

# Verification Report: Correlates of Risk Graphs

Di Lu

2021/06/04

## Description

This is the verification report for the `cor_graphical` folder of the `correlates_reporting` project for CoVPN.

In the verification process, the outputs of `cor_graphical_verification_code.R` were visually compared against the plots listed in the file `cor_graphical/verification/verification_plan.pdf`. The values presented in the original plots were also generated independently by the tester and compared against the outputs generated by the original programmer.

The files `cor_graphical/verification/input/longer_cor_data_plot1.csv`, and `cor_graphical/verification/input/plot.25sample1.csv`, were provided by the original programmer to the tester for verification purposes.

## Data Verification

Load `longer.cor.subset.plot1`

```
dat.longer.cor.subset.plot1_verification <- read.csv(  
  here("verification/output/dat.longer.cor.subset.plot1_verification.csv")  
) %>% arrange(Ptid,assay,time)  
  
original.longer.cor.subset.plot1<-read.csv(  
  here("verification/input/longer_cor_data_plot1.csv")  
) %>% arrange(Ptid,assay,time)
```

## Verification

```
data_clean_comparison <- compare_datasets(  
  cols = colnames(dat.longer.cor.subset.plot1_verification), index = "Ptid",  
  ds1 = dat.longer.cor.subset.plot1_verification, ds2 = original.longer.cor.subset.plot1  
)
```

## There are 0 mismatched fields of 39.

`longer.cor.subset.plot1` generated by using `cor_graphical_verification_code.R` was equivalent to the output generated by original programmer, and passes verification.

Load plot.25sample1

```
plot.25sample1_verification <- read.csv(  
  here("verification/output/plot.25sample1_verification.csv")  
) %>% arrange(Ptid,assay,time)  
  
original.plot.25sample1<-read.csv(  
  here("verification/input/plot.25sample1.csv")  
) %>% arrange(Ptid,assay,time)
```

## Verification

```
data_clean_comparison <- compare_datasets(  
  cols = colnames(plot.25sample1_verification), index = "Ptid",  
  ds1 = plot.25sample1_verification, ds2 = original.plot.25sample1  
)
```

## There are 0 mismatched fields of 39.

plot.25sample1 generated by using cor\_graphical\_verification\_code.R was equivalent to the output generated by original programmer, and passes verification.

## Verification of lineplot of Binding Antibody to Spike: baseline negative vaccine arm (2 time-points)

```
data_clean_comparison_boxplot <- compare_datasets(  
  cols = colnames(boxplots_neg_vaccine_bindSpike_2_verification), index = "Ptid",  
  ds1 = boxplots_neg_vaccine_bindSpike_2_verification,  
  ds2 = original.boxplots_neg_vaccine_bindSpike_2  
)
```

## There are 0 mismatched fields of 39.

```
data_clean_comparison_lineplot <- compare_datasets(  
  cols = colnames(lineplots_neg_vaccine_bindSpike_plot.25sample1_2_verification), index = "Ptid",  
  ds1 = lineplots_neg_vaccine_bindSpike_plot.25sample1_2_verification,  
  ds2 = original.lineplots_neg_vaccine_bindSpike_plot.25sample1_2  
)
```

## There are 0 mismatched fields of 39.

The violin plot, box plot and line plot generated by the tester were visually compared with the outputs generated by original programmer.

Key statistics(min, 25th percentile, median, 75th percentile, max) shown in the box plot calculated by tester were equivalent to the numbers provided by original programmer, and passes verification.

Input data for the line plot generated by tester were equivalent to the data provided by original programmer, and passes verification.

### Verification of lineplot of Pseudovirus Neutralization ID50: baseline negative vaccine arm (2 timepoints)

```
data_clean_comparison_boxplot <- compare_datasets(  
  cols = colnames(boxplots_neg_vaccine_pseudoneutid50_2_verification), index = "Ptid",  
  ds1 = boxplots_neg_vaccine_pseudoneutid50_2_verification,  
  ds2 = original.boxplots_neg_vaccine_pseudoneutid50_2  
)
```

## There are 0 mismatched fields of 39.

```
data_clean_comparison_lineplot <- compare_datasets(  
  cols = colnames(lineplots_neg_vaccine_pseudoneutid50_plot.25sample1_2_verification), index = "Ptid",  
  ds1 = lineplots_neg_vaccine_pseudoneutid50_plot.25sample1_2_verification,  
  ds2 = original.lineplots_neg_vaccine_pseudoneutid50_plot.25sample1_2  
)
```

## There are 0 mismatched fields of 39.

The violin plot, box plot and line plot generated by the tester were visually compared with the outputs generated by original programmer.

Key statistics(min, 25th percentile, median, 75th percentile, max) shown in the box plot calculated by tester were equivalent to the statistics provided by original programmer, and passes verification.

Input data for the line plot generated by tester were equivalent to the data provided by original programmer, and passes verification.

### Verification of lineplot of Binding Antibody to Spike: baseline negative vaccine arm (3 timepoints)

```
data_clean_comparison_boxplot <- compare_datasets(  
  cols = colnames(boxplots_neg_vaccine_bindSpike_3_verification), index = "Ptid",  
  ds1 = boxplots_neg_vaccine_bindSpike_3_verification,  
  ds2 = original.boxplots_neg_vaccine_bindSpike_3  
)
```

## There are 0 mismatched fields of 39.

```
data_clean_comparison_lineplot <- compare_datasets(  
  cols = colnames(lineplots_neg_vaccine_bindSpike_plot.25sample1_3_verification), index = "Ptid",  
  ds1 = lineplots_neg_vaccine_bindSpike_plot.25sample1_3_verification,  
  ds2 = original.lineplots_neg_vaccine_bindSpike_plot.25sample1_3  
)
```

## There are 0 mismatched fields of 39.

The violin plot, box plot and line plot generated by the tester were visually compared with the outputs generated by original programmer.

Key statistics(min, 25th percentile, median, 75th percentile, max) shown in the box plot calculated by tester were equivalent to the statistics provided by original programmer, and passes verification.

Input data for the line plot generated by tester were equivalent to the data provided by original programmer, and passes verification.

## Signature

Role	Name	Signature	Date
Tester	Di Lu		