# Lab Book

*Cientific Iniciation - Coral Metagenomes*

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# Capítulo 1

# May 2018

## 1.1 13

### 1.1.1 Learning LaTeX

- Working folder: *path*

LaTeX is a high-quality typesetting system, available as free software, which allows to produce scientific or technical documents [?]. I am using LaTeX to create a Bioinformatics Lab Book. To compile my Lab Book, I can use command lines (pdflatex and bibtex). Afterwards I can visualise the produced *.pdf* file with evince or another reader. Alternatevily, I can use a Latex editor, such as TexWorks (`https://www.tug.org/texworks/`), which allows me to write the code and control the *pdf* file in the same environment (Figure 8.1).

To compile the *.tex* file in the command line:

$pdflatex lab-book
$bibtex lab-book
$pdflatex lab-book
$pdflatex lab-book

To visualise the *.pdf*:

$evince lab-book.pdf &

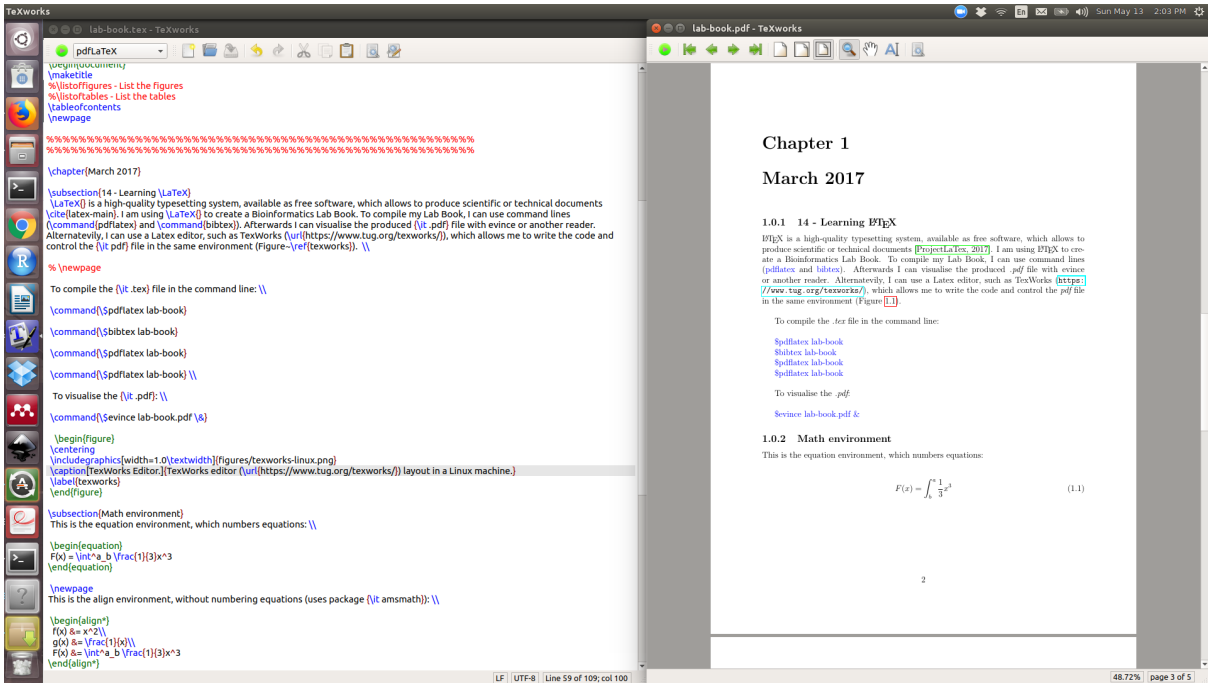


Figura 1.1: TexWorks editor (`https://www.tug.org/texworks/`) layout in a Linux machine.

### 1.1.2 Math environment

This is the equation environment, which numbers equations:

$$F(x) = \int_b^a \frac{1}{3}x^3 \tag{1.1}$$

This is the align environment, without numbering equations (uses package *amsmath*):

$$f(x) = x^2$$
$$g(x) = \frac{1}{x}$$
$$F(x) = \int_b^a \frac{1}{3}x^3$$

### 1.1.3 15 - Short-term project proposal

Some text here. Incluing and referencing a table (table 1.1).

- First numbered list item
- Second numbered list item

Tabela 1.1: table0

| species | changes | score |
|---|---|---|
| Macaque | 4 | 0.0 |
| Human | 2 | 14.9 |
| Orangutan | 0 | 0.0 |
| Pan | 0 | 0.0 |
| Gorilla | 0 | 0.0 |

# Capítulo 2

# Creation of data base of metagenomes and genomes

## 2.1 28

### 2.1.1 Bibliographic search for genomes

Found a new possibility of phyla list. Because of this, there are four possibilities of list of microorganisms phyla, one of them, the SILVA database, is based in RNA sequences:

- The list of Prokariotic names with stading nomenclature `http://www.bacterio.net/-classifphyla.html`
- SILVA database LSU(large subunit of ribosome) `https://www.arb-silva.de/browser/lsu/`
- SILVA database SSU(small subunit of ribosome) `https://www.arb-silva.de/browser/ssu/`
- PATRIC GENOMES `https://www.patricbrc.org/view/Taxonomy/2#view_tab=taxontree`

The list of articles used until now is:

- 10.1038/nature14486
- 10.1038/ismej.2013.111
- 10.1038/ismej.2013.174
- 10.1038/ismej.2016.43
- 10.1038/nature12352
- 10.1038/nature14486
- 10.1038/nature21031
- 10.1038/ismej.2015.233

- 10.1038/ncomms13219
- 10.1073/pnas.0801980105
- 10.1111/1462-2920.13362
- 10.1126/science.1132690
- 10.1186/s40168-015-0077-6

The list os correspondent phyla and articles is above

Tabela 2.1: table 1

| DOI | Phylum |
|---|---|
| 10.1038/nature14486 | Candidatus Falkowbacteria |
| 10.1038/nature14486 | Candidatus Kuenenbacteria |
| 10.1038/nature14486 | Candidatus Magasanikbacteria |
| 10.1038/nature14486 | Candidatus Uhrbacteria |
| 10.1038/nature14486 | Candidatus Moranbacteria |
| 10.1038/nature14486 | Candidatus Azambacteria |
| 10.1038/nature14486 | Candidatus Yanofskybacteria |
| 10.1038/nature14486 | Candidatus Jorgensenbacteria |
| 10.1038/nature14486 | Candidatus Wolfebacteria |
| 10.1038/nature14486 | Candidatus Giovannonibacteria |
| 10.1038/nature14486 | Candidatus Nomurabacteria |
| 10.1038/nature14486 | Candidatus Campbellbacteria |
| 10.1038/nature14486 | Candidatus Adlerbacteria |
| 10.1038/nature14486 | Candidatus Kaiserbacteria |
| 10.1038/nature14486 | C. S. yataiensis |
| 10.1038/nature14486 | Pacebacteria |
| 10.1038/nature14486 | Candidatus Collierbacteria |
| 10.1038/nature14486 | Candidatus Beckwithbacteria |
| 10.1038/nature14486 | Candidatus Roizmanbacteria |
| 10.1038/nature14486 | Candidatus Saphirobacteria |
| 10.1038/nature14486 | Candidatus Amesbacteria |
| 10.1038/nature14486 | Candidatus Woesebacteria |
| 10.1038/nature14486 | Candidatus Gottesmanbacteria |
| 10.1038/nature14486 | Candidatus Levybacteria |
| 10.1038/nature14486 | Candidatus Daviesbacteria |
| 10.1038/nature14486 | Candidatus Curtissbacteria |
| 10.1038/nature14486 | WWE3 |
| 10.1038/nature14486 | CPR3 |
| 10.1038/nature14486 | WS6 |
| 10.1038/nature14486 | Candidatus Berkelbacteria |
| 10.1038/nature14486 | Candidatus Peregrinibacteria |
| 10.1038/nature14486 | Candidatus Gracilibacteria |
| 10.1038/nature14486 | CPR2 |
| 10.1038/nature14486 | Kazan |
| 10.1038/nature14486 | Saccharibacteria (TM7) |
| 10.1038/nature14486 | SR1 |
| 10.1038/ncomms13219 | Candidatus Kerfeldbacteria |
| 10.1038/ncomms13219 | Candidatus Komeilibacteria |
| 10.1038/ncomms13219 | Candidatus Andersenbacteria |
| 10.1038/ncomms13219 | Candidatus Ryanbacteria |
| 10.1038/ncomms13219 | Candidatus Niyogibacteria |

| | |
|---|---|
| 10.1038/ncomms13219 | Candidatus Tagabacteria |
| 10.1038/ncomms13219 | Candidatus Terrybacteria |
| 10.1038/ncomms13219 | Candidatus Vogelbacteria |
| 10.1038/ncomms13219 | Candidatus Zambryskibacteria |
| 10.1038/ncomms13219 | Candidatus Taylorbacteria |
| 10.1038/ncomms13219 | Candidatus Sungbacteria |
| 10.1038/ncomms13219 | Candidatus Brennerbacteria |
| 10.1038/ncomms13219 | Candidatus Spechtbacteria |
| 10.1038/ncomms13219 | Candidatus Staskawiczbacteria |
| 10.1038/ncomms13219 | Candidatus Wildermuthbacteria |
| 10.1038/ncomms13219 | Candidatus Portnoybacteria |
| 10.1038/ncomms13219 | Candidatus Woykebacteria |
| 10.1038/ncomms13219 | Candidatus Blackburnbacteria |
| 10.1038/ncomms13219 | Candidatus Chisholmbacteria |
| 10.1038/ncomms13219 | Candidatus Buchananbacteria |
| 10.1038/ncomms13219 | Candidatus Jacksonbacteria |
| 10.1038/ncomms13219 | Candidatus Veblenbacteria |
| 10.1038/ncomms13219 | Candidatus Nealsonbacteria |
| 10.1038/ncomms13219 | Candidatus Colwellbacteria |
| 10.1038/ncomms13219 | Candidatus Liptonbacteria |
| 10.1038/ncomms13219 | Candidatus Harrisonbacteria |
| 10.1038/ncomms13219 | Candidatus Yonathbacteria |
| 10.1038/ncomms13219 | Candidatus Lloydbacteria |
| 10.1038/ncomms13219 | Candidatus Abawacabacteria |
| 10.1038/ncomms13219 | Candidatus Doudnabacteria |
| 10.1038/ismej.2013.111 | Candidatus Poribacteria |
| 10.1111/1462-2920.13362 | Candidatus Desantisbacteria |
| 10.1038/nature12352 | Candidatus Omnitrophica |
| 10.1038/nature12352 | Candidatus Aminicenantes |
| 10.1126/science.1132690 | Candidatus Micrarchaeota |
| 10.1038/nature14486 | Candidatus Magasanikbacteria |
| 10.1073/pnas.0801980105 | Candidatus Korarchaeota |
| 10.1038/nature12352 | Candidatus Fervidibacteria |
| 10.1038/nature12352 | Candidatus Aenigmarchaeota |
| 10.1038/ismej.2016.43 | Candidatus Fermentibacteria |
| 10.1038/ismej.2013.174 | Candidatus Bathyarchaeota |
| 10.1016/j.cub.2015.01.014 | Candidatus Woesearchaeota |
| 10.1016/j.cub.2015.01.014 | Candidatus Kryptonia |
| 10.1038/nature12352 | Candidatus Diapherotrites |
| 10.1038/nature12352 | Candidatus Latescibacteria |
| 10.1038/nature21031 10.1038/ismej.2015.233 | Candidatus Thorarchaeota |
| 10.1038/ncomms13219 | Candidatus Lindowbacteria |
| 10.1038/nature12352 | Candidatus Parvarchaeota |
| 10.1038/nature12352 | Candidatus Cloacimonetes |
| 10.1038/nature12352 | Candidatus Hydrogenedentes |
| 10.1038/nature12352 | Candidatus Acetothermia |

| | |
|---|---|
| 10.1038/nature12352 | Candidatus Nanohaloarchaeota |
| 10.1038/ncomms13219 | Candidatus Eisenbacteria |
| 10.1186/s40168-015-0077-6 | candidate division WOR-3 |
| 10.1038/nature21031 | Lokiarchaeota |
| 10.1038/nature21031 | Odinarchaeota |
| 10.1038/nature21031 | Heimdallarchaeota |

## 2.2 28

### 2.2.1 Bibliographic search for metagenomes

The reserarch for coral metagenomes started last year. The actual list is:

Tabela 2.2: table 1

| IDs |
|---|
| mgm4440319.3 |
| mgm4440370.3 |
| mgm4440371.3 |
| mgm4440372.3 |
| mgm4440373.3 |
| mgm4440374.3 |
| mgm4440375.3 |
| mgm4440376.3 |
| mgm4440377.3 |
| mgm4440378.3 |
| mgm4440379.3 |
| mgm4440380.3 |
| mgm4440381.3 |
| mgm4445755.3 |
| mgm4445756.3 |
| mgm4480739.3 |
| mgm4480740.3 |
| mgm4480741.3 |
| mgm4480748.3 |
| mgm4480750.3 |
| mgm4487909.3 |
| mgm4487910.3 |
| mgm4487911.3 |
| mgm4516541.3 |
| mgm4516694.3 |
| mgm4653307.3 |
| mgm4694757.3 |
| mgm4694758.3 |

mgm4694759.3
mgm4694760.3
SRR1275409
SRR1275449
SRR1283349
SRR1283371
SRR1283377
SRR1283433
SRR1283435
SRR1283437
SRR1286223
SRR1286225
SRR1286226
SRR1286227
SRR1286229
SRR1286232
SRR1822488
SRR1822516
SRR3499156
SRR3569370
SRR3694369
SRR3694370
SRR3694371
SRR3694372
SRR5215424
SRR5215454
SRR5215455
SRR5215456
SRR5215457
SRR5215458
SRR5215462
SRR5605611

I found these metagenomes in the article: "Metagenomic analysis reveals a green sulfur bacterium as a potential coral symbiont"

SRR2937345
SRR2937346
SRR2937347
SRR2937348
SRR2937349
SRR2937350
SRR2937351
SRR2937352

SRR2937353
SRR2937354
SRR2937355
SRR2937356

Espcie: Platygyra carnosa Healthy

I found other metagenomes of coral from article doi Ï0.3389/fmars.2018.00101Ï uptated the file pmc_results_1.txt in the repository Lab_book. I continue to look the articles in results. Estou atualizando a lista pmc_results_2.txt Na pesquisa bibliografica olhando o ttulo ja me faz perceber se devo descartar e olhar. E olho aqueles que marquei para olhar. Ao olhar, leio o resumo procurando por metodos. E vou para os metodos do artigo para checar. Checking the sizes of metagenomes files. The mg-rast metagenomes base have 72 Gb.

The pipeline of bioinformatic is different for MGRAST and NCBI. The size of NCBI should be superestimated, because the ncbi says the file size of sra file, but most of them is paired-end metagenomes, so when we apply fastq-dump, its generate two files fastq.

# Capítulo 3

# Download of metagenomes

## 3.1 Download of mg-rast files

Espao no SDU Disponvel para o ebiodiv: 10Tb Bia: 5Tb Rilquer: 2T Remanescente: 3Tb

- Working folder: *scratch/ebiodiv/leticia.cavalcante/mg_rast*

I insert the list of metagenomes in the files before using it. After this, I used the following command line:

- Command: *nohup bash download_curl_mgrast_corais.sh ¿ download_curl_mgrast_corais.nohupout &*

## 3.2 Download of NCBI metagenomes

I use the script download_sra_wget_corais.sh, libs folder. I used the wget, because the curl is getting some problem in SDU. I noted that the size of the files is different:

Tabela 3.1: Comparing sizes of files

| ID of metagenome | the size in NCBI site | size of file in SDU |
|---|---|---|
| SRR6785058 | 317.00 Mb | 318M |
| SRR6785057 | 364.00 Mb | 365M |
| SRR6785056 | 560.00 Mb | 561M |
| SRR6785055 | 624.00 Mb | 625M |

So I checked the others files:

A Bia me informou que o SDU arrendonda os valores de tamanho dos arquivos, entao at o momento nao tive problemas com o download dos arquivos do mg_rast

Tabela 3.2: Comparing sizes of files 2

| ID of metagenome | the size in NCBI site | size of file in SDU | size of cleanned file |
|---|---|---|---|
| mgm4440319.3.299.1 | 30M | 29.1 MB | 28M |
| mgm4440370.3.299.1 | 3,6M | 3.5 MB | 3,5M |
| mgm4440371.3.299.1 | 5,0M | 4.9 MB | 4,8M |
| mgm4440372.3.299.1 | 6,0M | 6.0 MB | 5,9M |
| mgm4440373.3.299.1 | 6,2M | 6.1 MB | 6,0M |
| mgm4440374.3.299.1 | 4,1M | 4.1 MB | 4,0M |
| mgm4440375.3.299.1 | 3,8M | 3.7 MB | 3,7M |
| mgm4440376.3.299.1 | 3,9M | 3.9 MB | 3,8M |
| mgm4440377.3.299.1 | 3,5M | 3.5 MB | 3,4M |
| mgm4440378.3.299.1 | 6,2M | 6.2 MB | 6,1M |
| mgm4440379.3.299.1 | 7,0M | 7.0 MB | 6,9M |
| mgm4440380.3.299.1 | 5,2M | 5.2 MB | 5,2M |
| mgm4440381.3.299.1 | 6,4M | 6.4 MB | 6,4M |
| mgm4445755.3.299.1 | 158M | 157.0 MB | 155M |
| mgm4445756.3.299.1 | 150M | 149.9 MB | 147M |
| mgm4480739.3.299.1 | 8,0M | 7.9 MB | 7,9M |
| mgm4480740.3.299.1 | 12M | 11.3 MB | 12M |
| mgm4480741.3.299.1 | 8,5M | 8.5 MB | 8,5M |
| mgm4480742.3.299.1 | 10M | 12.9 MB | 10M |
| mgm4480743.3.299.1 | 15M | 10.0 MB | 14M |
| mgm4484839.3.299.1 | 13M | 14.1 MB | 13M |
| mgm4487909.3.299.1 | 17M | 16.5 MB | 17M |
| mgm4487910.3.299.1 | 36M | 35.6 MB | 36M |
| mgm4487911.3.299.1 | 12M | 11.4 MB | 12M |
| mgm4516541.3.299.1 | 161M | 160.2 MB | 163M |
| mgm4516694.3.299.1 | 193M | 192.9 MB | 193M |
| mgm4653307.3.299.1 | 17M | 16.0 MB | 17M |
| mgm4694757.3.299.1 | 1,9G | 1.8 GB | 1,9G |
| mgm4694758.3.299.1 | 2,2G | 2.1 GB | 2,2G |
| mgm4694759.3.299.1 | 1,7G | 1.7 GB | 1,8G |
| mgm4694760.3.299.1 | 592M | 1.6 GB | 597M |

# Capítulo 4

# Format Conversion of NCBI metagenomes

Adaptei o script da Bia para fazer a conversao do dos arquivos .sra
Inicialmente submeti apenas um na cpu_dev para testar:

Script: *teste_slurm_job_fastq_dump_corais.sh*
Numero do job: *220896*

Deu certo.
O Rilquer me ajudou a criar um script que cria jobs de anotacao com o kraken2 para cada dois metagenomas.
O nome do script 'creatijobfile.sh', ele unir dois scripts: 'header' e 'ending'
Adaptei para criar jobs do fastq-dump para cada 2 arquivos .sra, haja visto que no tenho uma boa ideia do quanto cada fastq-dump demorar.

Jobs submetidos dia 27/09/2018:

- job_0.sh - job 221475
- job_100.sh - job 221476
- job_102.sh - job 221477
- job_104.sh - job 221478
- job_106.sh - job 221480
- job_108.sh - job 221481
- job_10.sh - job 221482
- job_110.sh - job 221483
- job_112.sh - job 221484
- job_114.sh - job 221485

- job_116.sh - job 221486
- job_118.sh - job 221487
- job_120.sh - job 221488
- job_122.sh - job 221489
- job_124.sh - job 221490
- job_126.sh - job 221493
- job_12.sh - job 221495

# Capítulo 5

# Quality filter

This step is only required for NCBI metagenomes. The command line was proposed by Bia:

- trim_qual_left 25
- trim_qual_right 25

# Capítulo 6

# Uniformity filter (size and N bases)

## 6.1 Command line

Parameters:

- min_len 80
- ns_max_p 2
- out_format 1

- Command: *nohup bash slurm_job_prinseq_single_corais_FASTA.bash &¿ slurm_prinseq_corais.out &*

Deu erro o job nohup: ignorando entrada

Location of PRINSEQ dir and scripts: /scratch/app/prinseq/0.20.4/bin srun Warning: can't run 1 processes on 21 nodes, setting nnodes to 1 srun Requested partition configuration not available now srun job 212425 queued and waiting for resources srun Force Terminated job 212425 srun Job has been cancelled srun error: Unable to allocate resources: No error srun Warning: can't run 1 processes on 21 nodes, setting nnodes to 1 srun Requested partition configuration not available now srun job 212428 queued and waiting for resources srun Force Terminated job 212428 srun Job has been cancelled

Ressubmeti o job com:

- Command: *sbatch slurm_job_prinseq_single_corais_FASTA.bash*

09-35-27.png

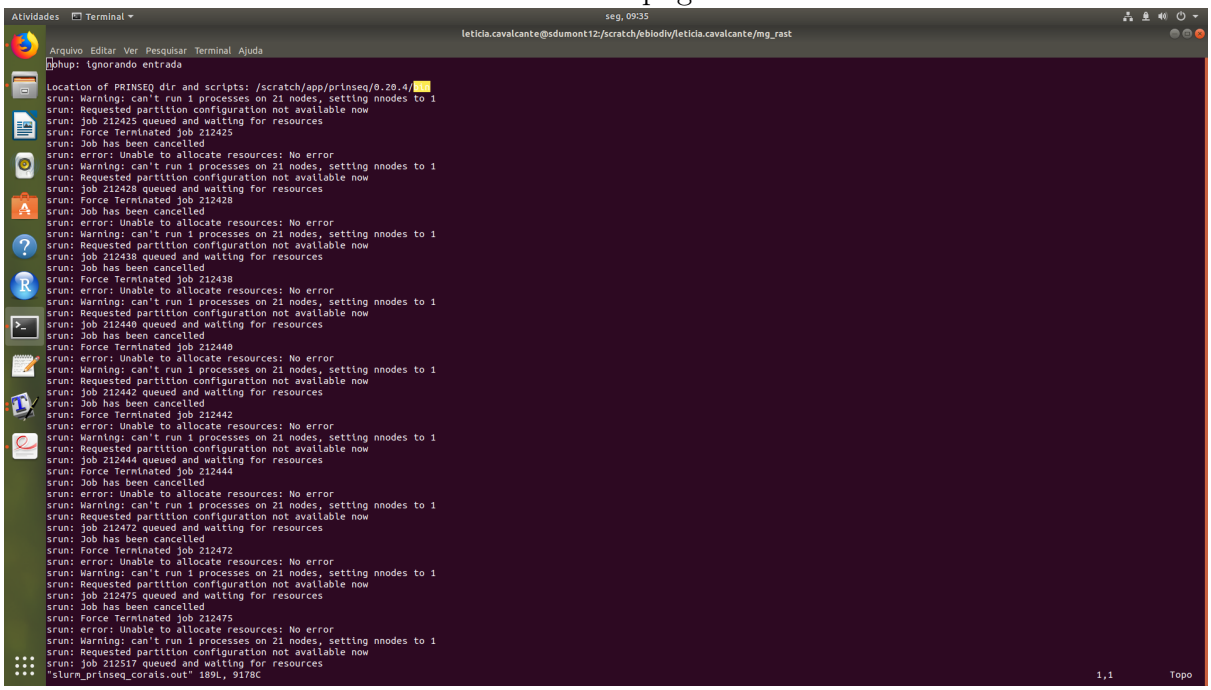


Figura 6.1: Erro no job no SDU

# Capítulo 7

# Profilling metagenomes

## 7.1 Mg-Rast metagenomes

I used the following script in the following folder:

- Folder: *scratch/ebiodiv/leticia.cavalcante/mg_rast/filtered_prinseq_good*
- Command: *sbatch slurm_job_kraken2_corais.sh*

The job doesn't work, o erro aparece na proxima figura

Ressubmeti o job, modificando a localizacao da DB do Kraken para a home do Rilquer. Numero do job: 216410

Esse problema foi resolvido modificando o endereco da base para o scratch do Rilquer.

## 7.2 Kraken-biom

Pasta onde est instalado kraken-biom:
/home/leticia/.local/bin

Para executar: python2.7 .kraken-biom

Executar o help do kraken-biom:
kraken-biom -h

Abrir no vim o arquivo .bashrc e inserir:
export PATH=$PATH:/home/leticia/.local/bin/kraken-biom

Executar o help do kraken-biom:
kraken-biom -h

Eu fiz um teste da etapa "Creation of BIOM table of abundances"da pipeline da bia com os seguintes passos: Na pasta /home/leticia/Documentos/libs/leticia_profiling_metagenomes:

- kraken-biom selected_file -o table.biom –max D –min P
- biom convert -i table.biom -o table.from_biom_with_taxonomy.txt –to-tsv –header-key taxonomy

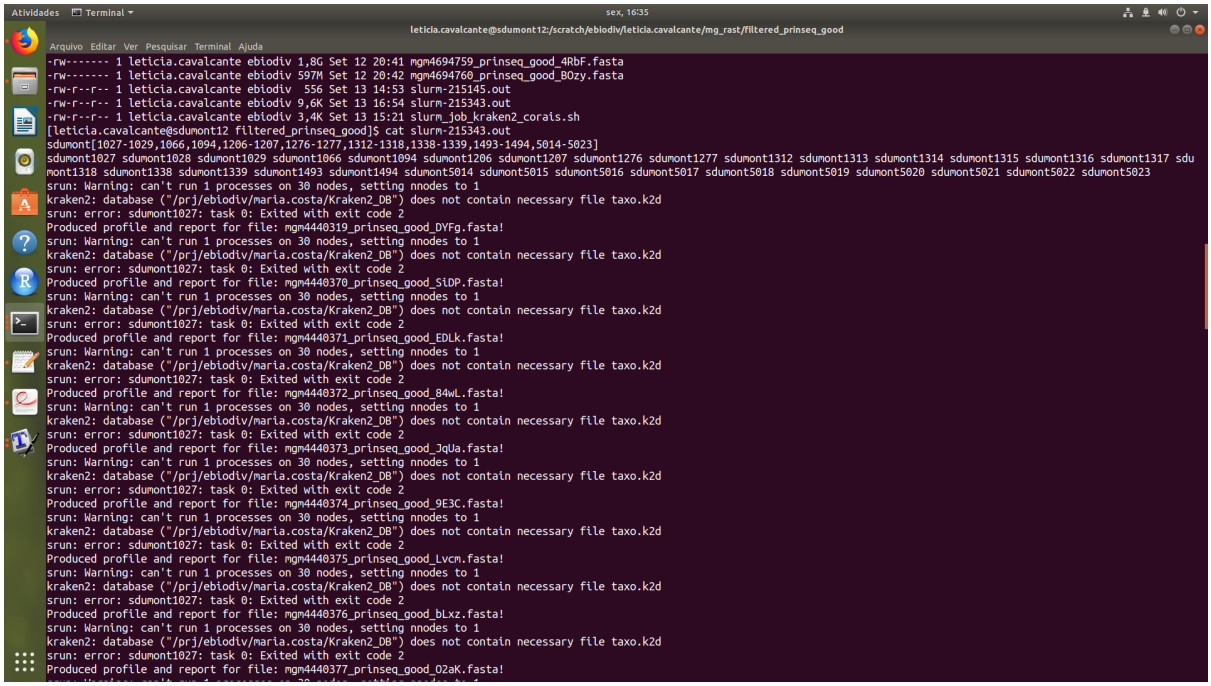


Figura 7.1: 2o erro no job no SDU

- perl filterRank.pl input table.from_biom_with_taxonomy.txt –rank p ¿ abundance.matrix

## 7.3 Teste com o kraken no scratch

Linha de teste:
perl selectGroups.pl input mgm4440370_prinseq_good_SiDP.fasta_kraken.report –file_groups groups.txt ¿ selected_file

- First Command: *sbatch slurm_job_kraken2_corais.sh*
- Second Command:
*kraken2 –db /prj/ebiodiv/rilquer.silva/Serrapilheira /Kraken2_custom_DB/ mgm4440370_prinseq_good_SiDP.fasta –output mgm4440370_prinseq_good_SiDP.fasta_kraken.profiled –use-names –report mgm4440370_prinseq_good_SiDP.fasta_kraken.report*

Ja testei o comando acima na home do SDU e agora no scratch

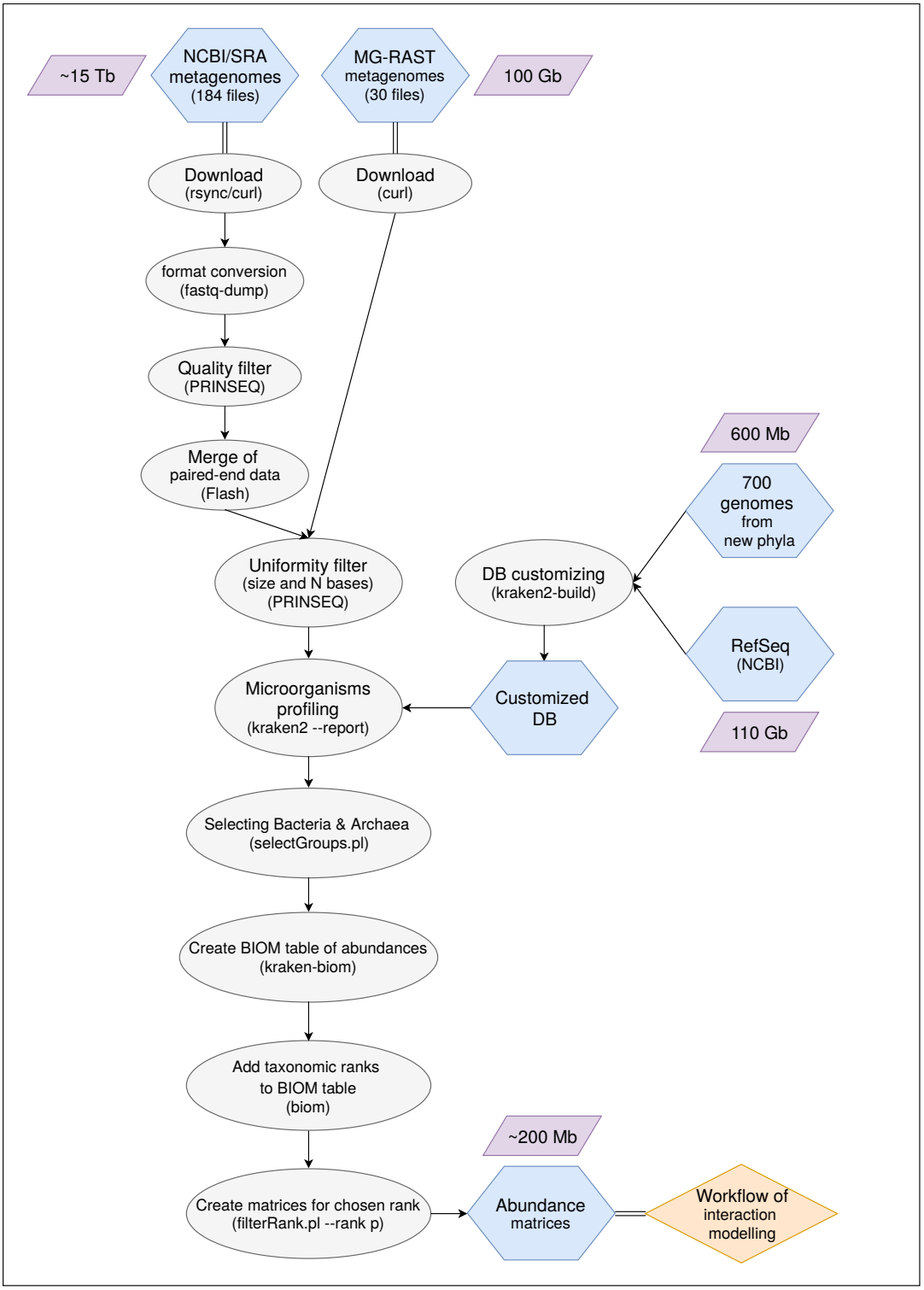


Figura 7.2: Pipeline of taxonomic annotation

## 7.4 Analises e obtencao de figuras

Apliquei o tutorial do professor para obteno de figuras no R para visualizao dos resultados.

- Script: *analisys.R*
- Folder: */home/leticia/Documentos/libs/R*

Figuras obtidas:

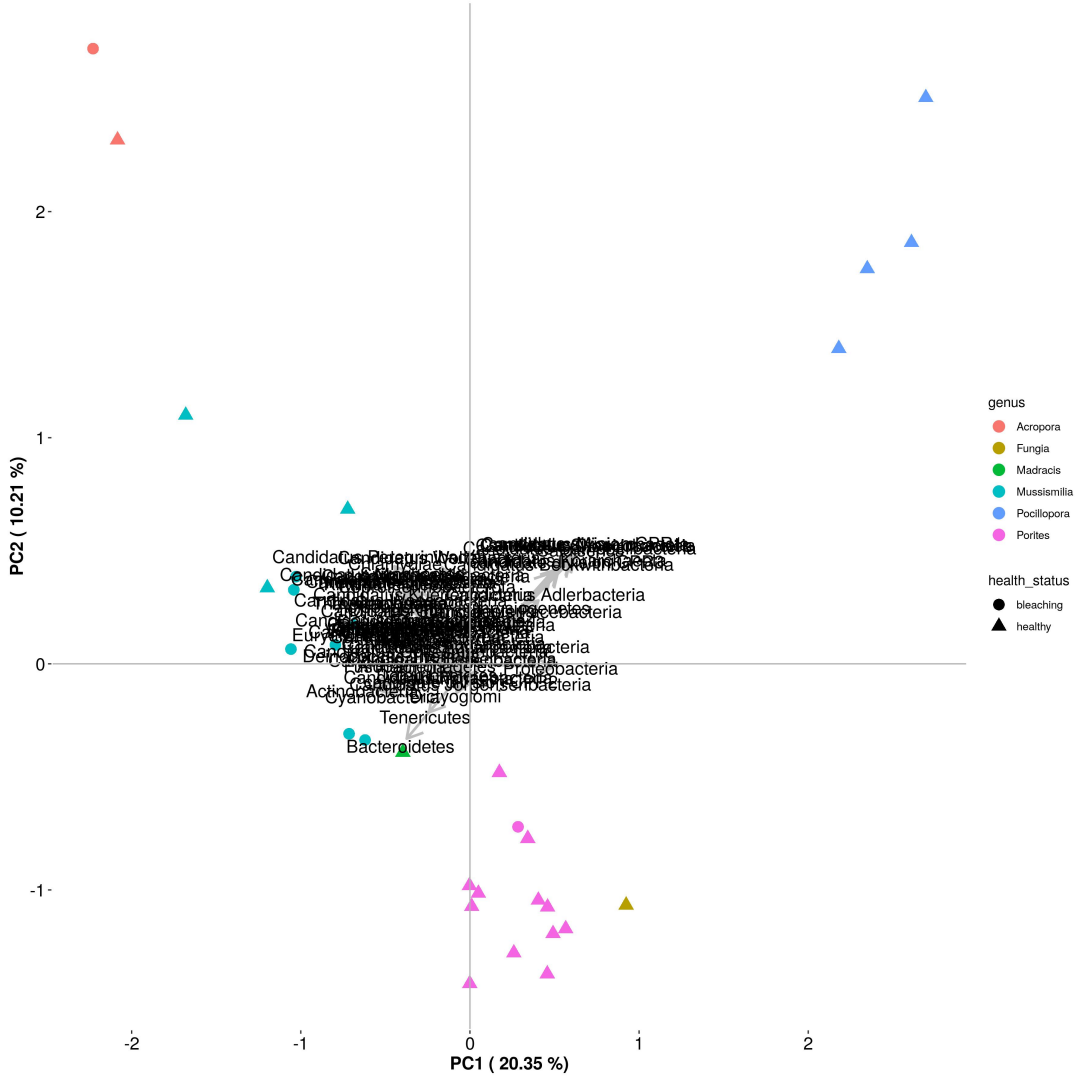


Figura 7.3: Anlise de componentes principais com todos os filos como variaveis

Na analise acima, as variaveis so muitas e ficam muito sobrepostas, fazendo com que haja grande poluicao visual. O professor recomendou em marco a utilizar uma analise de Random Forest, para que as variaveis mais importantes para os metagenomas que trabalho sejam ranqueadas.

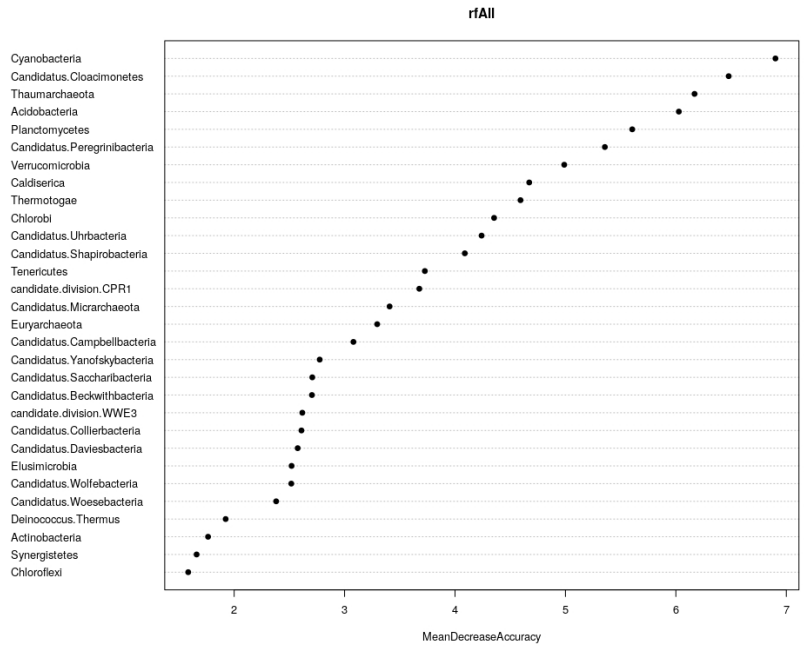


Figura 7.4: Random Forest ranqueando filos

Eu utilizei os 20 primeiros filos ranqueados para fazer o PCA. Segue esse PCA abaixo:

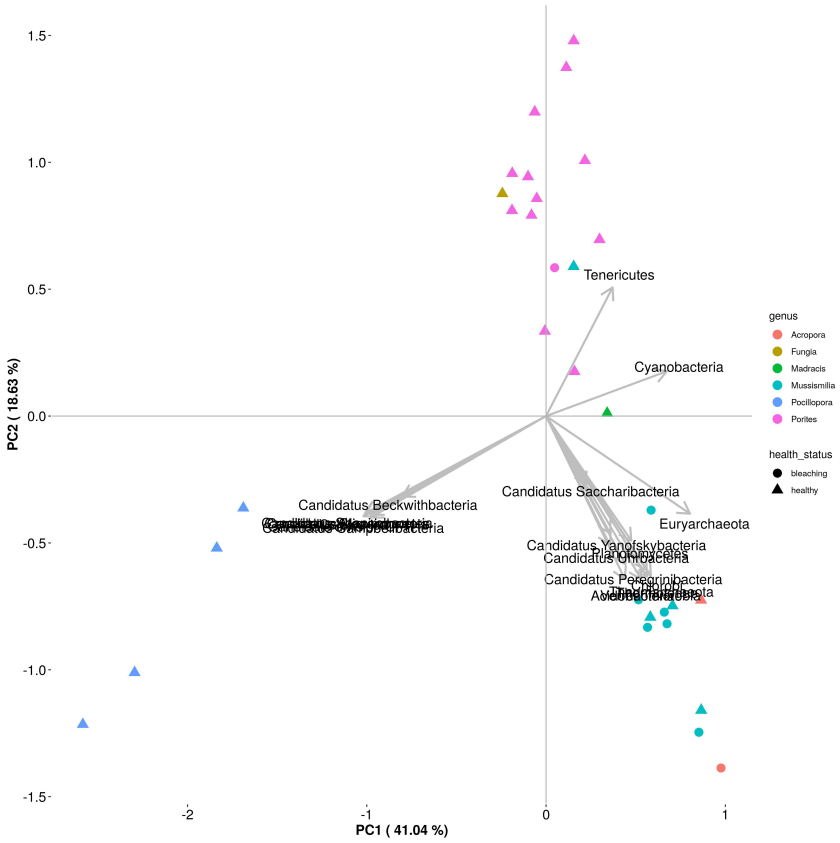


Figura 7.5: PCA com 20 filos utilizados no PCA

Uma tendencia se manteve: foi a separao das amostras por genero. Mas a poluicao visual ainda continuou, por isso fiz um random forest com os 15 primeiros filos indicados pelo random forest. Segue abaixo:

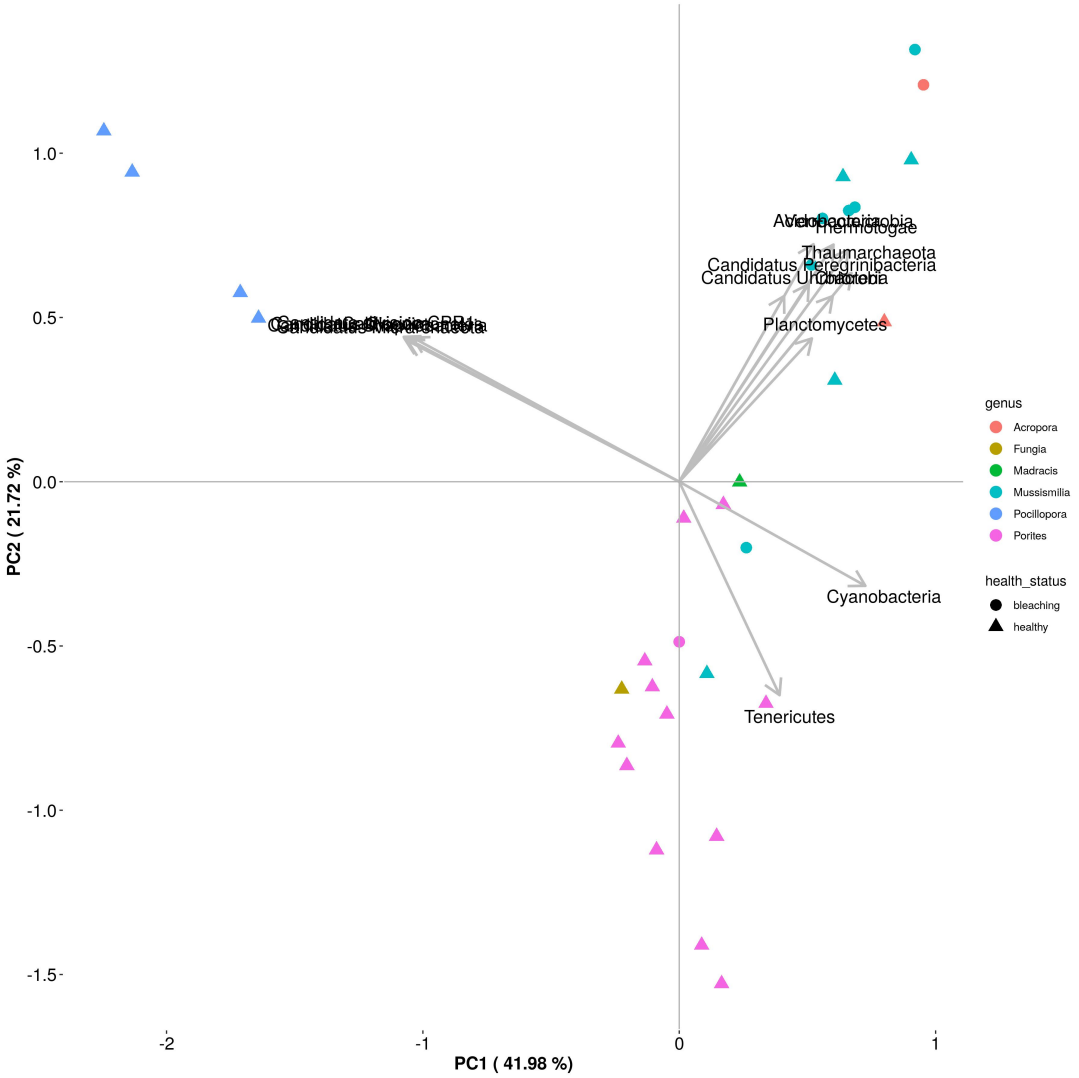


Figura 7.6: PCA com 15 filos como variaveis

Algumas tendencias tambem se mantiveram e a explicao dos eixos melhorou levemente. As amostras agrupadas no quadrante direito superior so mais diferentes das que esto no quadrante esquerdo do que das que esto no quadrante inferior direito. Na reuniao feita no dia 03/10/2018, o Amaro, o professor e Miguel me sinalizaram que existe uma separacao forte entre generos, indicando que os grupos candidatos podem ser genero - especficos. Surgiu a sugesto de leitura de textos em core microbiome e especificidade de filos entre generos.

# Capítulo 8

# Functional annotation of metagenomes

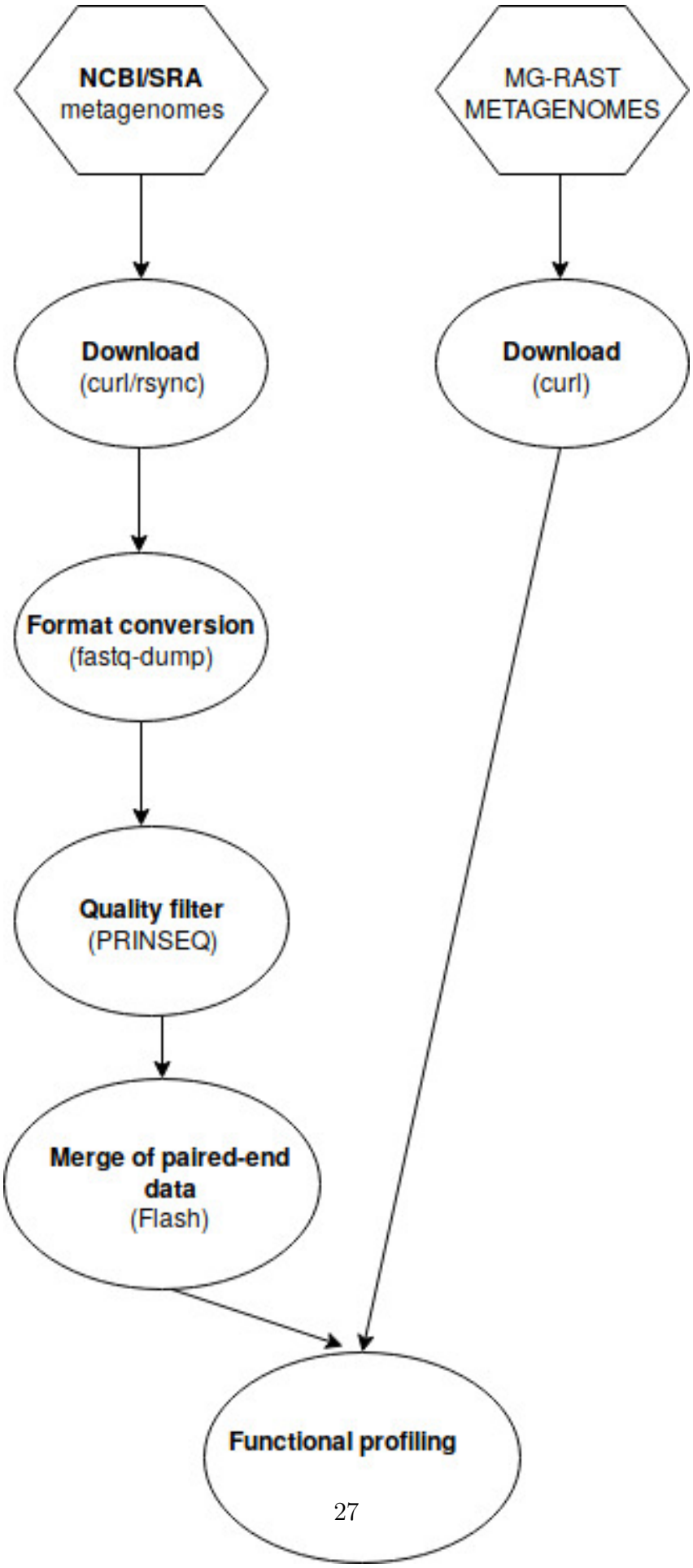




Figura 8.1: Pipeline of functional annotation

# Capítulo 9

# references

Articles list:

- 10.1371/journal.pone.0071301: Relata resultados que eu acreditava ter sido a primeira a encontrar
- 10.1038/nature14486: reconstruction of microorganism's genomes we use
- 10.1038/nmicrobiol.2016.48: three of life, including the Candidate Phyla Radiation
- 10.1146/annurev.micro.57.030502.090759: speaks about the uncultured majority of microorganisms
- 10.1038/ismej.2016.174: revision of rare biosphere
- 10.1038/nrmicro3400: another revision of rare biosphere
- 10.1126/science.1224041: metabolic activities of Candidatus Parcubacteria, one of super-phyla of CPR
- 10.1128/MMBR.00009-08: Revision of bioinformatic methods and steps for metagenomic
- 10.1186/s40168-018-0428-1: Sponge as holobiont. Note: This article has a important information about microbial ecology: "Network and modeling analyses aim to disentangle the strength and nature (positive, negative, or neutral) of the interactions and predict their dynamics. Bacteria-bacteria network analysis of the core microbiota in different sponge species has revealed a low connective network with very few strong and many weak unidirectional interactions (i.e., amensalism [/0] and commensalism [+/0] prevailed over cooperation [+/+] and competition [/]. These findings are consistent with mathematical models that predict that weak and non-cooperative interactions help to stabilize highly diverse microbial communities, whereas cooperation yields instability in the long term by fueling positive feedbacks"
- 10.1016/j.tim.2009.09.004: Microbial disease and the coral holobiont
- 10.3389/fmicb.2017.00618: Comparative Metagenomics of the Polymicrobial Black Band Disease of Corals

- 10.1038/nrmicro1643: The role of ecological theory in microbial ecology
- 10.1038/nrmicro3218: Explaining microbial genomic diversity in light of evolutionary ecology
- 10.1111/j.1462-2920.2009.01935.x: Metagenomic analysis of stressed coral holobionts
- 10.1038/nature06810: Functional metagenomic profiling of nine biomes
- 10.3389/fcimb.2014.00176: Microbes in the coral holobiont: partners through evolution, development, and ecological interactions
- 10.1038/ismej.2015.39: The coral core microbiome identifies rare bacterial taxa as ubiquitous endosymbionts
- 10.1111/j.1462-2920.2007.01383.x: Metagenomic analysis of the microbial community associated with the coral Porites astreoides
- 10.1038/nmicrobiol.2015.32: Metagenomics uncovers gaps in amplicon-based detection of microbial diversity
- 10.1038/ismej.2016.45: Challenges in microbial ecology: building predictive understanding of community function and dynamics
- 10.1111/j.1462-2920.2009.02113.x: Microbial functional structure of Montastraea faveolata, an important Caribbean reef-building coral, differs between healthy and yellow-band diseased colonies
- 10.1111/j.1758-2229.2010.00234.x:
- 10.1038/ismej.2011.116: Assessing the complex sponge microbiota: core, variable and species-specific bacterial communities in marine sponges

# Capítulo 10

# Softwares, instalacao e linhas

## 10.1 Profilling metagenomes

# Capítulo 11

# Fundamentos teoricos

# Capítulo 12

# meetings

Instalar o kraken-biome

- Folder: */home/leticia*
- Command: *pip install kraken-biom*
- Site: *https://github.com/smdabdoub/kraken-biom*

Para atualizacao:
git commit
git push origin master

Para transferencia:
maquina remota para local: scp leticia.cavalcante@login.sdumont.lncc.br:/scratch/ebiodiv/leticia.cavalc
/home/leticia/Documentos/dados

# Referências Bibliográficas