Viral Beacon Statistics part 1

1   Stats on files

Statistics are calculated using `Filters`.

1. Number of runs (fastqs): total runIds= 1094

2. Number of runs (fastqs) with variants (we are keeping WT?)

3. Number of unique sequence/haplotypes: ?

option Split by sequence database: SRA=1094, GISIAD=0, GWH=0
   NO SHOW - Click on SRA

option Split by sequencing technology (platform): Illumina=1094, Nanopore=0

option Split by sequencing platform model

option Split by sequencing library layout

option Split by Individual geographic region (grouped by countries)

option Split by Individual sex

option Split by Individual age (grouped by age groups)

option Split by Individual disease (grouped by harmonized values)

option Split by Biosample collection date (grouped by month)

option Split by Biosample sample type (grouped by harmonized values)

1.1   Graphs
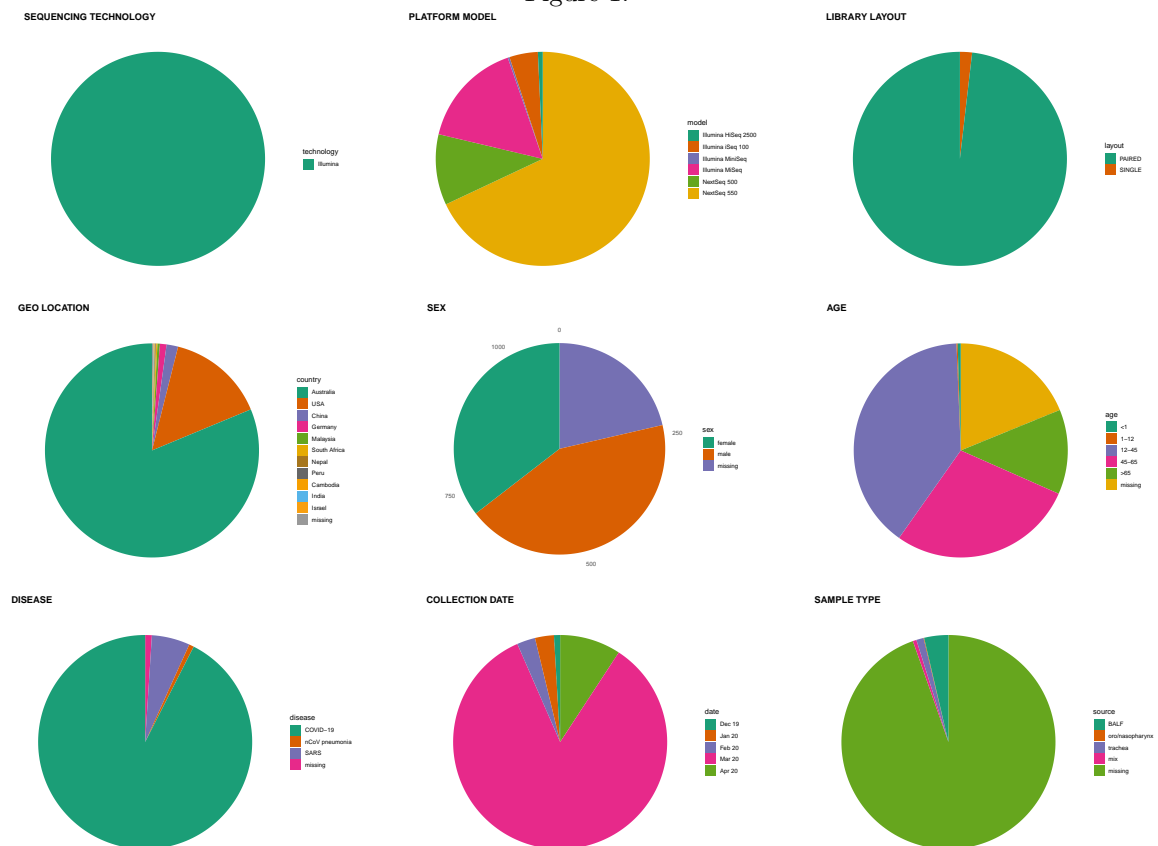
Show as pie charts 1 or bar charts 2.

Figure 1:

Figure 2: