Initial data survey $_{LJM}$ $_{2019-11-19}$

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Chapter 1

The data

```
rm(list=ls())
library(tidyverse)
```

What is in the files?

1.1 Which bins belong to which fOTUS?

```
fOTUs <- read_csv(file = "../data/fOTUs.csv", col_names = TRUE)

## Parsed with column specification:
## cols(
## cogOTU_0 = col_character(),
## `fMAG:Loc081215-8m_megahit_metabat_bin-2464;fMAG:Loc081215-5m_megahit_metabat_bin-1172
## )

glimpse(fOTUs)

## Observations: 2,810
## Variables: 2
## $ cogOTU_0
## $ `fMAG:Loc081215-8m_megahit_metabat_bin-2464;fMAG:Loc081215-5m_megahit_metabat_bin-1172

colnames(fOTUs)

## [1] "cogOTU_0"
## [2] "fMAG:Loc081215-8m_megahit_metabat_bin-2464;fMAG:Loc081215-5m_megahit_metabat_bin-117</pre>
```

1.2 What bin does each cluster of orthologous genes (COG) belong to?

```
bin2cogs <- read_csv(file = "../data/bin2cogs.csv", col_names = TRUE)</pre>
## Parsed with column specification:
              `Loclat_megahit_metabat_bin-01178` = col_character(),
               `COG_187551;COG_170313;COG_741993;COG_112861;COG_88993;COG_70779;COG_170312;COG_5458;COG_187551;COG_170312;COG_5458;COG_187551;COG_170312;COG_187551;COG_188993;COG_187551;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_188993;COG_1889935;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_188995;COG_
## )
glimpse(bin2cogs)
## Observations: 29,614
## Variables: 2
## $ `Loclat_megahit_metabat_bin-01178`
## $ `COG_187551;COG_170313;COG_741993;COG_112861;COG_88993;COG_70779;COG_170312;COG_5458;CO
colnames(bin2cogs)
## [1] "Loclat_megahit_metabat_bin-01178"
## [2] "COG_187551;COG_170313;COG_741993;COG_112861;COG_88993;COG_70779;COG_170312;COG_5458
                   Stats on all fOTUed bins
stats_on_all_fOTUed_bins <- read_csv(file = "../analyses/stats_on_all_fOTUed_bins.csv", col
## Warning: Missing column names filled in: 'X1' [1]
## Parsed with column specification:
## cols(
         X1 = col_character(),
##
## length = col_double(),
## nb_contigs = col_double(),
## nb_proteins = col_double(),
##
           coding_density = col_double(),
##
          GC = col_double(),
##
           vir_fract = col_double(),
```

##

)

fOTU = col_character()

glimpse(stats_on_all_fOTUed_bins)

```
## $ nb_contigs
                  <dbl> 1, 1, 5, 1, 1, 1, 2, 2, 1, 5, 3, 6, 10, 4, 6, 8...
## $ nb_proteins
                  <dbl> 64, 55, 80, 65, 55, 39, 55, 12, 19, 27, 21, 23,...
## $ coding_density <dbl> 0.9361077, 0.9678284, 0.9031046, 0.9190103, 0.9...
                  <dbl> 0.4203425, 0.4260087, 0.4239431, 0.4202987, 0.4...
## $ GC
## $ vir_fract
                  ## $ fOTU
                  <chr> "cogOTU_0", "cogOTU_0", "cogOTU_0", "cogOTU_0",...
colnames(stats_on_all_fOTUed_bins)
## [1] "X1"
                      "length"
                                      "nb_contigs"
                                                     "nb_proteins"
## [5] "coding_density" "GC"
                                     "vir_fract"
                                                     "fOTU"
```

1.4 Stats on representative bins

```
stats_on_representative_bins <- read_csv(file = "../analyses/stats_on_representative_bins.cs
## Warning: Missing column names filled in: 'X1' [1]
## Parsed with column specification:
## cols(
    X1 = col_character(),
##
##
    length = col_double(),
    nb_contigs = col_double(),
##
##
    nb_proteins = col_double(),
     coding_density = col_double(),
##
##
    GC = col_double(),
##
     vir_fract = col_double(),
##
     fOTU = col_character(),
##
     other_members = col_character()
## )
glimpse(stats_on_representative_bins)
## Observations: 2,430
## Variables: 9
## $ X1
                    <chr> "Loc081215-5m_megahit_metabat_bin-1172", "Loc08...
                    <dbl> 30213, 13170, 44529, 14195, 23811, 70833, 24419...
## $ length
## $ nb_contigs
                    <dbl> 1, 3, 9, 1, 5, 1, 3, 1, 3, 3, 2, 8, 19, 1, 5, 9...
## $ nb_proteins
                    <dbl> 55, 23, 71, 24, 29, 121, 30, 32, 16, 27, 19, 45...
## $ coding_density <dbl> 0.9678284, 0.8018223, 0.8892407, 0.9256781, 0.8...
                    <dbl> 0.4260087, 0.4763857, 0.6836219, 0.6211342, 0.5...
## $ GC
## $ vir_fract
                    <dbl> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 83076, 0, 0...
## $ fOTU
                    <chr> "cogOTU_0", "cogOTU_1", "cogOTU_2", "cogOTU_3",...
## $ other_members <chr> "fMAG:Loc081215-8m_megahit_metabat_bin-2464;fMA...
colnames(stats_on_representative_bins)
```

[1] "X1" "length" ## [5] "coding_density" "GC" ## [9] "other_members" "nb_contigs"
"vir_fract" "nb_proteins" "fOTU"