pour créer les dossiers de chaque chromosomes :

for i in `seq 2 19`; do mkdir 'chr'$i;done

remplacement des virgule par des tab

for i in `seq 2 19` Y; do cp ../Data/mouse/chr$i/mart\_export.txt ../Data/mouse/chr$i/MM\_transcript\_unspliced\_chr$i.txt;done

boucle pour tout les chromosomes:

for i in `seq 2 19` Y; do sed -i -e "s/,/\t/g" ../Data/mouse/chr$i/mart\_export.txt > ../Data/mouse/chr$i/MM\_transcript\_unspliced\_chr$i.txt;done

supprimer

for i in `seq 1 19` Y; do rm ../Data/mouse/chr$i/mart\_export.txt;done

pour faire une boucle et créer les fichiers pour l'analyse :

for i in `seq 1 19` Y; do time python ReplaceInformation.py --chromosome $i;done

rm -f virtenv

virtualenv --no-site-packages virtenv

source virtenv/bin/activate

[Wiki Graham](https://docs.computecanada.ca/wiki/Graham/fr)

**ssh** [**vana2406@graham.computecanada.ca**](mailto:vana2406@graham.computecanada.ca)

sbatch simple\_job.sh

scp -r -p mouse/ vana2406@graham.computecanada.ca:~/Data

Monter graham comme disque dur

sshfs -o follow\_symlinks,ServerAliveInterval=10 vana2406@graham.computecanada.ca:/project/6003961/vana2406 graham

Pour unmount

fusermount -u *mountpoint*

[Graham storage](https://docs.computecanada.ca/wiki/Storage_and_file_management#Filesystem_Quotas_and_Policies)

C’est caca :

for i in `seq 1 9`; do sbatch ../../../Script/G4Screener\_manuel.sh 15 "MM\_gene\_unspliced\_chr15\_0000"$i".fas"; done

for i in `seq 10 23`; do sbatch ../../../Script/G4Screener\_manuel.sh 15 "MM\_gene\_unspliced\_chr15\_000"$i".fas"; done

sbatch ../../../Script/G4Screener\_manuel.sh 5 "MM\_gene\_unspliced\_chrX\_00017.fas"

for i in `seq 31 32`; do sbatch ../../../Script/G4Screener\_manuel.sh 8 "MM\_gene\_unspliced\_chr8\_000"$i".fas"; done

for i in `seq 1 19` X Y; do cp chr$i\_split/\*.csv chr$i\_csv/;done

for i in `seq 1 19` X Y; do time ../../Script/G4Annotation.py -CHR "$i" -specie MM ;done

for i in `seq 1 19` X Y; do grep ">" transcriptType\_chr$i.fas > transcriptType\_chr$i.txt;done