)  
...     a, b = b, a+b  
...  
0  
1  
1  
2  
3  
5  
8  
13  
21  
>>>
```

The `print()` function writes the value of the argument(s) it is given.

The body of the loop is indented: indentation is Python's way of grouping statements. At the interactive prompt, **you have to type a tab for each indented line**. In practice you will prepare more complicated input for Python with a text editor; all decent text editors have an auto-indent facility. When a compound statement is entered interactively, it must be followed by a blank line to indicate completion (since the parser cannot guess when you have typed the last line). Note that each line within a basic block must be indented by the same amount.

The `print()` function

The `print()` function handles multiple arguments, **floating-point quantities**, and strings. Strings are printed without quotes, and a space is inserted between items, so you can format things nicely, like this:

```
>>> i = 256 ** 2
>>> i
65536
>>> print('The value of i is', i)
The value of i is 65536
>>> a, b = 0, 1
>>> while a < 1000:
...     print(a, end=', ')
...     a, b = b, a+b
...
0,1,1,2,3,5,8,13,21,34,55,89,144,233,377,610,987,>>>
>>>
```

The keyword argument `end` can be used to avoid the newline after the output, or end the output with a different string:

Il programma alimenti.py

```
piero@piero-XPS-9320:~$ cd Scaricati/
piero@piero-XPS-9320:~/Scaricati$ wget
https://github.com/pierorivoira/COMPUTER-SCIENCE/raw/refs/heads/main/ALIMENTI.tar.gz
--2025-05-15 10:35:28-- https://github.com/pierorivoira/COMPUTER-SCIENCE/raw/refs/heads/main/
ALIMENTI.tar.gz
Risoluzione di github.com (github.com) ... 140.82.121.4
Connessione a github.com (github.com) |140.82.121.4| :443... connesso.
Richiesta HTTP inviata, in attesa di risposta... 302 Found
Posizione: https://raw.githubusercontent.com/pierorivoira/COMPUTER-SCIENCE/refs/heads/main/
ALIMENTI.tar.gz [segue]
--2025-05-15 10:35:28-- https://raw.githubusercontent.com/pierorivoira/COMPUTER-SCIENCE/refs/
heads/main/ALIMENTI.tar.gz
Risoluzione di raw.githubusercontent.com (raw.githubusercontent.com) ... 185.199.109.133,
185.199.111.133, 185.199.108.133, ...
Connessione a raw.githubusercontent.com (raw.githubusercontent.com) |185.199.109.133| :443...
connesso.
Richiesta HTTP inviata, in attesa di risposta... 200 OK
Lunghezza: 16456 (16K) [application/octet-stream]
Salvataggio in: 'ALIMENTI.tar.gz'

ALIMENTI.tar.gz      100%[=====] 16,07K --.-KB/s    in 0,008s

2025-05-15 10:35:29 (2,05 MB/s) - 'ALIMENTI.tar.gz' salvato [16456/16456]

piero@piero-XPS-9320:~/Scaricati$
```

Il programma alimenti.py

```
piero@piero-XPS-9320:~/Scaricati$ tar -xvzf ALIMENTI.tar.gz
ALIMENTI/
ALIMENTI/Leguminosa.py
ALIMENTI/Foraggio.py
ALIMENTI/Sottoprodotto.py
ALIMENTI/Farina_di_estrazione.py
ALIMENTI/Fonte_di_fibra.py
ALIMENTI/Cereale.py
ALIMENTI/importa_fieno_prato_stabile_primo_taglio.py
ALIMENTI/alimenti.py
piero@piero-XPS-9320:~/Scaricati$
```

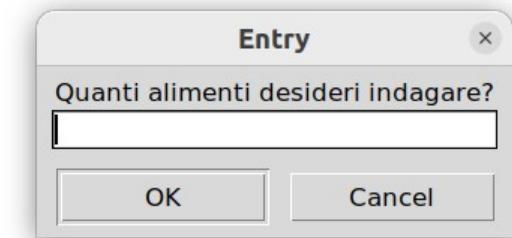
Il programma alimenti.py

```
piero@piero-XPS-9320:~/Scaricati$ cd  
piero@piero-XPS-9320:~$ pwd  
/home/piero  
piero@piero-XPS-9320:~$ python3 Scaricati/ALIMENTI/alimenti.py
```

Il programma alimenti.py

*
*
* * * * *

agrumi_pastazzo_secco
birra_lievito
calcio_saponi
cocco_pannello
frumento_tenero_germe
latte_magro_polvere
latte_siero
manioca
melasso_barbabietola
melasso_canna
patate_essiccate
proteina_patata
riso_gemma
riso_grana_verde
riso_pula_commerciale
riso_pula_verGINE
riso_rottura



Escape Sequences Represent Special Characters

- Sono caratteri speciali che consentono di inserire in una stringa caratteri che non possono essere digitati facilmente con la tastiera
- Il carattere < \ >, ed uno o più caratteri che lo seguono nella sequenza, viene sostituito da un *singolo* carattere nell'oggetto di tipo stringa risultante
- La combinazione di escape specifica il numero binario corrispondente a quel determinato carattere

```
>>> s = "piero\ninsegna\tall'Istituto\v Agrario\a\\"
>>> s
"piero\ninsegna\tall'Istituto\x0b Agrario\x07\\"
>>> print(s)
piero
insegna all'Istituto
                    Agrario\
>>>
```

Escape Sequences Represent Special Characters

\a bell

\n new line

\t horizontal tab

\v vertical tab

ESERCIZIO:

Scrivere un programma che disegni un quadrato di asterischi (10 per lato)

Escape Sequences Represent Special Characters

SOLUZIONE:

```
# script3.py
l = '*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *'
print('*' * 10)
print(l)
print('*' * 10)
```

Escape Sequences Represent Special Characters

SOLUZIONE:

```
# script3.py
l = '*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *\n*\t\t *'
print('*' * 10)
print(l)
print('*' * 10)
```

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 script3.py
```

A grid of 100 black asterisks arranged in a perfect square. Each row contains exactly 10 asterisks, and there are 10 such rows. The asterisks are evenly spaced both horizontally and vertically.

ESERCIZIO: **scrivere un programma che disegni un triangolo rettangolo**

Suggerimento:

```
print('*' * 10)  
# traccia la base
```

SOLUZIONE 1: triangolo pieno

```
print('*')
print('*' * 2)
print('*' * 3)
print('*' * 4)
print('*' * 5)
print('*' * 6)
print('*' * 7)
print('*' * 8)
print('*' * 9)
print('*' * 10)
```

SOLUZIONE 1: triangolo pieno

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3 disegna_triangolo_pieno.py
*
* *
* * *
* * * *
* * * * *
* * * * * *
* * * * * * *
* * * * * * * *
* * * * * * * * *
* * * * * * * * * *
```

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$
```

SOLUZIONE 2: triangolo vuoto

```
print('*')
print('* *')
print('*   *')
print('*       *')
print('*           *')
print('*               *')
print('*                     *')
print('*                           *')
print('*                                 *')
print('*                                     *')
print('*   *   *   *   *   *   *   *   *   *   *')
```

SOLUZIONE 2: triangolo vuoto

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3  
disegna_triangolo_vuoto_1.py  
*  
* *  
*   *  
*     *  
*       *  
*         *  
*           *  
*             *  
*               *  
*                 *  
*                   *  
*                     *  
* * * * * * * * * * *  
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$
```

SOLUZIONE 3: triangolo vuoto (due sole righe di codice)

Files binari

Contengono stringhe di bytes (*binary data*) che possono essere creati ed estratti con il modulo `struct`

I dati in Python

“Oggetti” (*objects*), porzioni di memoria alle quali sono associati valori ed insiemi di operazioni

Il numero pi

```
>>> import math  
>>> math.pi  
3.141592653589793  
>>>
```

Pi (π) is the **ratio of a circle's circumference (c) to its diameter (d)**:

$$\pi = c/d$$

- This ratio is always the same for any circle.
- Pi is an irrational number, which means it can't be expressed as a simple fraction. Therefore, pi has an infinite number of decimal places, but it can be approximated as 22/7, or 3.141.
- The pi value is given to fifteen decimal places in Python (the number of digits provided depends on the underlying C compiler); Python prints the first fifteen digits by default, and `math.pi` always returns a float value.

Il numero pi

```
>>> import math
>>> r = 3
>>> circumference = 2 * math.pi * r
>>> f"Circumference of a Circle = 2 * {math.pi:.4} * {r} = {circumference:.4}"
'Circumference of a Circle = 2 * 3.14159 * 3 = 18.85'
>>> f"Circumference of a Circle = 2 * {math.pi:.6} * {r} = {circumference:.4}"
'Circumference of a Circle = 2 * 3.141592 * 3 = 18.85'
>>> r = 5
>>> area = math.pi * r ** 2
>>> f"Area of a Circle = {math.pi:.4} * {r}^2 = {area:.4}"
'Area of a Circle = 3.14159 * 5^2 = 78.54'
>>>
```

Il numero tau

```
>>> import math  
>>> math.tau  
6.283185307179586  
>>>
```

Il numero magico <e> (numero di Euler)

```
>>> import math  
>>> math.e  
2.718281828459045  
>>>
```

Il numero magico <e>

```
> 10*9*8*7*6*5*4*3*2*1  
[1] 3628800  
> factorial(10)  
[1] 3628800  
> Euler = function(n, z)  
+ {  
+   result = NULL  
+   numbers = seq(1:n)  
+   for (i in numbers)  
+   {  
+     result[i] = (z^i)/factorial(i)  
+   }  
+   return(1 + sum(result))  
+ }
```

Esempio:

```
> Euler(100,10)  
[1] 22026.47  
> exp(10)  
[1] 22026.47
```

Esercizio: per quale valore di z si ottiene e?

```
> Euler(100,?)
```

Per $z = 10$:

$$\begin{aligned} e^z &= 1 + z/1! + z^2/2! + z^3/3! + z^4/4! + \dots \cong \\ e^{10} &= 1 + 10/1! + 10^2/2! + 10^3/3! + 10^4/4! + \dots \cong \\ &\cong 22026.47 \end{aligned}$$

Il numero magico <e>

```
> 10*9*8*7*6*5*4*3*2*1  
[1] 3628800  
> factorial(10)  
[1] 3628800  
> Euler = function(n, z)  
+ {  
+   result = NULL  
+   numbers = seq(1:n)  
+   for (i in numbers)  
+   {  
+     result[i] = (z^i)/factorial(i)  
+   }  
+   return(1 + sum(result))  
+ }
```



```
> Euler(100,1)  
[1] 2.718282
```

Per $z = 1$:

$$e = \frac{1}{0!} + \frac{1}{1!} + \frac{1}{2!} + \frac{1}{3!} + \frac{1}{4!} + \dots \cong 2.718282$$

Per $z = 10$:

$$e^z = 1 + z/1! + z^2/2! + z^3/3! + z^4/4! + \dots \cong$$

$$e^{10} = 1 + 10/1! + 10^2/2! + 10^3/3! + 10^4/4! + \dots \cong \\ \cong 22026.47$$

Il numero magico <e>

```
> 10*9*8*7*6*5*4*3*2*1  
[1] 3628800  
> factorial(10)  
[1] 3628800  
> Euler = function(n, z)  
+ {  
+   result = NULL  
+   numbers = seq(1:n)  
+   for (i in numbers)  
+   {  
+     result[i] = (z^i)/factorial(i)  
+   }  
+   return(1 + sum(result))  
+ }  
  
> Euler(100,1)  
[1] 2.718282
```

Per $z = 1$:

$$e = \frac{1}{0!} + \frac{1}{1!} + \frac{1}{2!} + \frac{1}{3!} + \frac{1}{4!} + \dots \cong 2.718282$$

Per $z = 10$:

$$e^z = z^0/0! + z^1/1! + z^2/2! + z^3/3! + z^4/4! + \dots \cong$$

$$e^{10} = 1 + 10/1! + 10^2/2! + 10^3/3! + 10^4/4! + \dots \cong \\ \cong 22026.47$$

Per $z < 1$:

$$e^z \cong 1 + z$$

Es.

se $z = 0.1$

$$e^{0.1} \cong 1 + 0.1 \cong 1.1$$

```
> exp(0.1)
```

```
[1] 1.105171
```

```
> Euler(10,0.1)
```

```
[1] 1.105171
```

Il numero magico <e>

```
>>> import math
>>> math.factorial(10)
3628800
>>> somma = []
>>> for i in range(1, 100):
...     result = 1 / math.factorial(i)
...     somma.append(result)
...     output = 1 + sum(somma)
...
>>> output
2.7182818284590455
>>> math.e
2.718281828459045
>>>
```

Esercizio: modificare la funzione in modo da non dover aggiungere <1> al risultato

Il numero magico <e>

```
>>> import math
>>> math.factorial(10)
3628800
>>> somma = []
>>> for i in range(0, 100):
...     result = 1 / math.factorial(i)
...     somma.append(result)
...     output = sum(somma)
...
>>> output
2.7182818284590455
>>> math.e
2.718281828459045
>>>
```

Il numero magico <e>

```
>>> import math
>>> z = 10
>>> n = 100
>>> somma = []
>>> for i in range(n):
...     result = z**i / math.factorial(i)
...     somma.append(result)
...     output = sum(somma)
```

```
...
>>> output
```

22026.46579480671

```
>>> math.exp(10)
```

22026.465794806718

Quindi...

```
>>> for i in range(1,10):  
...     print(i)  
...  
1  
2  
3  
4  
5  
6  
7  
8  
9  
>>>
```

Quindi...

```
>>> for i in range(0,10):  
...     print(i)  
...  
0  
1  
2  
3  
4  
5  
6  
7  
8  
9  
>>>
```

Quindi...

```
>>> for i in range(10):  
...     print(i)  
...  
0  
1  
2  
3  
4  
5  
6  
7  
8  
9  
>>>
```

Il numero magico <e>

```
>>> import math
>>> def eleva_a_potenza(n, z):
...     somma = []
...     for i in range(n):
...         result = z**i / math.factorial(i)
...         somma.append(result)
...     output = sum(somma)
...     return output
...
>>> eleva_a_potenza(100,10)
22026.46579480671
>>>
```

Il programma eleva_a_potenza.py

```
import math
from tkinter.simpledialog import askfloat
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare (es. 100)')
z = askfloat('Entry', "Inserisci l'esponente")
print('La somma sarà effettuata su %d termini' % n)
print('La base dei logaritmi naturali %f sarà elevata alla %f-esima potenza' %
      (math.e, z))

def eleva_a_potenza(n, z):
    somma = []
    for i in range(n):
        result = z**i / math.factorial(i)
        somma.append(result)
    output = sum(somma)
    return output

output = eleva_a_potenza(n, z)
print('Il risultato è %f' % output)
```

Rappresentazione dei numeri in virgola mobile

$$13.25_{10} = \mathbf{1101.01}_2$$

$$1*2^3 + 1*2^2 + 0*2^1 + 1*2^0 + 0*2^{-1} + 1*2^{-2} = 8 + 4 + 1 + 0.25 = 13.25$$

Mantissa Esponente, in base 10, della forma normalizzata
 $\mathbf{1101.01}_2 = \mathbf{1.10101}_2 \cdot \mathbf{2^3}$

spostare la virgola di 3 posizioni verso sinistra significa dividere per 2^3
dividiamo e moltiplichiamo per 2^3 “normalizzando il numero”

calcoliamo l'esponente sommando 127 all'esponente della forma normalizzata:

$$(3+127)_{10} = \mathbf{130}_{10} = \mathbf{10000010}_2$$

$$1*2^7 + 1*2^1 = 128 + 2 = 130$$

```
>>> print(bin(130))
```

```
0b10000010
```

```
>>>
```

Rappresentazione dei numeri in virgola mobile: single precision

	SEGNO	ESPOENTE	MANTISSA	
	0	10000010	1010100000000000000000000	
bit	1	8	23	32

Il bit di segno è definito pari a:

- 0 per valori ≥ 0
- 1 per valori ≤ 0
- La mantissa è in forma normalizzata 1.xxxxx
- Essendo quell'1 sempre presente, solo la parte frazionaria del numero è memorizzata
- L'1 omesso viene detto bit nascosto (hidden bit)
- Abbiamo, così, un bit in più di precisione (23 bit memorizzati + 1 nascosto = 24 bit effettivi)

Il programma tartaglia.py

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare') n=1
N = n + 3
print('Il programma restituisce la riga del Triangolo di Tartaglia formata da
%d numeri' % N)
La riga del triangolo sarà formata da 4 numeri
sequenza_iniziale = [1, 2, 1]
unità = 1

for j in range(n): Ogni sequenza inizia con <1>
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
    sequenza_nuova.append(unità)
    sequenza_iniziale = sequenza_nuova

print(sequenza_nuova)
print(len(sequenza_nuova))
```

i assume prima il valore <0> poi il valore <1>
j può assumere solo il valore <0>

sequenza_nuova = [1]

Per j=0:

Per i = 0:

sequenza_iniziale[0] = 1
sequenza_iniziale[1] = 2
sequenza_iniziale[0]+sequenza_iniziale[1]=3
:sequenza_nuova=[1,3]

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3
Python 3.10.12 (main, Feb 4 2025, 14:57:36) [GCC 11.4.0] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>> n=1
>>> for j in range(n):
...     print(j)
...
0
>>>
```

Il programma tartaglia.py

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare') n=1
N = n + 3
print('Il programma restituisce la riga del Triangolo di Tartaglia formata da
%d numeri' % N)
sequenza_iniziale = [1,2,1]
unità = 1

for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
    sequenza_nuova.append(unità)
    sequenza_iniziale = sequenza_nuova

print(sequenza_nuova)
print(len(sequenza_nuova))
```

i assume prima il valore <0> poi il valore <1>
j può assumere solo il valore <0>

sequenza_nuova=[1,3]

Per j=0:

Per i = 1:

sequenza_iniziale[1] = 2

sequenza_iniziale[2] = 1

sequenza_iniziale[1]+sequenza_iniziale[2]=3

:sequenza_nuova=[1,3,3]

Il programma tartaglia.py

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare') n=1
N = n + 3
print('Il programma restituisce la riga del Triangolo di Tartaglia formata da
%d numeri' % N)
sequenza_iniziale = [1,2,1]
unità = 1

for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
sequenza_nuova.append(unità) Ogni sequenza finisce con <1>
sequenza_iniziale = sequenza_nuova

print(sequenza_nuova)
print(len(sequenza_nuova))
```

i assume prima il valore <0> poi il valore <1>
j può assumere solo il valore <0>
sequenza_iniziale=[1,3,3,1]

sequenza_nuova=[1,3,3,1]

Avendo esaurito i possibili valori di i, esco dal for annidato
Aggiungo un <1> finale alla sequenza nuova
Aggiorno la sequenza iniziale
Esco anche dal for esterno
Stampo la sequenza 1 3 3 1

```
piero@piero-XPS-9320:~/COMPUTER_SCIENCE/AI$ python3
Python 3.10.12 (main, Feb 4 2025, 14:57:36) [GCC 11.4.0] on linux
Type "help", "copyright", "credits" or "license" for more information.
>>> sequenza_iniziale=[1,3,3,1]
>>> len(sequenza_iniziale)
4
>>> for i in range(len(sequenza_iniziale)-1):
...     print(i)
...
0
1
2
>>>
```

Il programma tartaglia.py

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare') n=2
N = n + 3
print('Il programma restituisce la riga del Triangolo di Tartaglia formata da
%d numeri' % N)
sequenza_iniziale = [1,2,1]
unità = 1

for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
sequenza_nuova.append(unità) Ogni sequenza finisce con <1>
sequenza_iniziale = sequenza_nuova

print(sequenza_nuova)
print(len(sequenza_nuova))
```

i assume prima il valore <0> poi il valore <1> poi il valore <2>
j assume prima il valore <0> poi il valore <1>
sequenza_iniziale=[1,3,3,1]
Per j=1:
Per i = 0:
sequenza_iniziale[0] = 1
sequenza_iniziale[1] = 3
sequenza_iniziale[0]+sequenza_iniziale[1]=4
sequenza_nuova=[1,4]
Avendo esaurito i possibili valori di i, esco dal for annidato
Aggiungo un <1> finale alla sequenza nuova
Aggiorno la sequenza iniziale
Se n=2, j può assumere anche il valore <1>
Non posso uscire dal for esterno

Il programma tartaglia.py

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare') n=2
N = n + 3
print('Il programma restituisce la riga del Triangolo di Tartaglia formata da
%d numeri' % N)

sequenza_iniziale = [1,2,1]
unità = 1

for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
sequenza_nuova.append(unità) Ogni sequenza finisce con <1>
sequenza_iniziale = sequenza_nuova

print(sequenza_nuova)
print(len(sequenza_nuova))
```

i assume prima il valore <0> poi il valore <1> poi il valore <2>
sequenza_iniziale=[1,3,3,1]

Per j=1:

Per i = 1:

sequenza_iniziale[1] = 3

sequenza_iniziale[2] = 3

sequenza_iniziale[1]+sequenza_iniziale[2]=6

sequenza_nuova=[1,4,6]

Avendo esaurito i possibili valori di i, esco dal for annidato

Aggiungo un <1> finale alla sequenza nuova

Aggiorno la sequenza iniziale

Se n=2, j può assumere anche il valore <1>

Non posso uscire dal for esterno

Il programma tartaglia.py

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare') n=2
N = n + 3
print('Il programma restituisce la riga del Triangolo di Tartaglia formata da
%d numeri' % N)

sequenza_iniziale = [1,2,1]
unità = 1

for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
sequenza_nuova.append(unità) Ogni sequenza finisce con <1>
sequenza_iniziale = sequenza_nuova

print(sequenza_nuova)
print(len(sequenza_nuova))
```

i assume prima il valore <0> poi il valore <1> poi il valore <2>
sequenza_iniziale=[1,3,3,1]

Per j=1:

Per i = 2:

sequenza_iniziale[2] = 3
sequenza_iniziale[3] = 1
sequenza_iniziale[2]+sequenza_iniziale[3]=4
sequenza_nuova=[1,4,6,4]

Avendo esaurito i possibili valori di i, esco dal for annidato
sequenza_nuova=[1,4,6,4,1]

Aggiungo un <1> finale alla sequenza nuova

Aggiorno la sequenza iniziale

Avendo esaurito I possibili valori di j, esco dal for esterno

ESERCIZIO:

Modificare il programma <tartaglia.py> affinché stampi in output l'intero triangolo di Tartaglia

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare')
N = n + 3
print('Il programma restituisce la riga del Triangolo di Tartaglia formata da %d numeri' % N)

sequenza_iniziale = [1,2,1]
unità = 1

for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
    sequenza_nuova.append(unità)
    sequenza_iniziale = sequenza_nuova

print(sequenza_nuova)
```

SOLUZIONE 1:

Modificare il programma <tartaglia.py> affinché stampi in output l'intero triangolo di Tartaglia

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare')
N = n + 1
print('Il programma restituisce il Triangolo di Tartaglia formata da %d righe' % N)
triangolo = []
sequenza_iniziale = [1,2,1]
unità = 1

print('[1, 2, 1]')

for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
    sequenza_nuova.append(unità)
    sequenza_iniziale = sequenza_nuova
print(sequenza_nuova)
```

SOLUZIONE 2:

Modificare il programma <tartaglia.py> affinché stampi in output l'intero triangolo di Tartaglia

```
from tkinter.simpledialog import askinteger
n = askinteger('Entry', 'Inserisci il numero di termini da sommare')
N = n + 1
print('Il programma restituisce il Triangolo di Tartaglia formata da %d righe' % N)
triangolo = []
sequenza_iniziale = [1,2,1]
unità = 1
for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
    sequenza_nuova.append(unità)
    sequenza_iniziale = sequenza_nuova
    triangolo.append(sequenza_nuova)
print('\n')
print('[1, 2, 1]')
print('\n')
for k in range(len(triangolo)):
    print(triangolo[k])
    print('\n')
```

Il modulo tartaglia_triangolo_modulo.py

```
from tkinter.simpledialog import askinteger
# n = askinteger('Entry', 'Inserisci il numero di termini da sommare')
n = 97
N = n + 3
print('Il programma restituisce la riga del Triangolo di Tartaglia formata da %d numeri' % N)
sequenza_iniziale = [1, 2, 1]
triangolo = []
unità = 1

for j in range(n):
    sequenza_nuova = [1]
    for i in range(len(sequenza_iniziale)-1):
        sequenza_nuova.append(sequenza_iniziale[i]+sequenza_iniziale[i+1])
    sequenza_nuova.append(unità)
    sequenza_iniziale = sequenza_nuova
    triangolo.append(sequenza_nuova)
```

Il modulo tartaglia_triangolo_modulo.py

```
>>> from tartaglia_triangolo_modulo import triangolo
```

Il programma restituisce la riga del Triangolo di Tartaglia formata da 100 numeri

```
>>> triangolo[0]
```

```
[1, 3, 3, 1]
```

```
>>> triangolo[1]
```

```
[1, 4, 6, 4, 1]
```

```
>>> triangolo[10]
```

```
[1, 13, 78, 286, 715, 1287, 1716, 1716, 1287, 715, 286, 78, 13, 1]
```

```
>>> triangolo[37]
```

```
[1, 40, 780, 9880, 91390, 658008, 3838380, 18643560, 76904685, 273438880,  
847660528, 2311801440, 5586853480, 12033222880, 23206929840, 40225345056,  
62852101650, 88732378800, 113380261800, 131282408400, 137846528820,  
131282408400, 113380261800, 88732378800, 62852101650, 40225345056,  
23206929840, 12033222880, 5586853480, 2311801440, 847660528, 273438880,  
76904685, 18643560, 3838380, 658008, 91390, 9880, 780, 40, 1]
```

```
>>>
```

L'effetto additivo dei fattori genetici ed ambientali

gene normale A -> effetto fenotipico = 8 p = 0,5

allele mutante A' -> effetto fenotipico = 4 q = 0,5

omozigoti AA -> valore fenotipico = 16 F = 0,25

omozigoti A'A' -> valore fenotipico = 8 F = 0,25

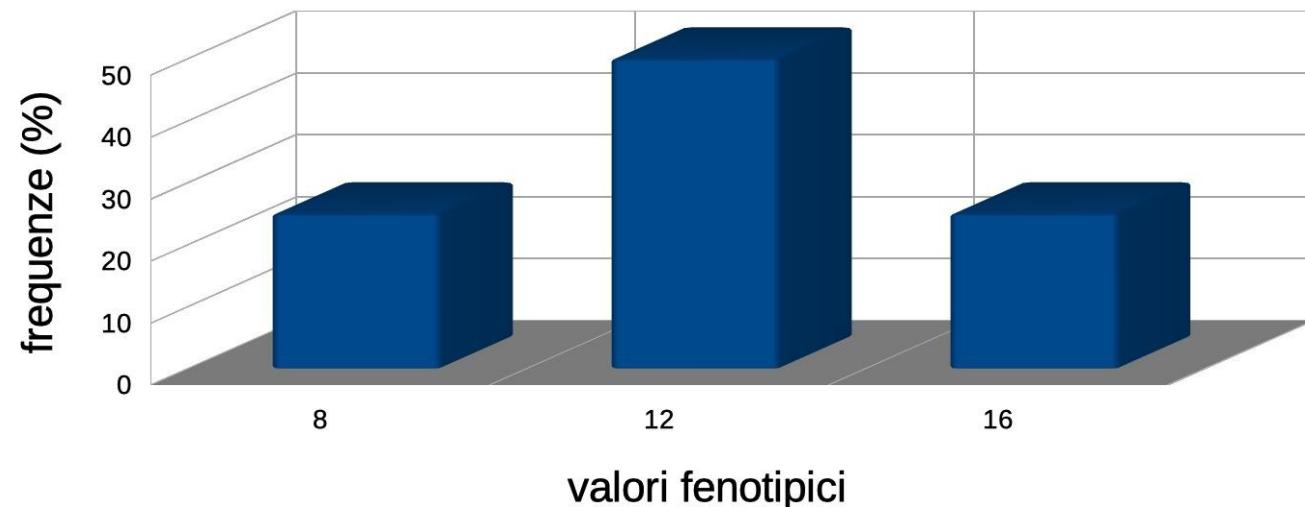
eterozigoti AA' -> valore fenotipico = 12 F = 0,25

eterozigoti A'A -> valore fenotipico = 12 F = 0,25

L'effetto additivo dei fattori genetici ed ambientali

CLASSE GENOTIPICA	VALORE FENOTIPICO	FREQUENZA
AA	16	1/4 = 25%
AA' - A'A	12	2/4 = 50%
A'A'	8	1/4 = 25%

DISTRIBUZIONE DEI VALORI FENOTIPICI CON 1 COPPIA ALLELICA



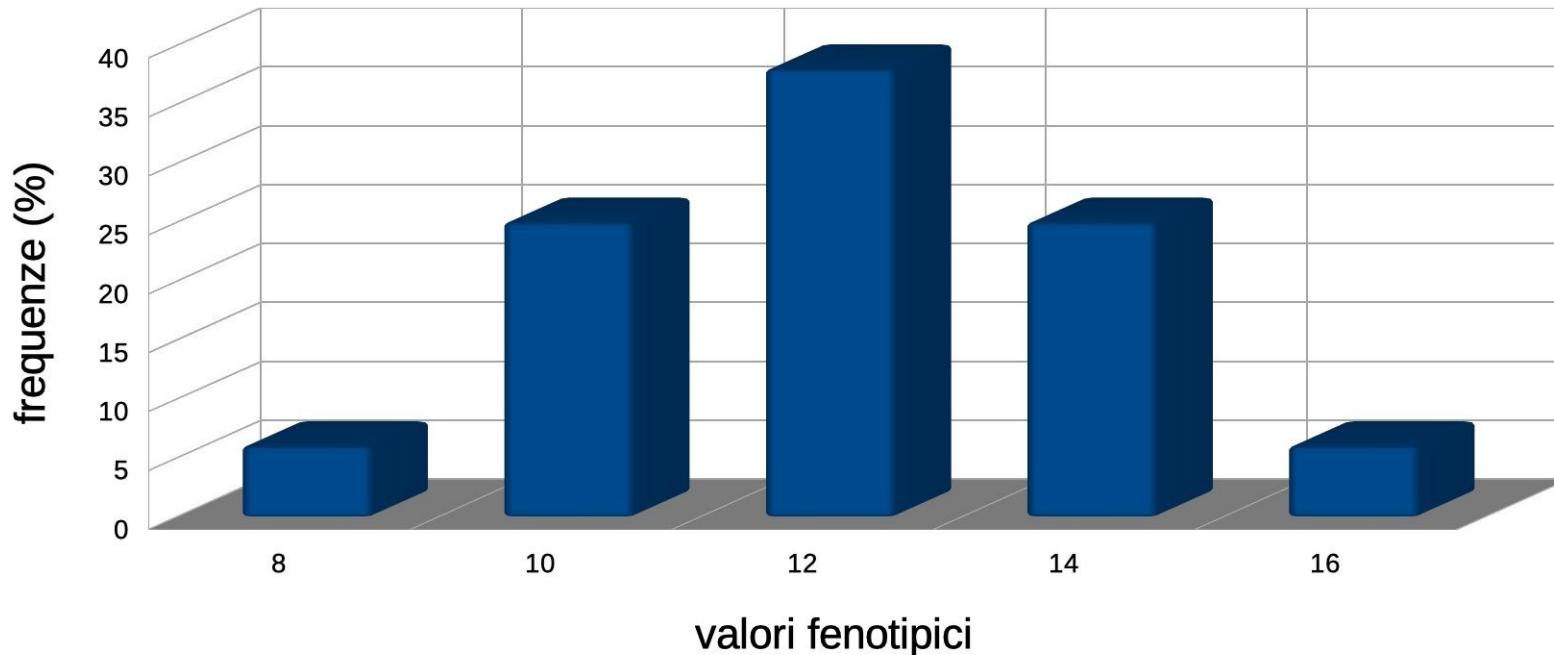
Due loci

Se, a parità di altre condizioni, si considerano **due copie di geni**, A-A' e B-B', dove gli alleli "normali" A e B hanno effetto 4 e gli alleli "mutanti" A' e B' effetto 2, le classi genotipiche e i relativi valori fenotipici saranno:

CLASSE GENOTIPICA	VALORE FENOTIPICO	FREQUENZA
AABB	16	1/16 = 6%
AABB' - AAB'B - AA'BB - A'ABB	14	4/16 = 25%
AAB'B' - AA'BB' - AA'B'B - A'ABB' - A'AB'B - A'A'BB	12	6/16 = 38%
A'A'BB' - A'A'B'B - AA'B'B - A'AB'B'	10	4/16 = 25%
A'A'B'B'	8	1/16 = 6%

Due loci

DISTRIBUZIONE DEI VALORI FENOTIPICI CON 2 COPPIE ALLELICHE



Valori e frequenze dei possibili genotipi nel caso in cui un carattere quantitativo è controllato da due/loci («A» e «B»)

Tre loci

Aumentando ulteriormente il numero di coppie alleliche interessate, aumenta in numero delle classi di valori ma diminuiscono le differenze fra i valori delle varie classi

Se si considerano tre coppie di geni, A-A', B-B' e C-C', dove gli alleli «normali» A, B e C hanno effetto 2 e gli alleli «mutanti» A', B' e C' effetto 1, le classi genotipiche e i relativi valori fenotipici saranno:

Tre loci

Quali sono i valori fenotipici intermedi?

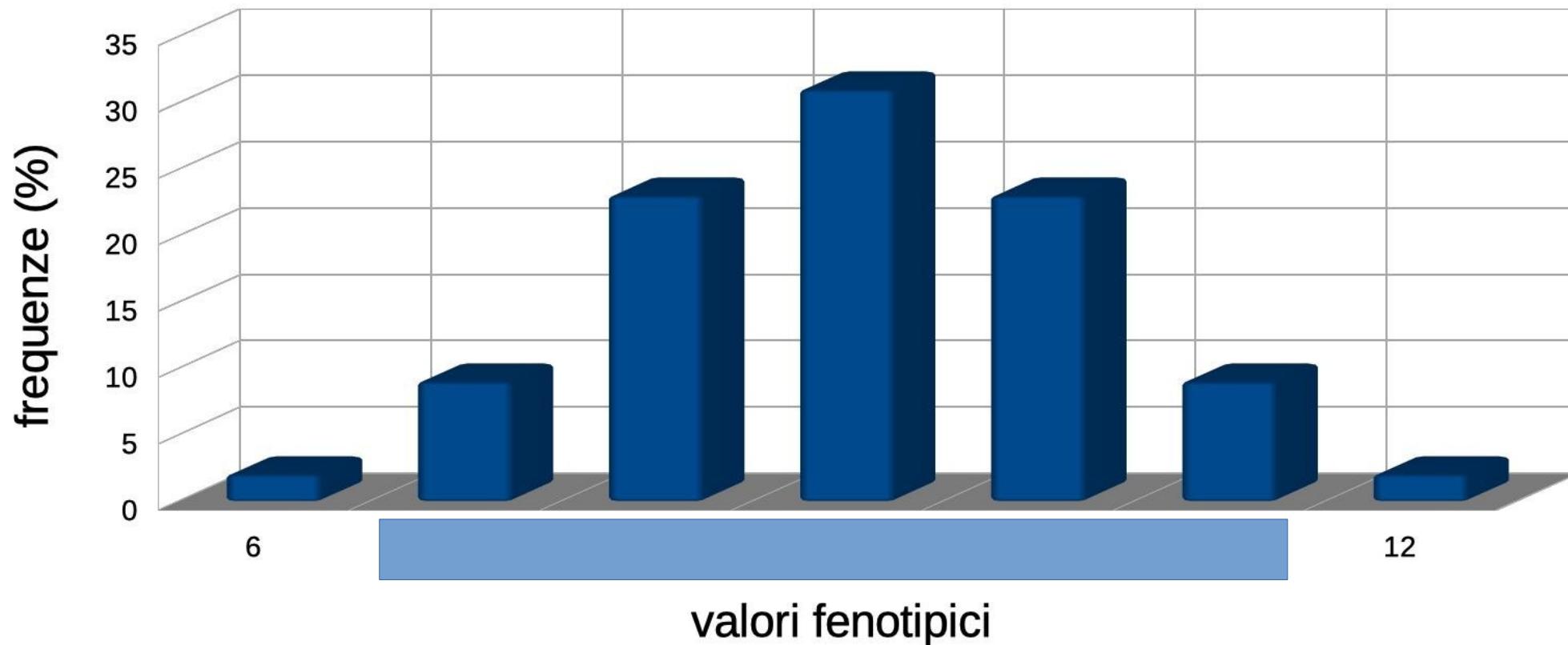
CLASSE GENOTIPICA	VALORE FENOTIPICO	FREQUENZA
AABBCC	12	1/64 = 2%
AABBCC' – AABBC'C – AABB'CC AAB'BCC – AA'BBCC – A'ABBCC		6/64 = 9%
AABBC'C' – AABB'CC' – AAB'BCC' AA'BBCC' – A'ABBCC' – AABB'C'C AAB'BC'C – AA'BBC'C – A'ABC'C AAB'B'CC – AA'BB'CC – A'ABB'CC AA'B'BCC – A'AB'BCC – A'A'BBCC		15/64 = 23%
AABB'C'C' – AAB'BC'C' – AAB'B'CC' AAB'B'C'C – AA'BBC'C' – AA'BB'CC' AA'B'BCC' – AA'BB'C'C – AA'B'BC'C AA'B'B'CC – A'ABBC'C' – A'ABB'CC' A'AB'BCC' – A'ABB'C'C – A'AB'BC'C A'AB'B'CC – A'A'B'BCC – A'A'BB'CC, A'ABBC'C – A'A'BBCC'		20/64 = 31%
AAB'B'C'C' – AA'BB'C'C' – A'ABB'C'C' A'ABBC'C' – AA'B'BC'C' – A'AB'BC'C' A'A'B'BCC' – AA'B'B'CC' – A'AB'B'CC' A'A'B'BC'C – AA'B'B'C'C – A'AB'B'C'C A'A'B'B'CC – A'A'BB'CC' – A'A'BB'C'C		15/64 = 23%
AA'B'B'C'C' – A'AB'B'C'C' – A'A'B'B'C'C A'A'B'B'CC' – A'A'BB'C'C' – A'A'BC'C'C		6/64 = 9%
A'A'B'B'C'C'	6	1/64 = 2%

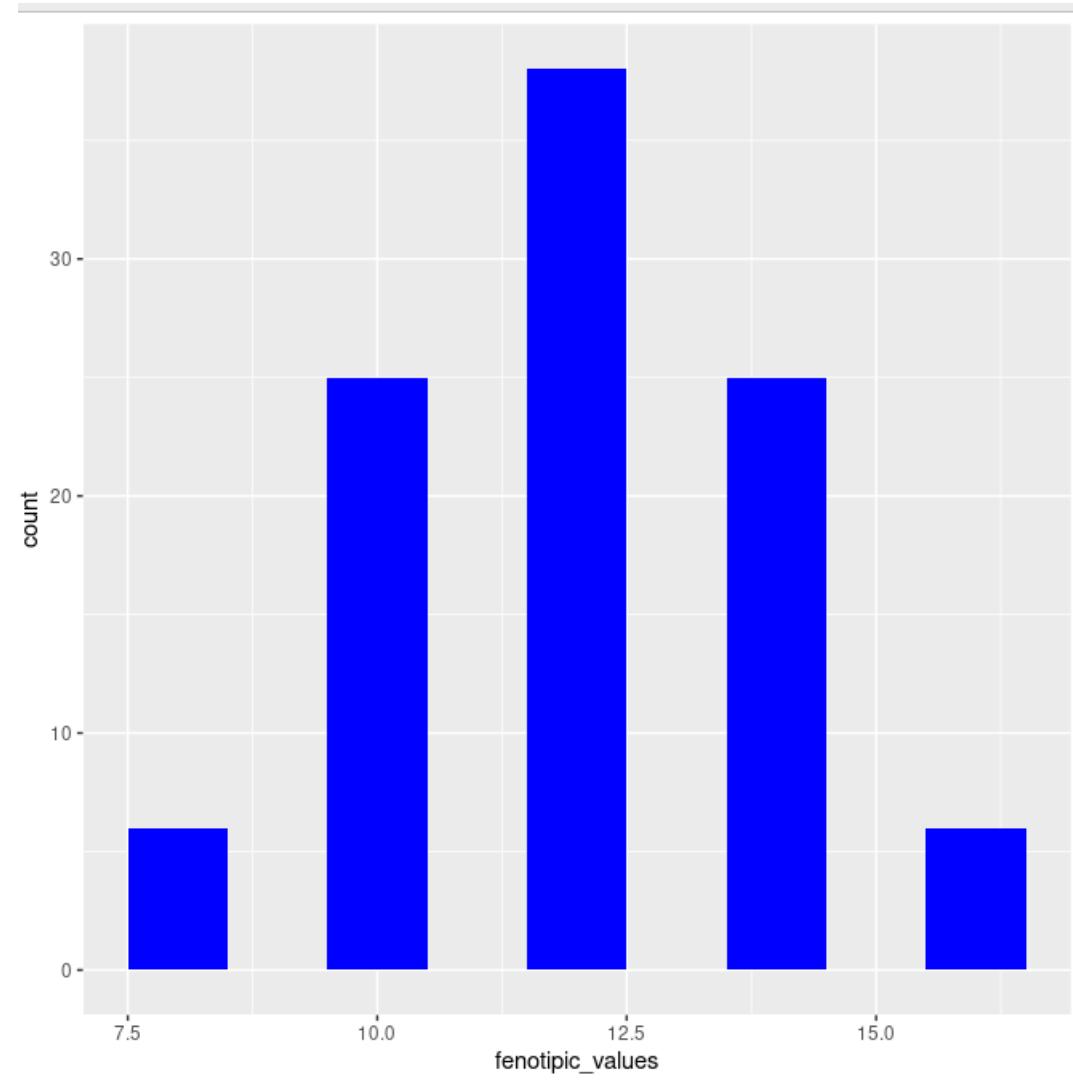
Tre loci

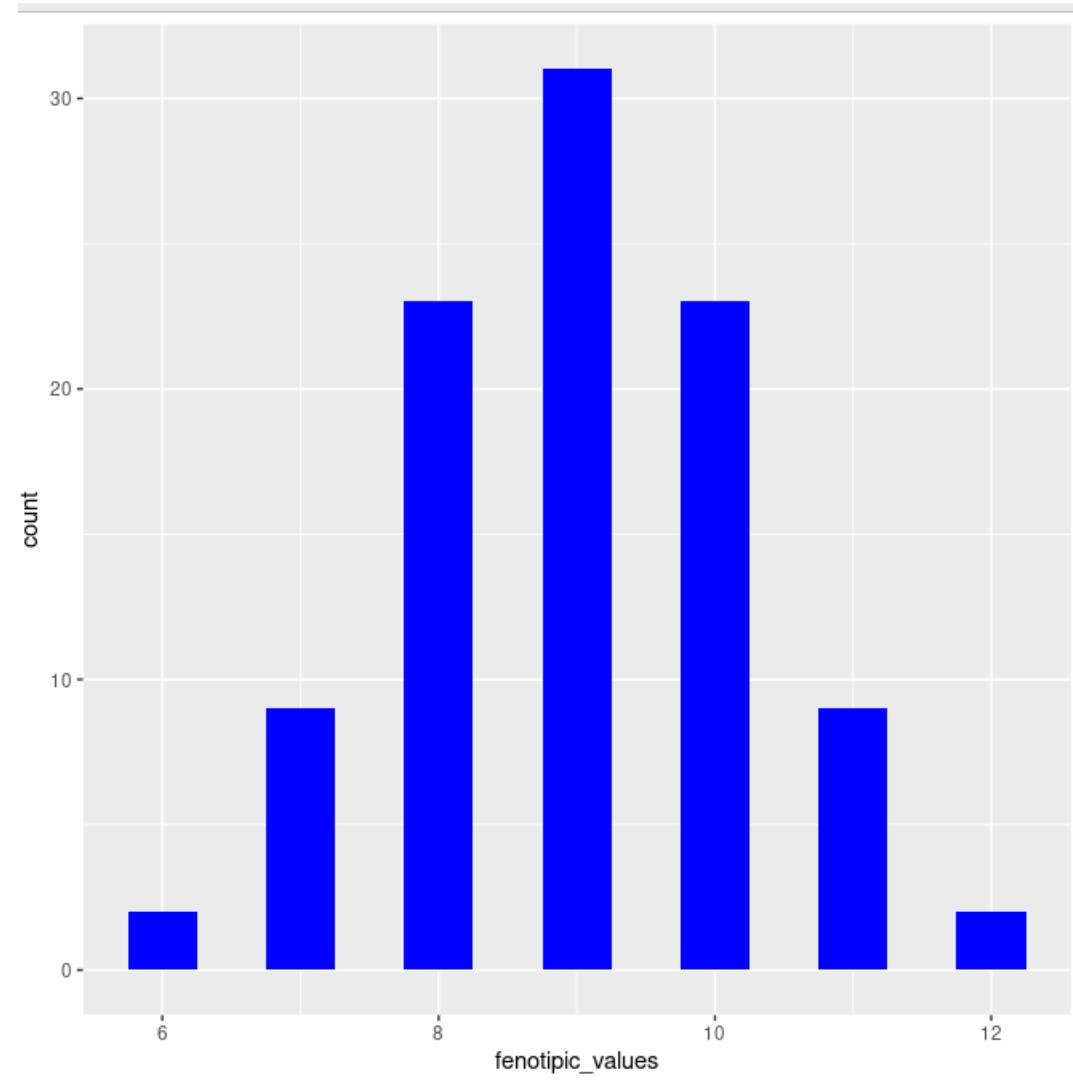
Quali sono i valori fenotipici intermedi?

CLASSE GENOTIPICA	VALORE FENOTIPICO	FREQUENZA
AABBCC	12	1/64 = 2%
AABBCC' – AABBC'C – AABB'CC AAB'BCC – AA'BBCC – A'ABBCC	11	6/64 = 9%
AABBC'C' – AABB'CC' – AAB'BCC' AA'BBCC' – A'ABBCC' – AABB'C'C AAB'BC'C – AA'BBC'C – A'ABC'C AAB'B'CC – AA'BB'CC – A'ABB'CC AA'B'BCC – A'AB'BCC – A'A'BBCC	10	15/64 = 23%
AABB'C'C' – AAB'BC'C' – AAB'B'CC' AAB'B'C'C – AA'BBC'C' – AA'BB'CC' AA'B'BCC' – AA'BB'C'C – AA'B'BC'C AA'B'B'CC – A'ABBC'C' – A'ABB'CC' A'AB'BCC' – A'ABB'C'C – A'AB'BC'C A'AB'B'CC – A'A'B'BCC – A'A'BB'CC, A'ABBC'C – A'A'BBCC'	9	20/64 = 31%
AAB'B'C'C' – AA'BB'C'C' – A'ABB'C'C' A'ABBC'C' – AA'B'BC'C' – A'AB'BC'C' A'A'B'BCC' – AA'B'B'CC' – A'AB'B'CC' A'A'B'BC'C – AA'B'B'C'C – A'AB'B'C'C A'A'B'B'CC – A'A'BB'CC' – A'A'BB'C'C	8	15/64 = 23%
AA'B'B'C'C' – A'AB'B'C'C' – A'A'B'B'C'C A'A'B'B'CC' – A'A'BB'C'C' – A'A'BC'C'C	7	6/64 = 9%
A'A'B'B'C'C'	6	1/64 = 2%

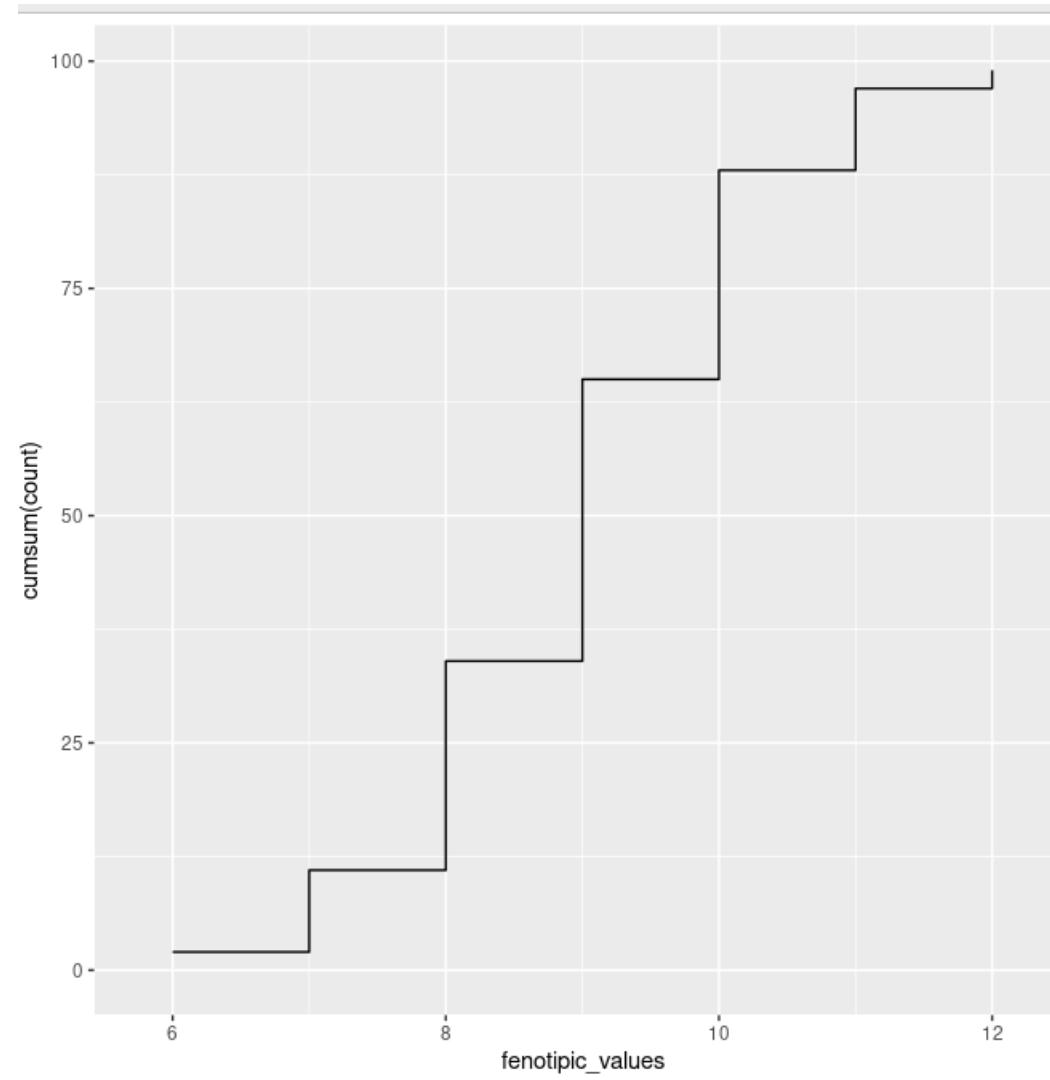
DISTRIBUZIONE DEI VALORI FENOTIPICI CON 3 COPPIE ALLELICHE







```
> cp = ggplot(data,aes(x=fenotipic_values)) +  
+ stat_bin(data=data,aes (y=cumsum(..count..)),geom="step", binwidth=0.5)  
> cp  
>
```

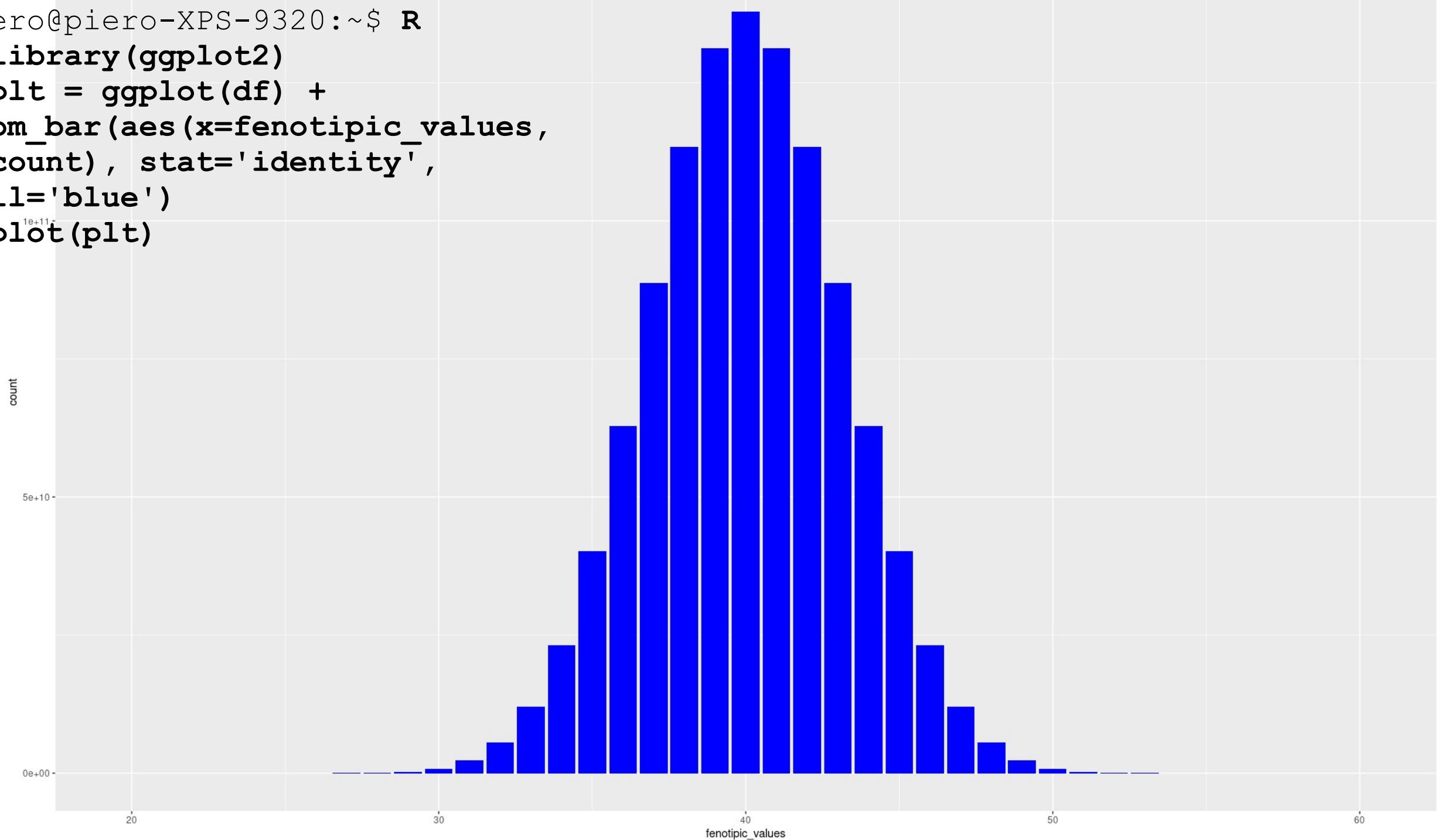


```
>>> from tartaglia_triangolo_modulo import triangolo
>>> triangolo[37]
[1, 40, 780, 9880, 91390, 658008, 3838380, 18643560, 76904685, 273438880,
847660528, 2311801440, 5586853480, 12033222880, 23206929840, 40225345056,
62852101650, 88732378800, 113380261800, 131282408400, 137846528820,
131282408400, 113380261800, 88732378800, 62852101650, 40225345056,
23206929840, 12033222880, 5586853480, 2311801440, 847660528, 273438880,
76904685, 18643560, 3838380, 658008, 91390, 9880, 780, 40, 1]
>>>
```

```
> count = c(1, 40, 780, 9880, 91390, 658008, 3838380, 18643560, 76904685,  
273438880, 847660528, 2311801440, 5586853480, 12033222880, 23206929840,  
40225345056, 62852101650, 88732378800, 113380261800, 131282408400,  
137846528820, 131282408400, 113380261800, 88732378800, 62852101650,  
40225345056, 23206929840, 12033222880, 5586853480, 2311801440, 847660528,  
273438880, 76904685, 18643560, 3838380, 658008, 91390, 9880, 780, 40, 1)  
> fenotipic_values = seq(20,60,1)  
> fenotipic_values  
[1] 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44  
[26] 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60  
> length(fenotipic_values)  
[1] 41  
> df = data.frame(fenotipic_values, count)  
> head(df)  
  fenotipic_values count  
1              20      1  
2              21     40  
3              22    780  
4              23   9880  
5              24  91390  
6              25  658008  
>
```

```
piero@piero-XPS-9320:~$ R
```

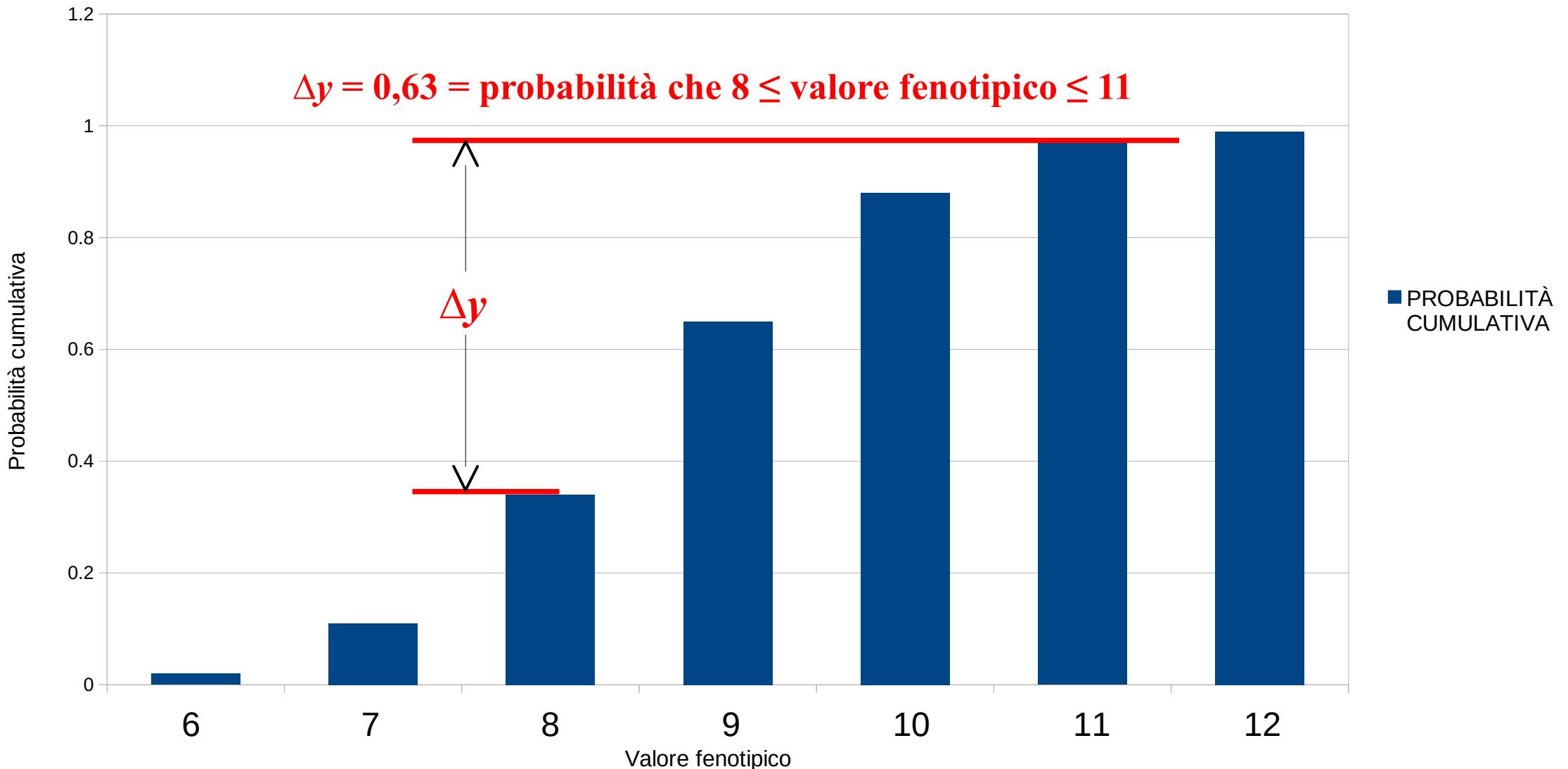
```
> library(ggplot2)
> plt = ggplot(df) +
  geom_bar(aes(x=fenotipic_values,
y=count), stat='identity',
fill='blue')
> plot(plt)
>
```



Tre loci

Distribuzione di probabilità cumulativa

Carattere quantitativo controllato da 3 loci

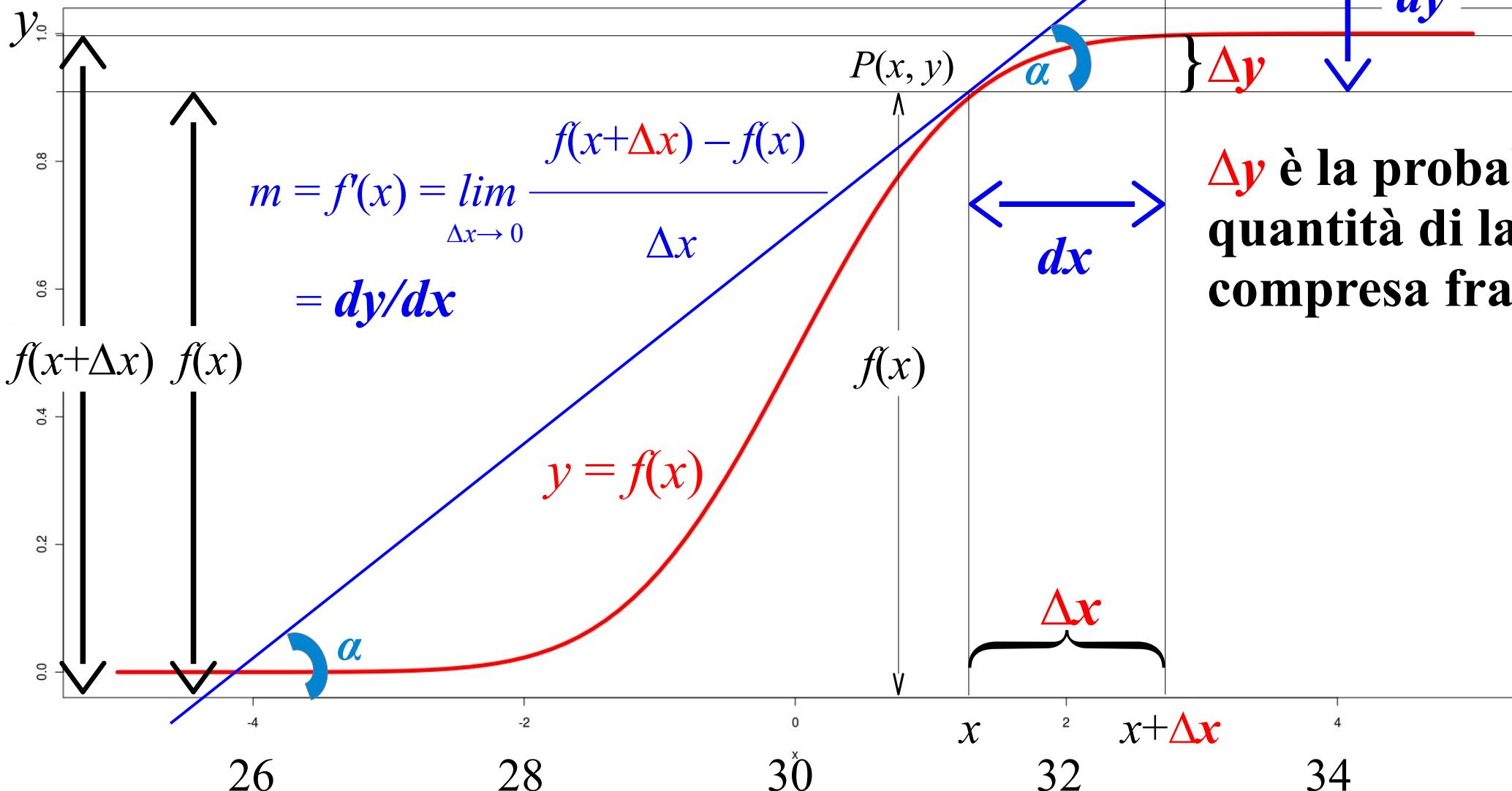


Un numero (quasi) infinito di fattori ambientali e genetici

$$y = mx + q$$

$y = f(x)$ → distribuzione di probabilità cumulativa

```
> curve(pnorm(x), -5, 5, col="red", lwd=5")
```



Δy è la probabilità che la quantità di latte sia compresa fra x e $x+\Delta x$

Usare Python all'interno di R

```
> install.packages('reticulate')
> library(reticulate)
> reticulate::py_config()
```

Would you like to create a default Python environment for the reticulate package? (Sì/no/annulla) Sì

Errore: Tools for managing Python virtual environments are not installed.

Install venv with:

```
$ sudo apt-get install python3-venv python3-pip python3-dev
```

```
> q()
```

```
piero@piero-XPS-9320:~$ sudo apt-get install python3-venv python3-pip python3-dev
```

```
>
```

Usare Python all'interno di R

```
> library(reticulate)
> reticulate::py_config()
Would you like to create a default Python environment for the reticulate
package? (Sì/no/annulla) Sì
...
Installing collected packages: numpy
Successfully installed numpy-2.2.3
Virtual environment 'r-reticulate' successfully created.
python:          /home/piero/.virtualenvs/r-reticulate/bin/python
libpython:
/usr/lib/python3.10/config-3.10-x86_64-linux-gnu/libpython3.10.so
pythonhome:
/home/piero/.virtualenvs/r-reticulate:/home/piero/.virtualenvs/r-reticulate
version:         3.10.12 (main, Jan 17 2025, 14:35:34) [GCC 11.4.0]
numpy:           /home/piero/.virtualenvs/r-reticulate/lib/python3.10/site-
packages/numpy
numpy_version:  2.2.3
> use_python('/bin/python3.10', required = TRUE)
>
```

Estrarre un numero (pseudo)casuale

```
>>> import random  
>>> random.random()  
0.8287089642821494  
>>>
```

Oggetti “built-in”: numeri

```
>>> for i in range(1,11):  
...     print(i)  
...  
1  
2  
3  
4  
5  
6  
7  
8  
9  
10  
>>>
```

Oggetti “built-in”: numeri

```
>>> import random  
>>> random.random()  
0.8287089642821494  
>>> for i in range(1,11):  
...     print(random.random())  
...  
0.8594926661744832  
0.06936841835168606  
0.5885420854284539  
0.965105117036638  
0.803728988120997  
0.7559884522057374  
0.17251377438513837  
0.5684117024306461  
0.39295735916522334  
0.7685184418536651  
>>>
```

Oggetti “built-in”: numeri

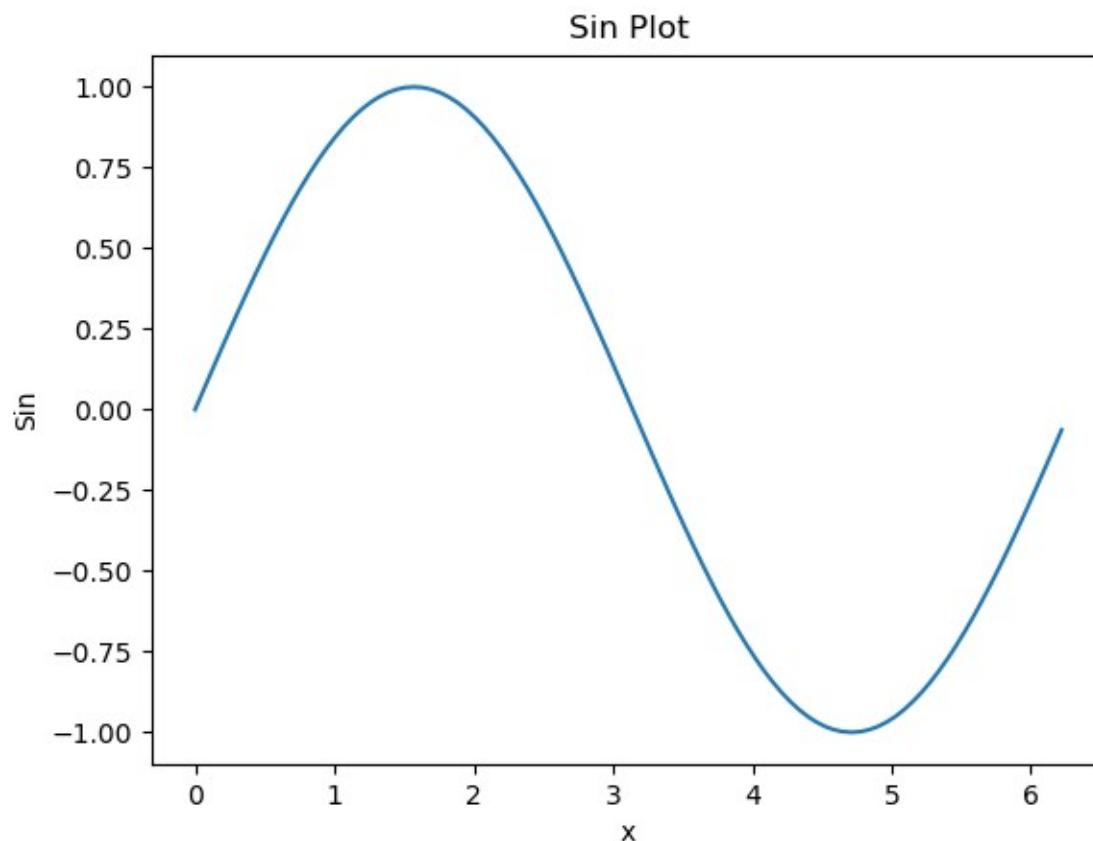
```
>>> import random
>>> randomlist = []
>>> for i in range(1,11):
...     n = random.random()
...     randomlist.append(n)
...
>>> randomlist
[0.31984567728569424, 0.5487040462281298, 0.6358083181180593,
0.9734906064546093, 0.6468907310587074, 0.21312048593018285,
0.8358032488432969, 0.18960849552618586, 0.6494585694906477,
0.5224444465761785]
>>>
```

Costruire il grafico di una funzione

```
>>> import matplotlib.pyplot as plt
>>> import numpy as np
>>> x = [i for i in range(100)]
>>> x
[0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 16, 17, 18, 19, 20, 21,
22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40,
41, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59,
60, 61, 62, 63, 64, 65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78,
79, 80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95, 96, 97,
98, 99]
>>> x = np.array(x)
>>> x
array([ 0,  1,  2,  3,  4,  5,  6,  7,  8,  9, 10, 11, 12, 13, 14, 15, 16,
       17, 18, 19, 20, 21, 22, 23, 24, 25, 26, 27, 28, 29, 30, 31, 32,
       33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47, 48,
       49, 50, 51, 52, 53, 54, 55, 56, 57, 58, 59, 60, 61, 62, 63, 64,
       65, 66, 67, 68, 69, 70, 71, 72, 73, 74, 75, 76, 77, 78, 79,
       80, 81, 82, 83, 84, 85, 86, 87, 88, 89, 90, 91, 92, 93, 94, 95,
       96, 97, 98, 99])
>>> x = 2 * np.pi * x * 0.01
>>> np.pi
3.141592653589793
```

Costruire il grafico di una funzione

```
>>> y = np.sin(x)
>>> plt.plot(x, y)
[<matplotlib.lines.Line2D object at 0x75a000587490>]
>>> plt.title('Sin Plot')
Text(0.5, 1.0, 'Sin Plot')
>>> plt.xlabel('x')
Text(0.5, 0, 'x')
>>> plt.ylabel('Sin')
Text(0, 0.5, 'Sin')
>>> plt.show()
>>>
```



Oggetti “built-in”: dictionaries

Python **dictionaries**, also known as **mappings**, are collections of other objects which are **stored by key** instead of by relative position. Mappings don't maintain any reliable left-to-right order; they simply map keys to associated values and are also mutable: like lists, they may be changed in place and can grow and shrink on demand. Also like lists, they are a flexible tool for representing collections, but their more mnemonic keys are better suited when a collection's items are named or labeled – fields of a database record, for example.

```
>>>
```

Dictionaries: import_fieno_prato_stabile_primo_taglio.py

```
import os
import numpy as np
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
from Foraggio import fieno_prato_stabile_I_taglio
print('<fieno_prato_stabile_I_taglio> importato con successo dal modulo <Foraggio>!')
FIEPRASTA1TA = list(np.float_(fieno_prato_stabile_I_taglio))
FIEPRASTA1TA_dict = {}
FIEPRASTA1TA_dict['DM'] = FIEPRASTA1TA[0]
FIEPRASTA1TA_dict['PG'] = FIEPRASTA1TA[1]
FIEPRASTA1TA_dict['RDP'] = FIEPRASTA1TA[2]
FIEPRASTA1TA_dict['RUP'] = FIEPRASTA1TA[3]
FIEPRASTA1TA_dict['FG'] = FIEPRASTA1TA[4]
FIEPRASTA1TA_dict['NDF'] = FIEPRASTA1TA[5]
FIEPRASTA1TA_dict['ADF'] = FIEPRASTA1TA[6]
FIEPRASTA1TA_dict['FAT'] = FIEPRASTA1TA[7]
FIEPRASTA1TA_dict['ASH'] = FIEPRASTA1TA[10]
FIEPRASTA1TA_dict['Ca'] = FIEPRASTA1TA[11]
FIEPRASTA1TA_dict['P'] = FIEPRASTA1TA[12]
FIEPRASTA1TA_dict['Mg'] = FIEPRASTA1TA[13]
FIEPRASTA1TA_dict['K'] = FIEPRASTA1TA[14]
FIEPRASTA1TA_dict['S'] = FIEPRASTA1TA[15]
FIEPRASTA1TA_dict['Na'] = FIEPRASTA1TA[16]
FIEPRASTA1TA_dict['UFC'] = FIEPRASTA1TA[17]
FIEPRASTA1TA_dict['UFL'] = FIEPRASTA1TA[18]
FIEPRASTA1TA_dict['kcal'] = FIEPRASTA1TA[19]
FIEPRASTA1TA_dict['Mj'] = FIEPRASTA1TA[20]
print(FIEPRASTA1TA_dict)
```

A list of dictionaries

```
>>> import os
>>> user = os.getlogin()
>>> user
'piero'
>>> os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
>>> from importa_fieno_prato_stabile_primo_taglio import FIEPRASTA1TA_dict
<fieno_prato_stabile_I_taglio> importato con successo dal modulo <Foraggio>!
{'DM': 87.0, 'PG': 9.5, 'RDP': 6.0, 'RUP': 3.5, 'FG': 30.0, 'NDF': 46.5, 'ADF': 34.8, 'FAT': 2.6,
'ASH': 7.7, 'Ca': 0.42, 'P': 0.23, 'Mg': 0.25, 'K': 1.3, 'S': 0.15, 'Na': 0.009, 'UFC': 0.41,
'UFL': 0.61, 'kcal': 1055.3, 'Mj': 4.42}
>>> from importa_fieno_prato_stabile_secondo_taglio import FIEPRASTA2TA_dict
<fieno_prato_stabile_II_taglio> importato con successo dal modulo <Foraggio>!
{'DM': 87.0, 'PG': 10.0, 'RDP': 6.3, 'RUP': 3.7, 'FG': 26.0, 'NDF': 45.0, 'ADF': 29.7, 'FAT': 3.2,
'ASH': 7.0, 'Ca': 0.6, 'P': 0.3, 'Mg': 0.25, 'K': 1.3, 'S': 0.15, 'Na': 0.009, 'UFC': 0.54, 'UFL': 0.65,
'kcal': 1124.5, 'Mj': 4.71}
>>> fieni = [FIEPRASTA1TA_dict, FIEPRASTA2TA_dict]
>>> fieni
[{'DM': 87.0, 'PG': 9.5, 'RDP': 6.0, 'RUP': 3.5, 'FG': 30.0, 'NDF': 46.5, 'ADF': 34.8, 'FAT': 2.6,
'ASH': 7.7, 'Ca': 0.42, 'P': 0.23, 'Mg': 0.25, 'K': 1.3, 'S': 0.15, 'Na': 0.009, 'UFC': 0.41,
'UFL': 0.61, 'kcal': 1055.3, 'Mj': 4.42}, {'DM': 87.0, 'PG': 10.0, 'RDP': 6.3, 'RUP': 3.7, 'FG': 26.0, 'NDF': 45.0, 'ADF': 29.7, 'FAT': 3.2,
'ASH': 7.0, 'Ca': 0.6, 'P': 0.3, 'Mg': 0.25, 'K': 1.3, 'S': 0.15, 'Na': 0.009, 'UFC': 0.54, 'UFL': 0.65,
'kcal': 1124.5, 'Mj': 4.71}]
>>>
```

A list of dictionaries

```
>>> fieni[1]
{'DM': 87.0, 'PG': 10.0, 'RDP': 6.3, 'RUP': 3.7, 'FG': 26.0, 'NDF': 45.0, 'ADF': 29.7, 'FAT': 3.2,
'ASH': 7.0, 'Ca': 0.6, 'P': 0.3, 'Mg': 0.25, 'K': 1.3, 'S': 0.15, 'Na': 0.009, 'UFC': 0.54, 'UFL':
0.65, 'kcal': 1124.5, 'Mj': 4.71}
>>> fieni[1][0]
Traceback (most recent call last):
  File "<stdin>", line 1, in <module>
KeyError: 0
>>> fieni[1]['DM']
87.0
>>>
```

Non è possibile accedere all'ingresso di un dizionario in base alla sua posizione!

Il programma systeminfo.py

```
import json, os
from tkinter.simpledialog import askstring
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
print("Puoi scegliere fra <sysname>, <nodename>, <release>, <version> e <machine>")
question = askstring('Entry', "Inserisci l'informazione desiderata")
info = os.uname()
info = "{0}".format(info)
with open("uname.txt", "w") as text_file:
    text_file.write("%s" % info)
with open('uname.txt') as f:
    newtext = f.read().replace("posix.uname_result(", "{'")
with open('uname.txt', 'w') as f:
    f.write(newtext)
with open('uname.txt') as f:
    newtext = f.read().replace("=", "':")
with open('uname.txt', 'w') as f:
    f.write(newtext)
with open('uname.txt') as f:
    newtext = f.read().replace(",", "", "")
with open('uname.txt', 'w') as f:
    f.write(newtext)
with open('uname.txt') as f:
    newtext = f.read().replace(")", "}")
with open('uname.txt', 'w') as f:
    f.write(newtext)
with open('uname.txt') as f:
    newtext = f.read().replace("'''", "''")
with open('uname.txt', 'w') as f:
    f.write(newtext)
```

Il programma systeminfo.py

```
with open('uname.txt', 'r') as file:  
    info = file.read()  
info = json.loads(info)  
if question == 'sysname':  
    output = info['sysname']  
    print("Il sistema operativo è <%s>" % output)  
elif question == 'nodename':  
    output = info['nodename']  
    print("Il nome del nodo è <%s>" % output)  
elif question == 'release':  
    output = info['release']  
    print("Il nome della release è <%s>" % output)  
  
elif question == 'version':  
    output = info['version']  
    print("Il nome della versione è <%s>" % output)  
elif question == 'machine':  
    output = info['machine']  
    print("Il nome della macchina è <%s>" % output)
```

ESERCIZIO:

modificare il programma **systeminfo.py** in modo tale che visualizzi in output **tutte le informazioni sul sistema contemporaneamente**

The range() function: email.py

The range() function

```
>>> import os
>>> from tkinter.simpledialog import askstring, askinteger
>>> user = os.getlogin()
>>> INDIRIZZO = askstring('Entry', 'Inserisci il tuo indirizzo e-mail senza il nome di battesimo')
>>> email = user + INDIRIZZO
>>> NUMERO = askinteger('Entry', 'Scegli un numero intero')
>>> for i in range(NUMERO):
...     print(email)
...
piero.rivoira@yahoo.it
piero.rivoira@yahoo.it
piero.rivoira@yahoo.it
>>>
```

The if statement

```
>>> the_world_is_flat = True  
>>> if the_world_is_flat:  
...     print("Be careful not to fall off!")  
...
```

Be careful not to fall off!

```
>>>
```

The if else statement: inserisci_gruppo.py

```
from tkinter.simpledialog import askstring
#global gruppo
gruppo = askstring('Entry', 'Scegli il GRUPPO di bovine (<F> per freschissime, <f> per
fresche, <s> per stanche)')
if gruppo == 'F' or gruppo == 'f' or gruppo == 's':
    print('GRUPPO di bovine <%s> inserito con SUCCESSO!' % gruppo)
    print('')
else:
    print('ERRORE: prova a reinserire il gruppo!')
if gruppo == 'F':
    print('La RAZIONE sarà calcolata per il GRUPPO <freschissime>!')
    print('(1^-9^ settimana di lattazione)')
    print('')
    print('<SETTIMANA DI GRAVIDANZA> impostata a 0 (zero)')
elif gruppo == 'f':
    print('La RAZIONE sarà calcolata per il GRUPPO <fresche>!')
    print('(10^-20^ settimana di lattazione)')
    print('')
elif gruppo == 's':
    print('La RAZIONE sarà calcolata per il GRUPPO <stanche>!')
    print('(dalla 21^ settimana di lattazione)')
    print('')
```

Funzioni: trova_massimo.py

```
from tkinter.simpledialog import askinteger, askfloat
DIMENSIONE = askinteger('Entry', 'Inserisci il numero delle osservazioni')
print(DIMENSIONE)
DATI = []
for i in range(DIMENSIONE):
    dato = askfloat('Entry', 'Inserisci i dati uno alla volta')
    print(dato)
    DATI.append(dato)
print(DATI)
def maxarray(lista):
    M = lista[0]
    for i in lista:
        if i > M:
            M = i
    return M
t = maxarray(DATI)
print('Il valore massimo è %f' % t)
```

[28.61, 127.73, 459.26, 35.74, 49.52]

M = 28.61

Per i = uno dei valori della list

Se i > M

M = i, es. M = 127.73

Leggere dati in Python

```
>>> import os
>>> import pandas as pd
>>> basal_metabolic_rate =
pd.read_csv('~/COMPUTER_SCIENCE/AI/DATA/metabolismo_basale.csv')
>>> basal_metabolic_rate.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 667 entries, 0 to 666
Data columns (total 6 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Unnamed: 0        30 non-null    object  
 1   species          634 non-null    object  
 2   BasalMetabolicRate_W  635 non-null    float64 
 3   BodyMass_g        635 non-null    float64 
 4   Body_temp         635 non-null    object  
 5   Ambient_temp      635 non-null    object  
dtypes: float64(2), object(4)
memory usage: 31.4+ KB
>>>
```

Leggere dati in Python

```
>>> basal_metabolic_rate.describe()
           BasalMetabolicRate_W      BodyMass_g
count          635.000000       635.000000
mean         4553.009559       6354.377039
std        21124.257254      31503.606291
min          0.040000        2.400000
25%        143.000000       29.800000
50%        378.000000      106.800000
75%       1354.500000      862.500000
max      286847.000000     407000.000000
>>> basal_metabolic_rate.columns
Index(['Unnamed: 0', 'species', 'BasalMetabolicRate_W', 'BodyMass_g',
       'Body_temp', 'Ambient_temp'],
      dtype='object')
```

Leggere dati in Python

```
>>> basal_metabolic_rate['species']
0                      NaN
1                      NaN
2                      NaN
3      Tachyglossus aculeatus
4          Zaglossus bruijni
...
662     Philantomba monticola
663     Raphicerus campestris
664          Taurotragus oryx
665                      NaN
666                      NaN
Name: species, Length: 667, dtype: object
>>>
```

Leggere dati in Python

```
>>> basal_metabolic_rate['BasalMetabolicRate_W']  
0           NaN  
1           NaN  
2           NaN  
3      2404.00  
4      6778.00  
      ...  
662     10075.00  
663    20619.00  
664     200.83  
665       NaN  
666     634.00  
Name: BasalMetabolicRate_W, Length: 667, dtype: float64  
>>> basal_metabolic_rate['BasalMetabolicRate_W'].count()  
635  
>>>
```

Leggere dati in Python

```
>>> basal_metabolic_rate['BodyMass_g']
0           NaN
1           NaN
2           NaN
3      2725.0
4     10300.0
...
662     4200.0
663     9600.0
664  150000.0
665       NaN
666     634.0
Name: BodyMass_g, Length: 667, dtype: float64
>>>
```

Leggere dati in Python

```
>>> import os
>>> import pandas as pd
>>> basal_metabolic_rate =
pd.read_csv('~/COMPUTER_SCIENCE/AI/DATA/metabolismo_basale.csv')
>>> basal_metabolic_rate.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 667 entries, 0 to 666
Data columns (total 6 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Unnamed: 0        30 non-null    object  
 1   species          634 non-null    object  
 2   BasalMetabolicRate_W  635 non-null    float64 
 3   BodyMass_g        635 non-null    float64 
 4   Body_temp         635 non-null    object  
 5   Ambient_temp      635 non-null    object  
dtypes: float64(2), object(4)
memory usage: 31.4+ KB
>>> BodyMass = basal_metabolic_rate['BodyMass_g']
>>> BodyMass_df = BodyMass.to_frame()
```

Leggere dati in Python

```
>>> BodyMass_df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 667 entries, 0 to 666
Data columns (total 1 columns):
 #   Column      Non-Null Count  Dtype  
--- 
 0   BodyMass_g    635 non-null    float64
dtypes: float64(1)
memory usage: 5.3 KB
>>> BodyMass_df
   BodyMass_g
0          NaN
1          NaN
2          NaN
3        2725.0
4       10300.0
..        ...
662      4200.0
663      9600.0
664     150000.0
665        NaN
666      634.0

[667 rows x 1 columns]
```

Leggere dati in Python

```
>>> BodyMass_df = BodyMass_df.rename(columns={'BodyMass_g': 'Body Mass (g)'})
>>> BodyMass_df
   Body Mass (g)
0           NaN
1           NaN
2           NaN
3        2725.0
4       10300.0
..         ...
662      4200.0
663      9600.0
664    150000.0
665       NaN
666      634.0

[667 rows x 1 columns]
>>> BodyMass_df.count()
BodyMass_g    635
dtype: int64
>>>
```

Leggere dati in Python

```
>>> import dill, os, pickle
>>> import pandas as pd
>>> basal_metabolic_rate =
pd.read_csv('~/COMPUTER_SCIENCE/AI/DATA/metabolismo_basale.csv')
>>> user = os.getlogin()
>>> os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
>>> with open("metabolic.pkl", "wb") as file:
...     dill.dump(basal_metabolic_rate, file)
...
>>> exit()
```

Leggere dati in Python

```
piero@piero-XPS-9320:~$ python3
>>> import dill, os, pickle
>>> import pandas as pd
>>> user = os.getlogin()
>>> os.chdir('/home/%s/COMPUTER_SCIENCE/AI' % user)
>>> with open("metabolic.pkl", "rb") as file:
...     basal_metabolic_rate = pickle.load(file)
...
>>> basal_metabolic_rate
      Unnamed: 0    ... Ambient_temp
0           NaN    ...        NaN
1  PROTOTHERIA: MONOTREMATA    ...        NaN
2      Order: Monotremata    ...        NaN
3           NaN    ...       19.7
4           NaN    ...       16.2
...
662          ...    ...        ...
663          NaN    ...       19.1
664          NaN    ...       21.5
665          NaN    ...        NaN
666          NaN    ...       576
[667 rows x 6 columns]
>>>
```

Leggere dati in Python

```
>>> BodyMass = basal_metabolic_rate['BodyMass_g']
>>> BodyMass_df = BodyMass.to_frame()
>>> BodyMass_df = BodyMass_df.rename(columns={'BodyMass_g': 'Body Mass (g)'})
>>> BodyMass_df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 667 entries, 0 to 666
Data columns (total 1 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Body Mass (g)    635 non-null    float64
dtypes: float64(1)
memory usage: 5.3 KB
>>> BodyMass_df.count()
BodyMass_g    635
dtype: int64
>>>
```

Leggere dati in Python

```
>>> BodyMass_df  
      Body Mass (g)  
0             NaN  
1             NaN  
2             NaN  
3            2725.0  
4           10300.0  
..          ...  
662         4200.0  
663         9600.0  
664        150000.0  
665           NaN  
666         634.0  
  
[667 rows x 1 columns]  
>>>
```

NaN = Not a Number

Leggere dati in Python

```
>>> BodyMass_df_clean = BodyMass_df.dropna(how='all')
>>> BodyMass_df_clean
   Body Mass (g)
3          2725.0
4         10300.0
5          693.0
8          329.0
9          935.0
..
       ...
661        69125.0
662        4200.0
663        9600.0
664      150000.0
666        634.0

[635 rows x 1 columns]
>>>
```

Leggere dati in Python

```
>>> BasalMetabolicRate = basal_metabolic_rate['BasalMetabolicRate_W']
>>> BasalMetabolicRate
0           NaN
1           NaN
2           NaN
3      2404.00
4      6778.00
...
662     10075.00
663    20619.00
664     200.83
665       NaN
666     634.00
Name: BasalMetabolicRate_W, Length: 667, dtype: float64
>>> BasalMetabolicRate_df = BasalMetabolicRate.to_frame()
>>>
```

Leggere dati in Python

```
>>> BasalMetabolicRate_df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 667 entries, 0 to 666
Data columns (total 1 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   BasalMetabolicRate_W  635 non-null    float64
dtypes: float64(1)
memory usage: 5.3 KB
>>> BasalMetabolicRate_df =
BasalMetabolicRate_df.rename(columns={'BasalMetabolicRate_W': 'Basal Metabolic Rate
(W)'})
>>> BasalMetabolicRate_df.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 667 entries, 0 to 666
Data columns (total 1 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Basal Metabolic Rate (W)  635 non-null    float64
dtypes: float64(1)
memory usage: 5.3 KB
>>>
```

Leggere dati in Python

```
>>> BasalMetabolicRate_df_clean = BasalMetabolicRate_df.dropna(how='all')
>>> BasalMetabolicRate_df_clean
   Basal Metabolic Rate (W)
3           2404.00
4           6778.00
5           1082.00
8           1255.00
9           2549.00
..
          ...
661        106663.00
662        10075.00
663        20619.00
664        200.83
666        634.00

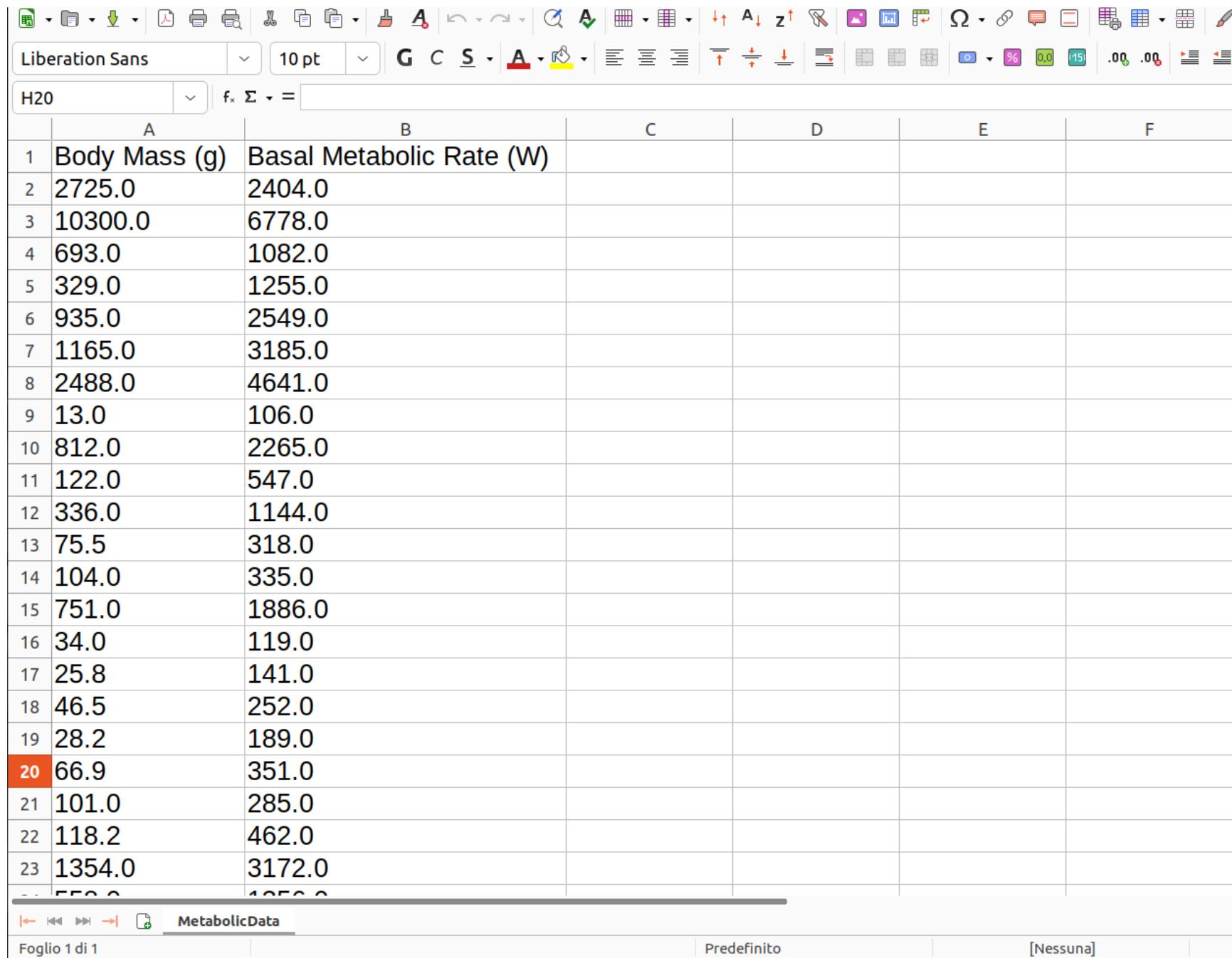
[635 rows x 1 columns]
>>>
```

Leggere dati in Python

```
>>> MetabolicData = pd.concat([BodyMass_df_clean, BasalMetabolicRate_df_clean], axis=1)
>>> MetabolicData
   Body Mass (g)  Basal Metabolic Rate (W)
3           2725.0          2404.00
4          10300.0         6778.00
5            693.0          1082.00
8            329.0          1255.00
9            935.0          2549.00
..           ...
661          69125.0        106663.00
662          4200.0          10075.00
663          9600.0          20619.00
664         150000.0         200.83
666          634.0           634.00

[635 rows x 2 columns]
>>> os.getcwd()
'/home/piero/COMPUTER_SCIENCE/AI'
>>> os.chdir('DATA')
>>> os.getcwd()
'/home/piero/COMPUTER_SCIENCE/AI/DATA'
>>> MetabolicData.to_csv('MetabolicData.csv', index=False)
>>>
```

Leggere dati in Python



The screenshot shows a Microsoft Word document with a table of metabolic data. The table has two columns: 'Body Mass (g)' and 'Basal Metabolic Rate (W)'. The data is as follows:

	A	B	C	D	E	F
1	Body Mass (g)	Basal Metabolic Rate (W)				
2	2725.0	2404.0				
3	10300.0	6778.0				
4	693.0	1082.0				
5	329.0	1255.0				
6	935.0	2549.0				
7	1165.0	3185.0				
8	2488.0	4641.0				
9	13.0	106.0				
10	812.0	2265.0				
11	122.0	547.0				
12	336.0	1144.0				
13	75.5	318.0				
14	104.0	335.0				
15	751.0	1886.0				
16	34.0	119.0				
17	25.8	141.0				
18	46.5	252.0				
19	28.2	189.0				
20	66.9	351.0				
21	101.0	285.0				
22	118.2	462.0				
23	1354.0	3172.0				
	552.0	1250.0				

Leggere dati in Python

```
>>> BodyMass_df_clean.info()
<class 'pandas.core.frame.DataFrame'>
Int64Index: 635 entries, 3 to 666
Data columns (total 1 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Body Mass (g)    635 non-null    float64
dtypes: float64(1)
memory usage: 9.9 KB
>>> BodyMass_df_clean.count()
Body Mass (g)    635
dtype: int64
>>> os.getcwd()
'/home/piero/COMPUTER_SCIENCE/AI'
>>> os.chdir('DATA')
>>> os.getcwd()
'/home/piero/COMPUTER_SCIENCE/AI/DATA'
>>> BodyMass_df_clean.to_csv('BodyMass.csv', index=False)
>>>
```

Leggere dati in Python

```
>>> import dill, os, pickle
>>> import pandas as pd
>>> basal_metabolic_rate =
pd.read_csv('~/COMPUTER_SCIENCE/AI/DATA/metabolismo_basale.csv')
>>> BodyMass_df = basal_metabolic_rate['BodyMass_g'].to_frame()
>>> BodyMass_df.count().item()
635
>>> range(BodyMass_df.count().item())
range(0, 635)
>>> for i in range(BodyMass_df.count().item()):
...     print(i)
...
0
1
2
3
...
632
633
634
>>>
```

Leggere dati in Python

```
>>> import dill, os, pickle
>>> import pandas as pd
>>> basal_metabolic_rate =
pd.read_csv('~/COMPUTER_SCIENCE/AI/DATA/metabolismo_basale.csv')
>>> BodyMass_df_clean =
basal_metabolic_rate['BodyMass_g'].to_frame().rename(columns={'BodyMass_g': 'Body Mass (g)'}) .dropna(how='all')
>>> BodyMass_ls_clean = BodyMass_df_clean['Body Mass (g)'].to_list()
>>> BodyMass_ls_clean[0]
2725.0
>>> len(BodyMass_ls_clean)
635
>>> somma = 0
>>> for i in range(len(BodyMass_ls_clean)):
...     somma = somma + BodyMass_ls_clean[i]
...
>>> somma
4035029.42
>>> media = somma / len(BodyMass_ls_clean)
>>> media
6354.377039370079
>>>
```

Leggere dati in Python

```
>>> BodyMass_df_clean.info()
<class 'pandas.core.frame.DataFrame'>
Int64Index: 635 entries, 3 to 666
Data columns (total 1 columns):
 #   Column           Non-Null Count  Dtype  
--- 
 0   Body Mass (g)    635 non-null    float64 
dtypes: float64(1)
memory usage: 9.9 KB
>>> BodyMass_df_clean['Body Mass (g)'].mean()
6354.377039370079
>>>
```

Il programma statistica.py

```
import dill, os, pickle
import pandas as pd
from tkinter.simpledialog import askstring
user = os.getlogin()
os.chdir('/home/%s/COMPUTER_SCIENCE/AI/DATA' % user)
file_name = askstring('Entry', 'Inserisci il nome del file csv con i dati (senza estensione)')
#print('Your dataframe will be named <df>')
df = pd.read_csv('%s.csv' % file_name)
print('Questa è la struttura dei tuoi dati:')
print(df.info())
column_name = askstring('Entry', 'Inserisci il nome della colonna che ti interessa')
DATA = df['%s' % column_name]
def maxarray(dataframe):
    M = dataframe[0]
    for i in dataframe:
        if i > M:
            M = i
    return M
MAX = maxarray(DATA)
print('Il valore massimo della variabile <%s> è %f' % (column_name, MAX))
```

Il programma statistica.py

```
def minarray(dataframe):
    m = dataframe[0]
    for i in dataframe:
        if i < m:
            m = i
    return m
MIN = minarray(DATA)
print('Il valore minimo della variabile <%s> è %f' % (column_name, MIN))

DATA_ls = DATA.to_list()
SUM = 0
for i in range(len(DATA_ls)):
    SUM = SUM + DATA_ls[i]
AVERAGE = SUM / len(DATA_ls)
print('La media della variabile <%s> è %f' % (column_name, AVERAGE))
```

Lo shell script statistica

```
#!/bin/bash
cd COMPUTER_SCIENCE/AI
python3 statistica.py

piero@piero-XPS-9320:~$ chmod +x statistica
# rendiamo eseguibile il file come programma
piero@piero-XPS-9320:~$ ./statistica
piero@piero-XPS-9320:~$ statistica
statistica: comando non trovato
piero@piero-XPS-9320:~$
```

Impostare la variabile ambientale PATH

```
piero@piero-XPS-9320:~$ echo $PATH  
/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/usr/games:/usr/  
local/games:/snap/bin:/snap/bin
```

```
piero@piero-XPS-9320:~$ PATH=$PATH:/home/piero
```

#oppure

```
piero@piero-XPS-9320:~$ export PATH="$PATH:/home/piero"
```

```
piero@piero-XPS-9320:~$ echo $PATH
```

```
/usr/local/sbin:/usr/local/bin:/usr/sbin:/usr/bin:/sbin:/bin:/usr/games:/usr/  
local/games:/snap/bin:/snap/bin:/home/piero
```

#ATTENZIONE: il cambiamento vale solo per la sessione corrente!

Impostare la variabile ambientale PATH

```
piero@piero-XPS-9320:~$ statistica
```

Questa è la struttura dei tuoi dati:

```
<class 'pandas.core.frame.DataFrame'>
```

RangeIndex: 635 entries, 0 to 634

```
Data columns (total 2 columns):
```

#	Column	Non-Null Count	Dtype
0	Body Mass (g)	635 non-null	float64
1	Basal Metabolic Rate (W)	635 non-null	float64

```
dtypes: float64(2)
```

```
memory usage: 10.0 KB
```

```
None
```

Il valore massimo della variabile <Body Mass (g)> è 407000.000000

Il valore minimo della variabile <Body Mass (g)> è 2.400000

La media della variabile <Body Mass (g)> è 6354.377039

```
piero@piero-XPS-9320:~$
```

What are the Shell Environment Variables?

They are...

Il programma statistica.py

```
import dill, os, pickle
import pandas as pd
from tkinter.simpledialog import askstring
# importiamo i necessari moduli
user = os.getlogin()
# usiamo la funzione getlogin() del modulo os per ottenere il nome utente e lo salviamo
# come stringa user
os.chdir('/home/%s/COMPUTER_SCIENCE/AI/DATA' % user)
# impostiamo come cartella di lavoro quella in cui è stato salvato il file dei dati
# usiamo l'operatore % per sostituire ad esso la stringa denominata user
file_name = askstring('Entry', 'Inserisci il nome del file csv con i dati
(senza estensione)')
# usiamo la funzione askstring affinché l'utente possa inserire il nome del file che
contiene i dati, che viene salvato nella stringa file_name
df = pd.read_csv('%s.csv' % file_name)
# usiamo la funzione del read_csv modulo pandas per leggere il file (il cui nome era stato
salvato nella stringa file_name) e salvarlo come dataframe df
# usiamo l'operatore % per sostituire ad esso la stringa denominata file_name
```

Il programma statistica.py

```
print(df.info())
# usiamo l'attributo info() del dataframe df per inviare all'output standard (lo schermo)
# alcune informazioni sulla struttura del dataframe (numero ed intestazione delle colonne)
# per l'utente
column_name = askstring('Entry', 'Inserisci il nome della colonna che ti
interessa')
# usiamo la funzione askstring affinché l'utente possa scegliere la variabile che gli
# interessa (ogni colonna contiene i valori di una variabile diversa) e salviamo il nome della
# variabile (intestazione della colonna corrispondente) nella stringa column_name
DATA = df['%s' % column_name]
# creiamo il dataframe DATA per immagazzinare i valori della variabile scelta
# usiamo l'operatore % per sostituire ad esso la stringa denominata column_name
def maxarray(dataframe):
    M = dataframe[0]
    for i in dataframe:
        if i > M:
            M = i
    return M
# creiamo la funzione maxarray che ha come argomento il dataframe dataframe
```

Il programma statistica.py

```
def maxarray(dataframe):  
    M = dataframe[0]  
    for i in dataframe:  
        if i > M:  
            M = i  
    return M
```

creiamo la funzione `maxarray` che ha come argomento il `dataframe` `dataframe`

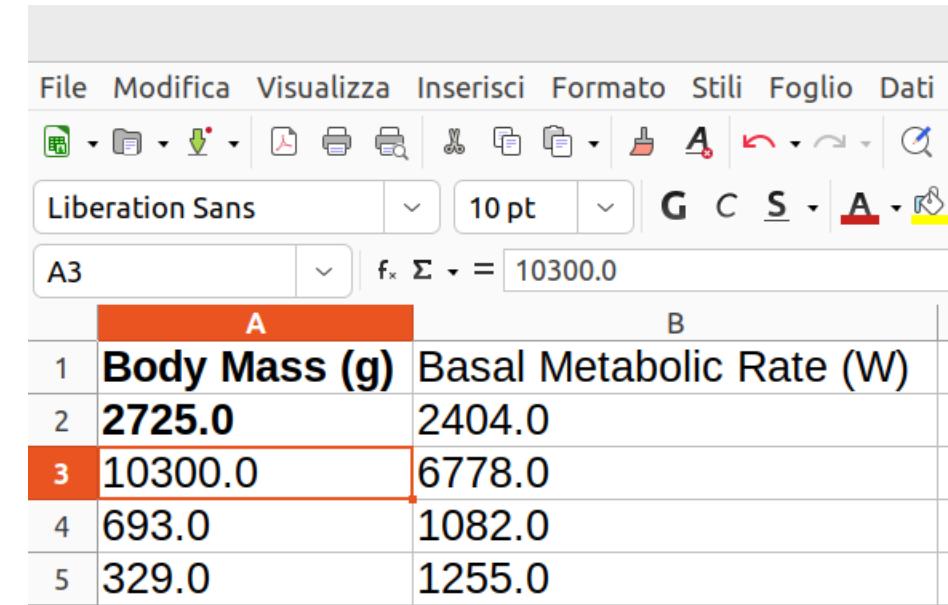
```
M = dataframe[0]
```

inizializziamo la variabile `M` facendole assumere il primo valore della variabile prescelta

A	B
1 Body Mass (g)	Basal Metabolic Rate (W)
2 2725.0	2404.0
3 10300.0	6778.0
4 693.0	1082.0
5 329.0	1255.0

Il programma `statistica.py`

```
def maxarray(dataframe):  
    M = dataframe[0]  
    for i in dataframe:  
        if i > M:  
            M = i  
    return M  
  
# usiamo il ciclo for e la variabile indicatrice i  
# ad ogni ripetizione del ciclo, i assume un valore del  
# dataframe  
# all'inizio i = M = 2725.0  
# nel ciclo successivo i = 10300.0, quindi i > M  
# M viene posta uguale ad i, ossia M = i = 10300.0  
# quindi il ciclo ricomincia: i diventa uguale a 693.0  
# poiché i < M, M rimane uguale a 10300.0  
# e così via
```



	A	B
1	Body Mass (g)	Basal Metabolic Rate (W)
2	2725.0	2404.0
3	10300.0	6778.0
4	693.0	1082.0
5	329.0	1255.0

Il programma `statistica.py`

```
MAX = maxarray(DATA)
# passiamo alla funzione maxarray l'argomento DATA (il dataframe che contiene i dati)
# e salviamo il risultato della stessa funzione nell'oggetto MAX

print('Il valore massimo della variabile <%s> è %f' % (column_name, MAX))

# usiamo gli operatori di formattazione %s e %f per sostituirli, rispettivamente, con i valori
della stringa column_name (che contiene il nome della variabile) e dell'oggetto di tipo float
(numero a virgola mobile) MAX, che rappresenta il risultato della funzione maxarray

def minarray(dataframe):
    m = dataframe[0]
    for i in dataframe:
        if i < m:
            m = i
    return m
MIN = minarray(DATA)
print('Il valore minimo della variabile <%s> è %f' % (column_name, MIN))
# stessa cosa per calcolare il minimo
```

Il programma `statistica.py`

```
DATA_ls = DATA.to_list()
# il dataframe DATA viene convertito nella list DATA_ls
SUM = 0
# la variabile SUM viene inizializzata a zero
for i in range(len(DATA_ls)):
    # per i che va da 0 a 634:
        SUM = SUM + DATA_ls[i]
# il valore di SUM viene aggiornato:
AVERAGE = SUM / len(DATA_ls)
# si applica la formula della media
print('La media della variabile <%s> è %f' % (column_name, AVERAGE))
# usiamo gli operatori di formattazione %s e %f per sostituirli, rispettivamente, con i valori
della stringa column_name (che contiene il nome della variabile) e dell'oggetto di tipo float
(numero a virgola mobile) AVERAGE, che rappresenta la media
```

Lo shell script <statistica>

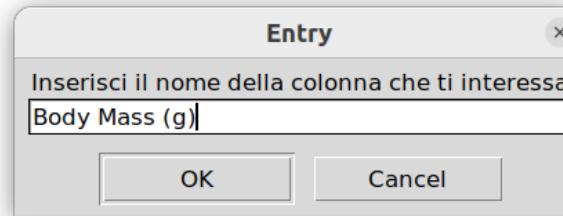
```
#!/bin/bash  
cd COMPUTER_SCIENCE/AI  
python3 statistica.py
```

Il programma statistica.py



Il programma statistica.py

```
piero@piero-XPS-9320:~$ ./statistica
Questa è la struttura dei tuoi dati:
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 635 entries, 0 to 634
Data columns (total 2 columns):
 #   Column           Non-Null Count   Dtype  
 ---  --  
 0   Body Mass (g)    635 non-null     float64 
 1   Basal Metabolic Rate (W) 635 non-null     float64 
dtypes: float64(2)
memory usage: 10.0 KB
None
```



Il programma **statistica.py**

```
piero@piero-XPS-9320:~$ ./statistica
```

Questa è la struttura dei tuoi dati:

```
<class 'pandas.core.frame.DataFrame'>
```

```
RangeIndex: 635 entries, 0 to 634
```

```
Data columns (total 2 columns):
```

#	Column	Non-Null Count	Dtype
0	Body Mass (g)	635 non-null	float64
1	Basal Metabolic Rate (W)	635 non-null	float64

```
dtypes: float64(2)
```

```
memory usage: 10.0 KB
```

```
None
```

Il valore massimo della variabile <Body Mass (g)> è 407000.000000

Il valore minimo della variabile <Body Mass (g)> è 2.400000

La media della variabile <Body Mass (g)> è 6354.377039

```
piero@piero-XPS-9320:~$
```

Python and R (<https://github.com/moderndatadesign/PyR4MDS>)

The screenshot shows the GitHub repository page for PyR4MDS. At the top, the URL https://github.com/moderndatadesign/PyR4MDS is displayed. The repository name is "moderndatadesign / PyR4MDS". The main navigation tabs include Code (selected), Issues (1), Pull requests (1), Actions, Projects, Security, and Insights. Below the tabs, the repository name "PyR4MDS" is shown with a ".R" icon and "Public" status. To the right are Watch (6), Fork (49), and Star (78) buttons. The code view shows the "master" branch with 1 branch and 0 tags. A search bar and a "Code" dropdown are also present.

About

Companion code repository for the O'Reilly "Python and R for the Modern Data Scientist" book.

moderndata.design

python r statistics dataviz
datascience machinelearning

Readme

Activity

Custom properties

78 stars

6 watching

49 forks

Report repository

File	Description	Time
boyanangelov Update book cover with final one	b07e521 · 4 years ago	9 Commits
ch02-r4py	Add files via upload	4 years ago
ch03-py4r	Add files via upload	4 years ago
ch04-format	Migrate code	4 years ago
ch05-workflow	Migrate code	4 years ago
ch06-reticulate	Migrate code	4 years ago
ch07-case-study	ch07	4 years ago
.gitignore	Migrate code	4 years ago
PyR4MDS.Rproj	ch07	4 years ago

Python and R: prepariamo i dati

piero@piero-XPS-9320:~\$ **R**

```
R version 4.4.2 (2024-10-31) -- "Pile of Leaves"
Copyright (C) 2024 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu
```

R è un software libero ed è rilasciato SENZA ALCUNA GARANZIA.
Siamo ben lieti se potrai redistribuirlo, ma sotto certe condizioni.
Scrivi 'license()' o 'licence()' per maggiori dettagli.

R è un progetto collaborativo con molti contributi esterni.
Scrivi 'contributors()' per maggiori informazioni e 'citation()' per sapere come citare R o i pacchetti nelle pubblicazioni.

Scrivi 'demo()' per una dimostrazione, 'help()' per la guida oppure 'help.start()' per la guida nel browser HTML.
Scrivi 'q()' per uscire da R.

[Caricato workspace precedentemente salvato]

>

Python and R: prepariamo i dati

```
> library(readxl)
> BasalMetabolicRate = read_excel('~/Scaricati/metabolismo_basale.xlsx')
> str(BasalMetabolicRate)
tibble [667 × 6] (S3: tbl_df/tbl/data.frame)
$ ...1 : chr [1:667] NA "PROTOTHERIA: MONOTREMATA" "Order: Monotremata" ...
$ species : chr [1:667] NA NA NA "Tachyglossus aculeatus" ...
$ BasalMetabolicRate_W: num [1:667] NA NA NA 2.4 6.78 ...
$ BodyMass_g : num [1:667] NA NA NA 2725 10300 ...
$ Body_temp : chr [1:667] NA NA NA "30.7" ...
$ Ambient_temp : chr [1:667] NA NA NA "19.7" ...
> tasso_metabolico_basale = BasalMetabolicRate$BasalMetabolicRate_W[!
is.na(BasalMetabolicRate$BasalMetabolicRate_W) ]
> str(tasso_metabolico_basale)
num [1:635] 2.4 6.78 1.08 1.25 2.55 ...
> massa_corporea = BasalMetabolicRate$BodyMass_g[ !is.na(BasalMetabolicRate$BodyMass_g) ]
> str(massa_corporea)
num [1:635] 2725 10300 693 329 935 ...
> df = data.frame(massa_corporea, tasso_metabolico_basale)
> str(df)
'data.frame': 635 obs. of  2 variables:
$ massa_corporea : num 2725 10300 693 329 935 ...
$ tasso_metabolico_basale: num 2.4 6.78 1.08 1.25 2.55 ...
```

Python and R: prepariamo i dati

```
> max(massa_corporea)
[1] 407000
> max(tasso_metabolico_basale)
[1] 634
> write.csv(df, "~/COMPUTER_SCIENCE/AI/DATA/data.csv", row.names=FALSE)
>
```