1.2_Dataset_Visualization_inR

September 9, 2020

1 1.2 Dataset Visualization in R

Author: Sandra Godinho Silva
Creation date: 07/09/2020
Version: 0.1

Input from **notebook 1.1 - Dataset Creation**: Dataset.csv

[1]:
```
library(ggplot2)
library(grid)
library(gridExtra)
library(dplyr)
library(plyr)
library(ggpubr)
```

```

Attaching package: ‘dplyr’

The following object is masked from ‘package:gridExtra’:

    combine

The following objects are masked from ‘package:stats’:

    filter, lag

The following objects are masked from ‘package:base’:

    intersect, setdiff, setequal, union

------------------------------------------------------------------------------
You have loaded plyr after dplyr - this is likely to cause problems.
If you need functions from both plyr and dplyr, please load plyr first, then
dplyr:
library(plyr); library(dplyr)
------------------------------------------------------------------------------

Attaching package: ‘plyr’
```

```
The following objects are masked from ‘package:dplyr’:

    arrange, count, desc, failwith, id, mutate, rename, summarise,
    summarize

Loading required package: magrittr

Attaching package: ‘ggpubr’

The following object is masked from ‘package:plyr’:

    mutate
```

[2]:

```
data <- read.csv("Dataset.csv", header=T, row.names="Genome_ID")
head(data)
```

	Bin_Id	Marker.lineage	Complete
GCA_000016645.1	GCA_000016645.1_ASM1664v1_genomic	f___Flavobacteriaceae (UID2817)	99.65
GCA_000023285.1	GCA_000023285.1_ASM2328v1_genomic	p___Bacteroidetes (UID2605)	100.00
GCA_000023465.1	GCA_000023465.1_ASM2346v1_genomic	s___algicola (UID2847)	99.62
GCA_000023725.1	GCA_000023725.1_ASM2372v1_genomic	o___Flavobacteriales (UID2815)	100.00
GCA_000024125.1	GCA_000024125.1_ASM2412v1_genomic	s___algicola (UID2846)	99.01
GCA_000060345.1	GCA_000060345.1_ASM6034v1_genomic	s___algicola (UID2847)	99.62

1.1 4 faceted bar plots

[9]:

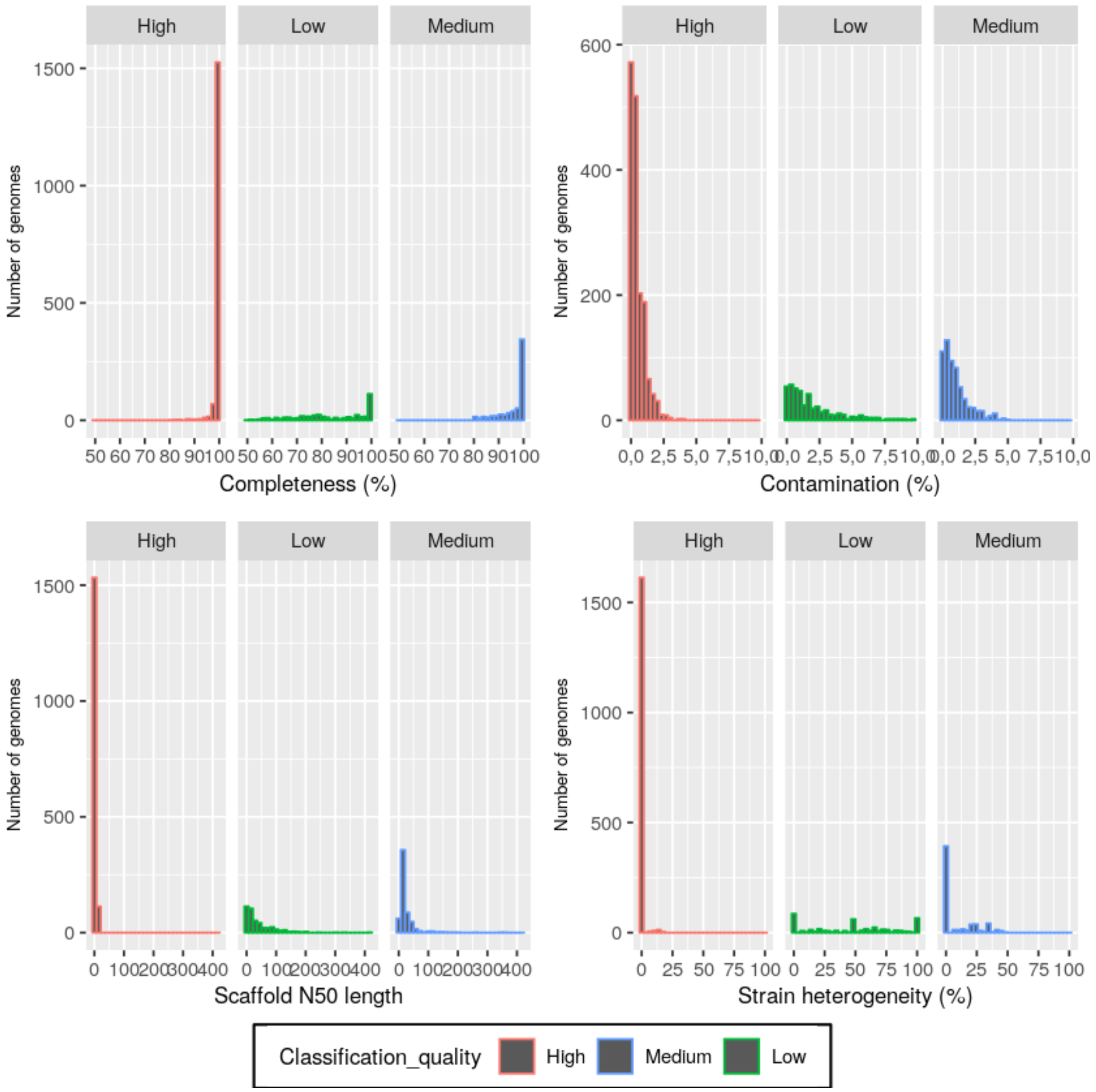
```
data <- as.data.frame(lapply(data, unlist))
data <- data %>% arrange(Quality_score)
data$Classification_f = factor(data$Classification_quality,␣
↪levels=c("High","Medium","Low"))
```

[13]:

```
#theme_set(theme_bw())
a <- ggplot(data, aes(x=Completeness, color=Classification_quality)) +
  geom_histogram(position="identity") +
  labs(y="Number of genomes", x="Completeness (%)") +
  theme(axis.title.y=element_text(size=8),
        axis.title.x=element_text(size=10),
        legend.box.background = element_rect(colour = "black", size = 0.6),
        legend.box.margin = margin(0.5, 6, 0.5, 6),
        legend.title = element_text(size=10))+
  scale_color_discrete(breaks=c("High","Medium","Low")) +
  facet_wrap(. ~ Classification_quality)

b <- ggplot(data, aes(x=Contamination, color=Classification_quality)) +
  geom_histogram(position="identity") +
  labs(y="Number of genomes", x="Contamination (%)") +
  theme(axis.title.y=element_text(size=8),
        axis.title.x=element_text(size=10),
        legend.box.background = element_rect(colour = "black", size = 0.6),
        legend.box.margin = margin(0.5, 6, 0.5, 6),
        legend.title = element_text(size=10))+
  scale_color_discrete(breaks=c("High","Medium","Low")) +
  facet_wrap(. ~ Classification_quality)

c <- ggplot(data, aes(x=scaf_N50, color=Classification_quality)) +
  geom_histogram(position="identity") +
  labs(y="Number of genomes", x="Scaffold N50 length") +
  theme(axis.title.y=element_text(size=8),
        axis.title.x=element_text(size=10),
        legend.box.background = element_rect(colour = "black", size = 0.6),
        legend.box.margin = margin(0.5, 6, 0.5, 6),
        legend.title = element_text(size=10),
        plot.margin=unit(c(5.5, 5.5, 7, 5.5), "pt"))+
  scale_color_discrete(breaks=c("High","Medium","Low"))+
  facet_wrap(. ~ Classification_quality)

d <- ggplot(data, aes(x=Strain_heterogeneity, color=Classification_quality)) +
  geom_histogram(position="identity") +
  labs(y="Number of genomes", x="Strain heterogeneity (%)") +
  theme(axis.title.y=element_text(size=8),
        axis.title.x=element_text(size=10),
        legend.box.background = element_rect(colour = "black", size = 0.6),
        legend.box.margin = margin(0.5, 6, 0.5, 6),
        legend.title = element_text(size=10),
        plot.margin=unit(c(5.5, 5.5, 7, 5.5), "pt"))+
  scale_color_discrete(breaks=c("High","Medium","Low"))+
  facet_wrap(. ~ Classification_quality)

ggarrange(a, b, c, d, ncol=2, nrow=2, common.legend = TRUE, legend="bottom")

ggsave("Comparison2", device="png",scale=1.3)
```

```
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
`stat_bin()` using `bins = 30`. Pick better value with `binwidth`.
```

```
Saving 8,67 x 8,67 in image
```

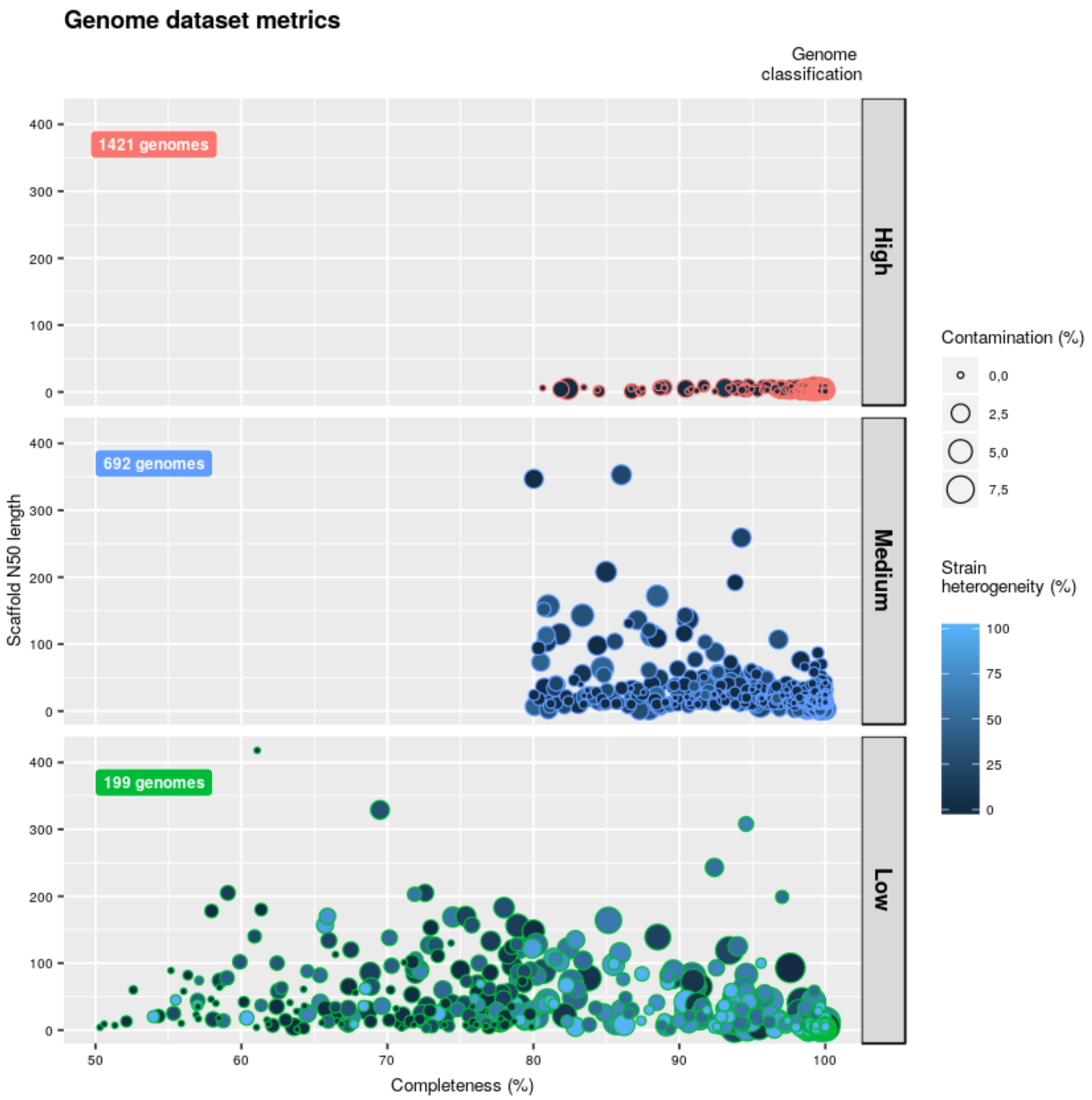


1.2 Plot 2

[14]:

```
g <- ggplot(data, aes(x=Completeness, y=scaf_N50,
                      fill=Strain_heterogeneity,␣
↪colour=Classification_quality,size=Contamination,))+
 geom_point(shape=21) +
 guides(color=FALSE) + #remove legend for Classification
 scale_color_discrete(breaks=c("High","Medium","Low"),␣
↪aes(fillcolour="black")) +
 scale_size_continuous(range=c(1,6)) +
 labs(y="Scaffold N50 length", x="Completeness (%)",
      subtitle = "Genome \nclassification",
```

```r
       title= "Genome dataset metrics",
       fill = "Strain \nheterogeneity (%) \n", size="Contamination (%)")+
  facet_grid(rows = vars(Classification_f))+
  theme(plot.title = element_text(size = 11, face="bold"),
        plot.subtitle= element_text(size=8, hjust = 1),
        legend.title = element_text(size=8),
        axis.title = element_text(size=8, colour="black"),
        axis.text.x = element_text(size=6, colour = "black"),
        axis.text.y = element_text(size=6, colour = "black"),
        legend.text = element_text(size=6),
        strip.text.y = element_text(size= 10, color = "black", face="bold"),
        strip.background = element_rect(color="black", linetype="solid"))

anno <- data.frame(lab = c("1421 genomes", "692 genomes", "199 genomes"),
                   Classification_f = c("High","Medium","Low"))

c <-g + geom_label(data = anno, mapping = aes(x = 54, y = 370, label = lab),␣
 ↪colour="white",
                   fill=c("#F8766D", "#619CFF", "#00BA38"),size=2.5,␣
 ↪fontface="bold",inherit.aes = FALSE)
c
```



[ ]:

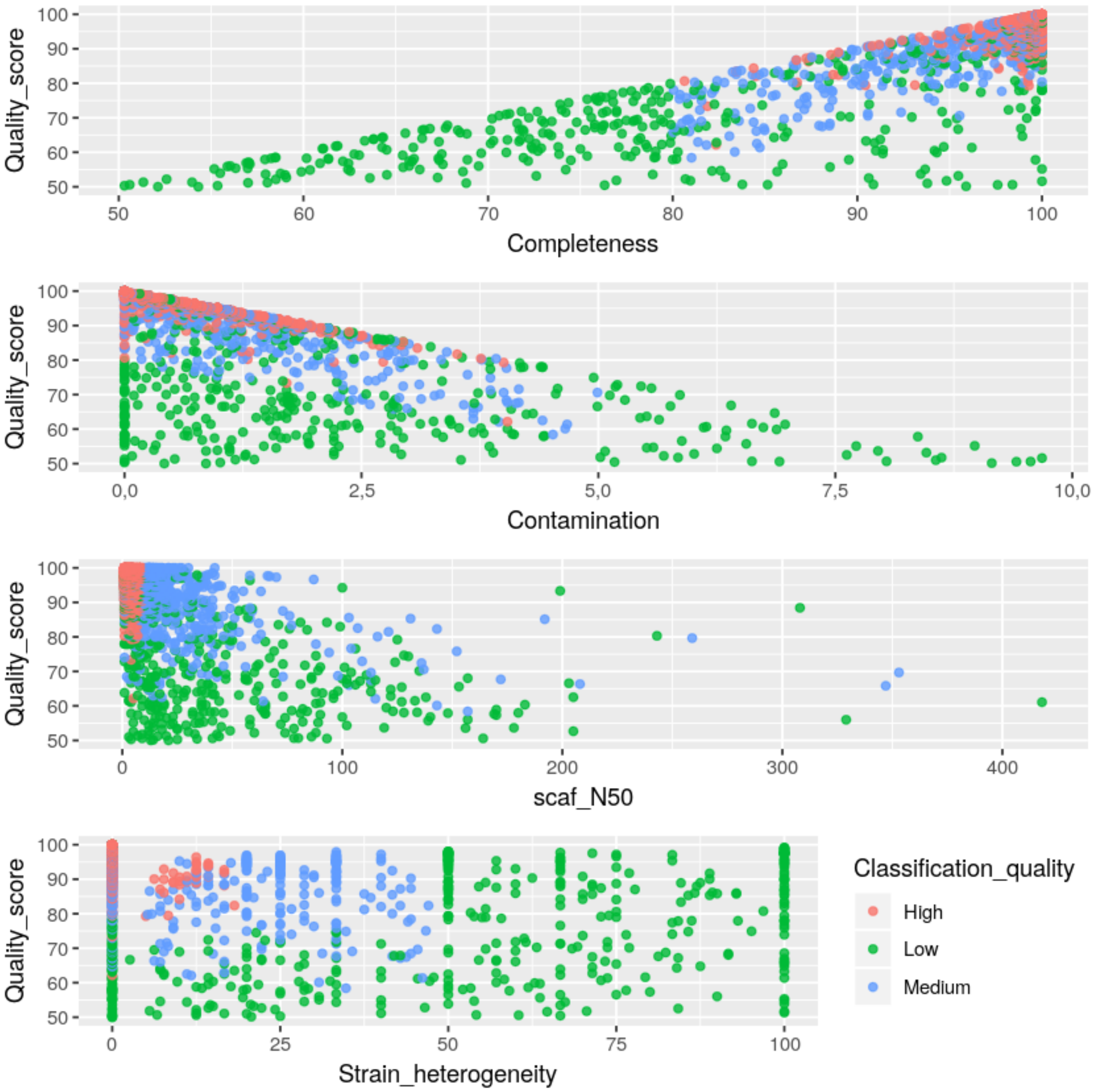
```
```

[16]:

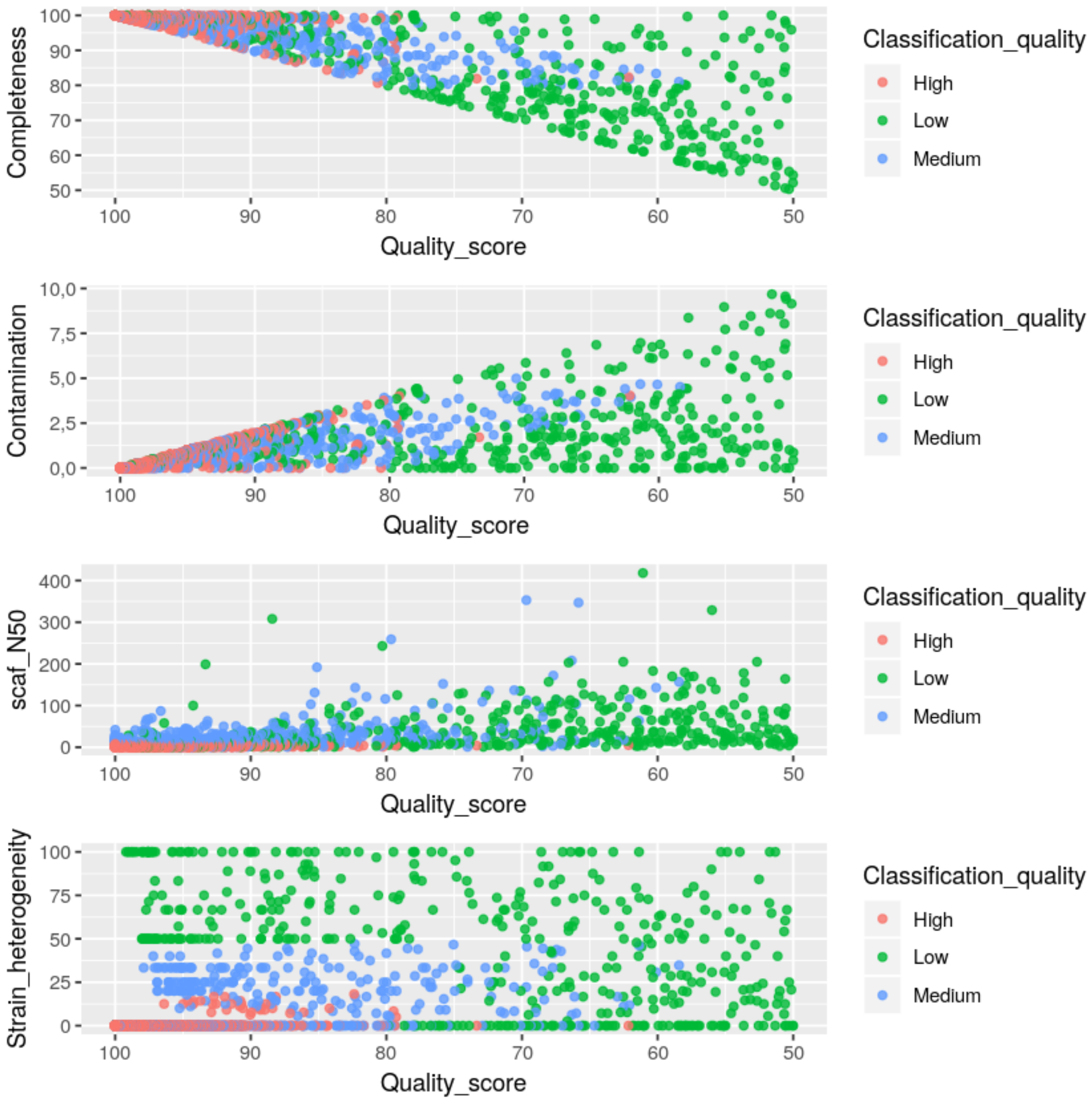
```
a <- ggplot(data, aes(y=Quality_score, x=Completeness,␣
↪color=Classification_quality, colour = clarity)) +
  geom_point(alpha=0.8)

b <- ggplot(data, aes(y=Quality_score, x=Contamination,␣
↪color=Classification_quality)) +
  geom_point(alpha=0.8)

c <- ggplot(data, aes(y=Quality_score, x=scaf_N50,␣
↪color=Classification_quality)) +
  geom_point(alpha=0.8)
```

```
d <- ggplot(data, aes(y=Quality_score, x=Strain_heterogeneity,␣
 ↪color=Classification_quality)) +
  geom_point(alpha=0.8)

grid.newpage()
grid.arrange(arrangeGrob(a + theme(legend.position="none"),
                         b + theme(legend.position="none"),
                         c+ theme(legend.position="none"),
                         d, nrow=4, ncol=1))

#ggarrange(a, b, c, d, ncol=1, nrow=4, common.legend = TRUE, legend="right")
```

```
Warning message:
"The plyr::rename operation has created duplicates for the following name(s):
(`colour`)"
```

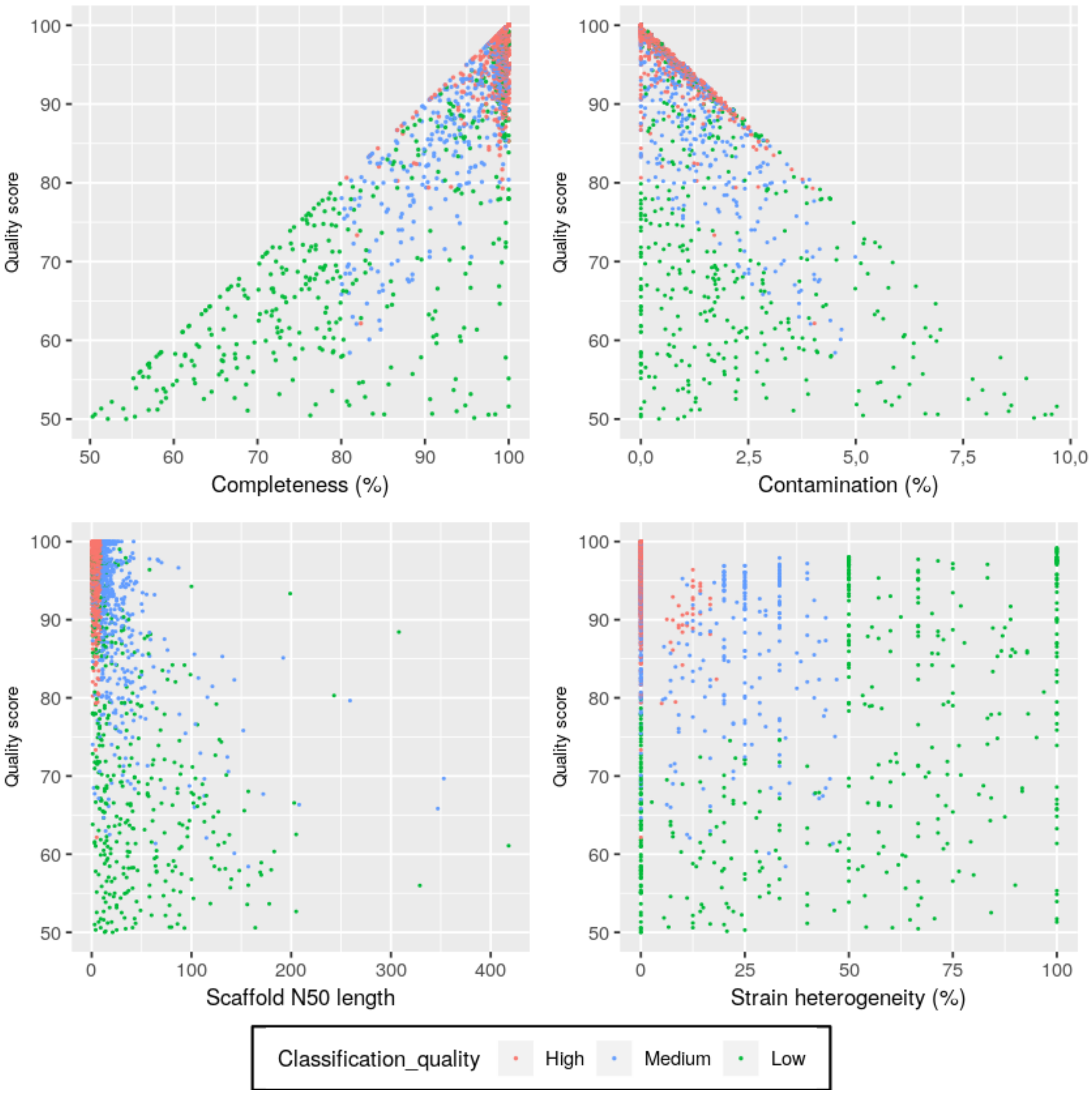


```
[17]: a <- ggplot(data, aes(x=Quality_score, y=Completeness,␣
       ↪color=Classification_quality)) +
        scale_x_reverse() +
        geom_point(alpha=0.8)

      b <- ggplot(data, aes(x=Quality_score, y=Contamination,␣
       ↪color=Classification_quality)) +
        scale_x_reverse() +
        geom_point(alpha=0.8)

      c <- ggplot(data, aes(x=Quality_score, y=scaf_N50,␣
       ↪color=Classification_quality)) +
        scale_x_reverse() +
        geom_point(alpha=0.8)

      d <- ggplot(data, aes(x=Quality_score, y=Strain_heterogeneity,␣
       ↪color=Classification_quality)) +
        scale_x_reverse() +
        geom_point(alpha=0.8)

      grid.newpage()
      grid.arrange(a, b, c, d, nrow = 4, ncol=1)
```



[18]:

```
a <- ggplot(data, aes(y=Quality_score, x=Completeness,␣
↪color=Classification_quality)) +
  geom_point(alpha=0.9, size=0.3 ) +
  labs(y="Quality score", x="Completeness (%)") +
  theme(axis.title.y=element_text(size=8),
        axis.title.x=element_text(size=10),
        legend.box.background = element_rect(colour = "black", size = 0.6),
        legend.box.margin = margin(0.5, 6, 0.5, 6),
        legend.title = element_text(size=10))+
  scale_color_discrete(breaks=c("High","Medium","Low"))

b <- ggplot(data, aes(y=Quality_score, x=Contamination,␣
 ↪color=Classification_quality)) +
  geom_point(alpha=1, size=0.2 ) +
  labs(y="Quality score", x="Contamination (%)") +
  theme(axis.title.y=element_text(size=8),
        axis.title.x=element_text(size=10),
        legend.box.background = element_rect(colour = "black", size = 0.6),
        legend.box.margin = margin(0.5, 6, 0.5, 6),
        legend.title = element_text(size=10))+
  scale_color_discrete(breaks=c("High","Medium","Low"))

c <- ggplot(data, aes(y=Quality_score, x=scaf_N50,␣
 ↪color=Classification_quality)) +
  geom_point(alpha=1, size=0.2 ) +
  labs(y="Quality score", x="Scaffold N50 length") +
  theme(axis.title.y=element_text(size=8),
        axis.title.x=element_text(size=10),
        legend.box.background = element_rect(colour = "black", size = 0.6),
        legend.box.margin = margin(0.5, 6, 0.5, 6),
        legend.title = element_text(size=10),
        plot.margin=unit(c(5.5, 5.5, 7, 5.5), "pt"))+
  scale_color_discrete(breaks=c("High","Medium","Low"))

d <- ggplot(data, aes(y=Quality_score, x=Strain_heterogeneity,␣
 ↪color=Classification_quality)) +
  geom_point(alpha=1, size=0.2 ) +
  labs(y="Quality score", x="Strain heterogeneity (%)") +
  theme(axis.title.y=element_text(size=8),
        axis.title.x=element_text(size=10),
        legend.box.background = element_rect(colour = "black", size = 0.6),
        legend.box.margin = margin(0.5, 6, 0.5, 6),
        legend.title = element_text(size=10),
        plot.margin=unit(c(5.5, 5.5, 7, 5.5), "pt"))+
  scale_color_discrete(breaks=c("High","Medium","Low"))

ggarrange(a, b, c, d, ncol=2, nrow=2, common.legend = TRUE, legend="bottom")

#ggsave("Comparison2", device="png",scale=1.3)
```



2 DataExplorer

```
[ ]: #For a quick way of visualizing the dataset constructed so far, I recommend the use of the DataExplorer R package, created for Exploratory Data Analysis.
     library(DataExplorer)
     create_report(data)
```