

Luminex Xponent: Plate- level Quality Control

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Aim

This code aims to do a plate- level quality control analysis for Luminex studies through bead counts, Background MFI, and Standard curve analysis.

R Markdown

This is an R Markdown document, areas that between the `{r}` frames that are require manual entries as described in the **bolded text**. When entries are completed, press the *knit* button at the top of the page.

Dependencies

- R version 4.3.1 (2023-06-16)
 - tidyverse (v. 2.0.0)
 - here (v. 1.0.1)

Required Inputs

1. Confirm working directory:

This is the project folder where the project is found. All folders and files added to the code will be within this folder. If needed you can set the working directory using the `setwd()` function.

Working directory: `/Users/sahal/Documents/R Projects/RTSS_Kisumu_Schisto`

2. Choose file (input required):

Chose the raw plate file from working directory by adding what folder within (in the quotes). In the example below, the plate csv is in the `Project/data/raw/luminex/` folder.

3. Set minimum bead count:

Set the **minimum bead count** as `min_beadcount`. In this example, the standard we have set here is 50. All bead counts `<50` will be identified.

4 Define the file_path:

For example, here “`Project/data/qc`” folder is where the *PlateName_beadqc_df.csv* will be saved

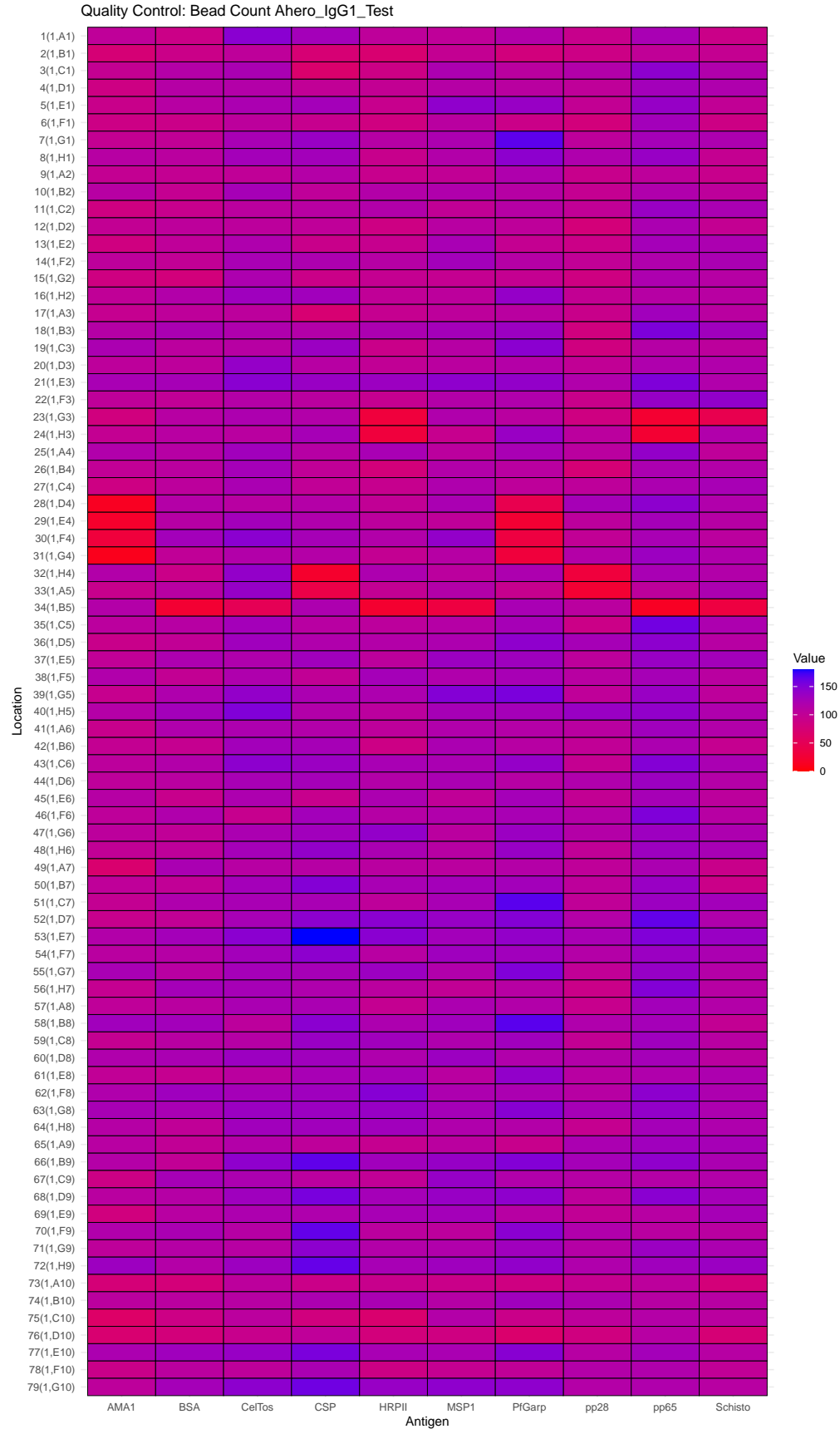
```
# Choose the input file
input_file <- "data/raw/luminex/Ahero_IgG1_Test.csv"
# Minimum bead count for analysis
min_beadcount <- 50

#Output file path
file_path <- "data/qc"
```

Quality Control

Bead count (Input required)

The bead QC report has been exported to data/qc/Ahero_IgG1_Test_beadqc.png



List of wells/analytes <50 beads

This code results in a list of wells, sample IDs, and analytes that are less than the minimum bead count set. This file is exported to `file_path` (chosen above) as `PlateName_beadqc_list.csv`. Values in this list will be Na in the Median MFI dataframe. `file_path`: data/qc (this can be edited in the **Bead Count** section)

The bead QC list has been exported to data/qc/Ahero_IgG1_Test_beadqc_list.csv

##	Location	Sample	Column
## 1	28(1,D4)	RAM-007	AMA1
## 2	29(1,E4)	RAC-007-T01	AMA1
## 3	30(1,F4)	RAC-007-T07	AMA1
## 4	31(1,G4)	RAC-007-T08	AMA1
## 5	32(1,H4)	RAM-008	pp28
## 6	33(1,A5)	RAC-008-T01	pp28
## 7	23(1,G3)	RAC-002-T07	Schisto
## 8	34(1,B5)	RAC-008-T07	Schisto
## 9	23(1,G3)	RAC-002-T07	pp65
## 10	24(1,H3)	RAC-002-T08	pp65
## 11	34(1,B5)	RAC-008-T07	pp65
## 12	34(1,B5)	RAC-008-T07	BSA
## 13	34(1,B5)	RAC-008-T07	MSP1
## 14	23(1,G3)	RAC-002-T07	HRPII
## 15	24(1,H3)	RAC-002-T08	HRPII
## 16	34(1,B5)	RAC-008-T07	HRPII
## 17	34(1,B5)	RAC-008-T07	CellTos
## 18	32(1,H4)	RAM-008	CSP
## 19	33(1,A5)	RAC-008-T01	CSP
## 20	28(1,D4)	RAM-007	PfGarp
## 21	29(1,E4)	RAC-007-T01	PfGarp
## 22	30(1,F4)	RAC-007-T07	PfGarp
## 23	31(1,G4)	RAC-007-T08	PfGarp

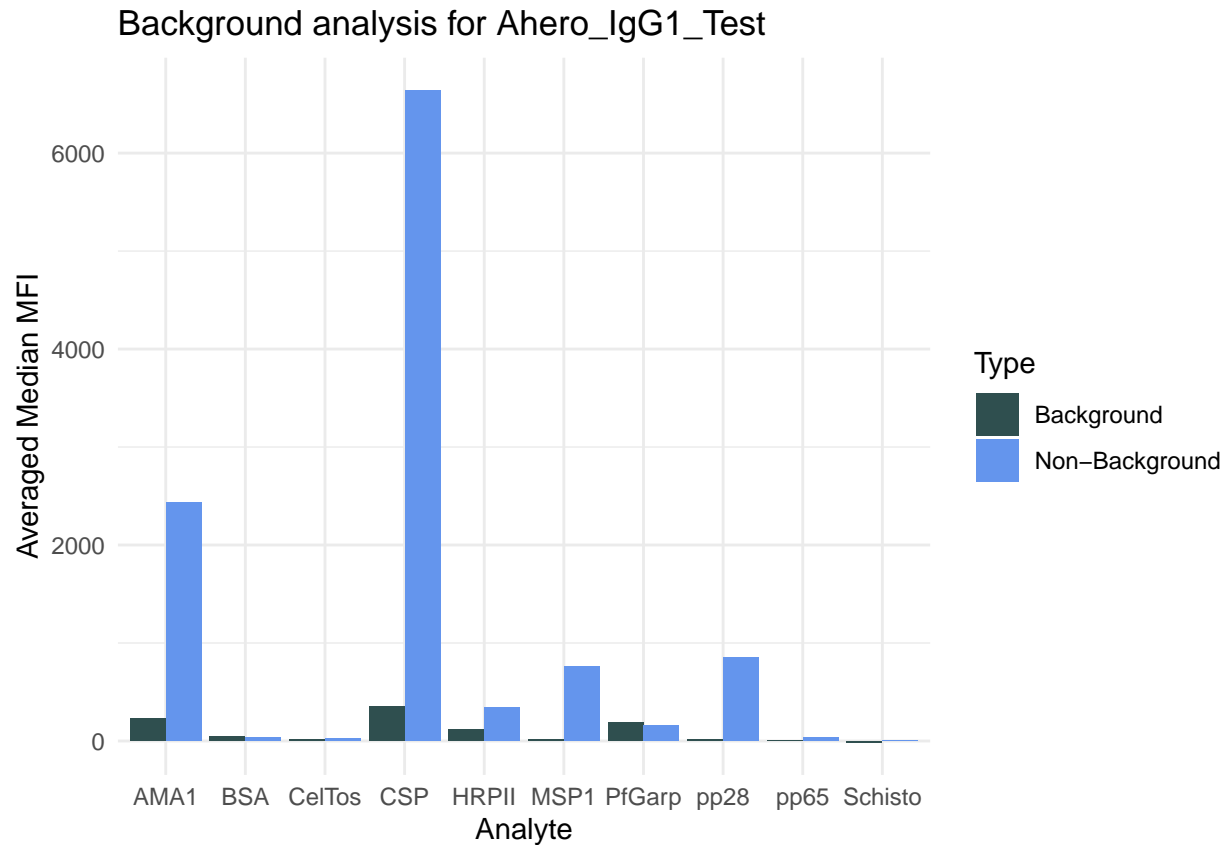
QC of median MFI data

This extracts the median MFI data, with all well-analyte combinations <50 beads/well replaced with NA. It completes the BSA MFI subtraction as well

note: negative values are kept

Background MFI

This code averages the median MFI values for all background and non-background samples. This requires all Background samples to have “Background” within the characters in the **Sample** column



Standard curve

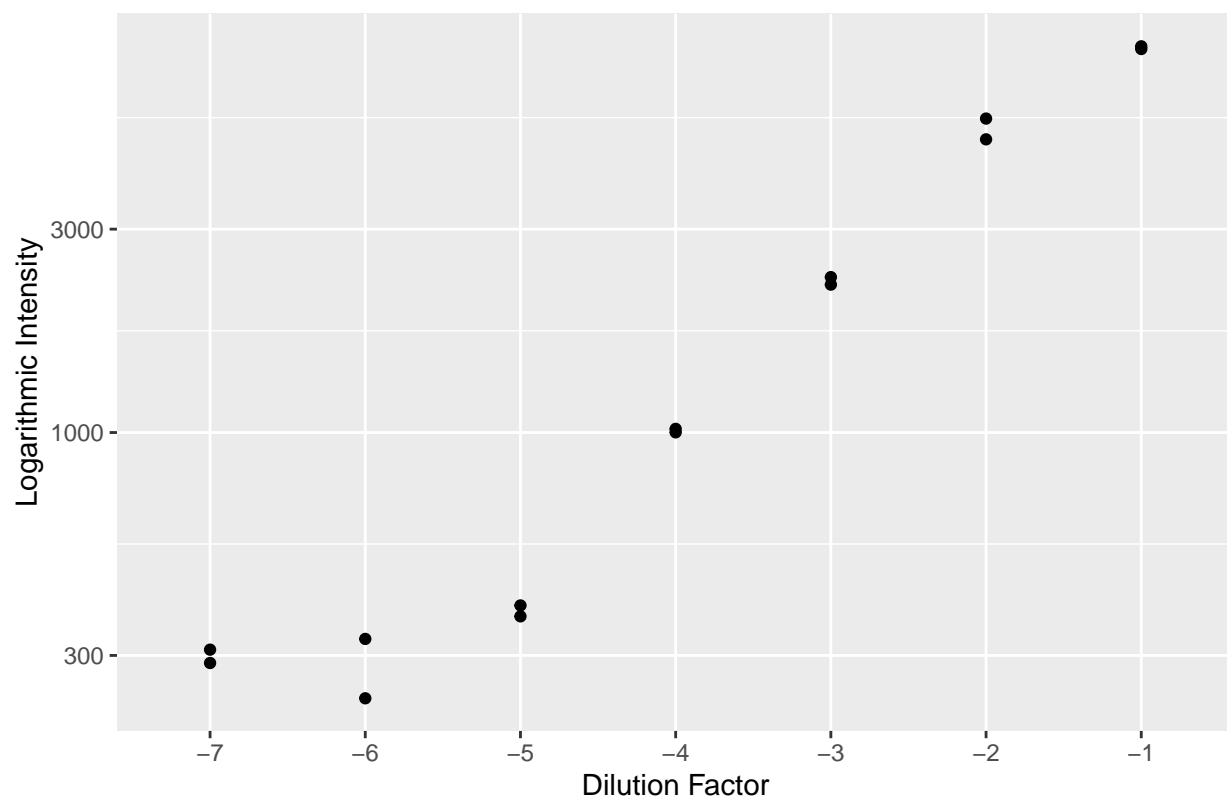
This code will attempt to create standard curves. This requires the samples have “Standard” within the characters in the **Sample** column. This will extraction **Dilution_Factor** as the number within the name (x -1).

For example: *Standard 2* will have a **Dilution_factor** of -2

This code will run for all **analyte**

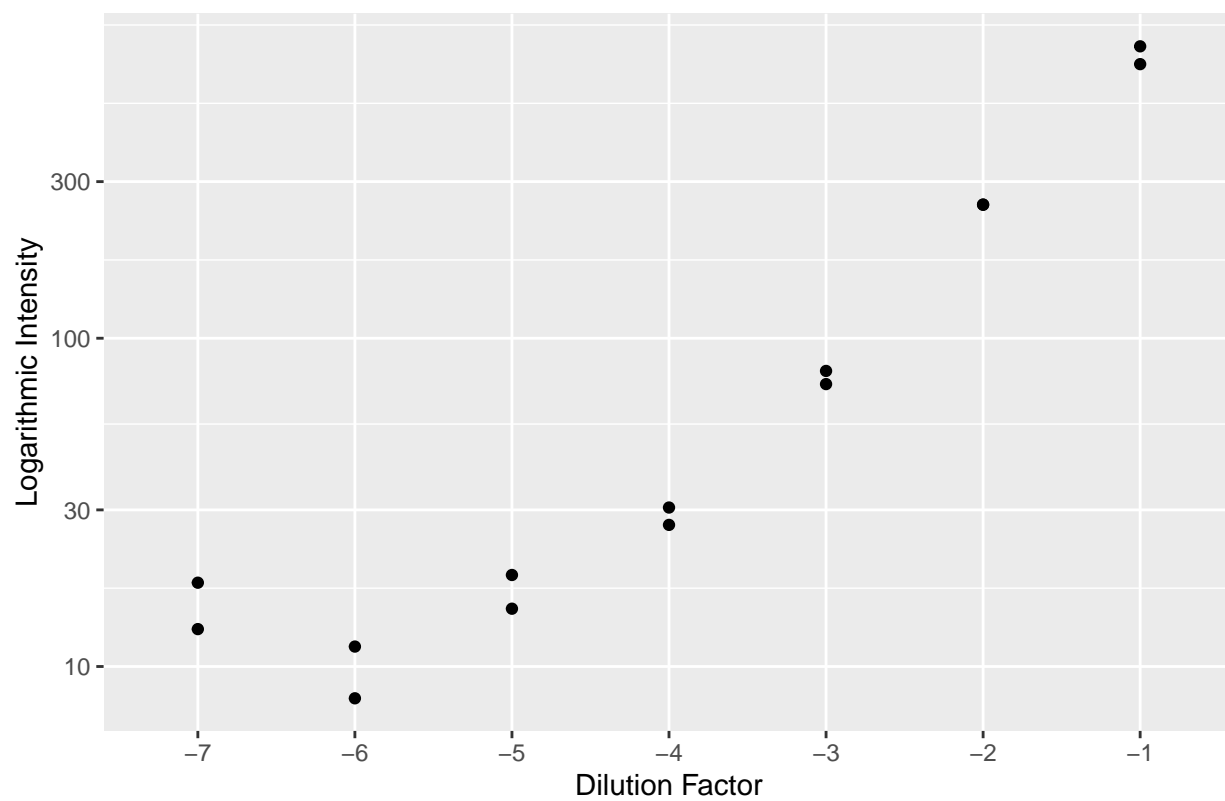
```
## [[1]]
```

AMA1 standard curve for Ahero_IgG1_Test

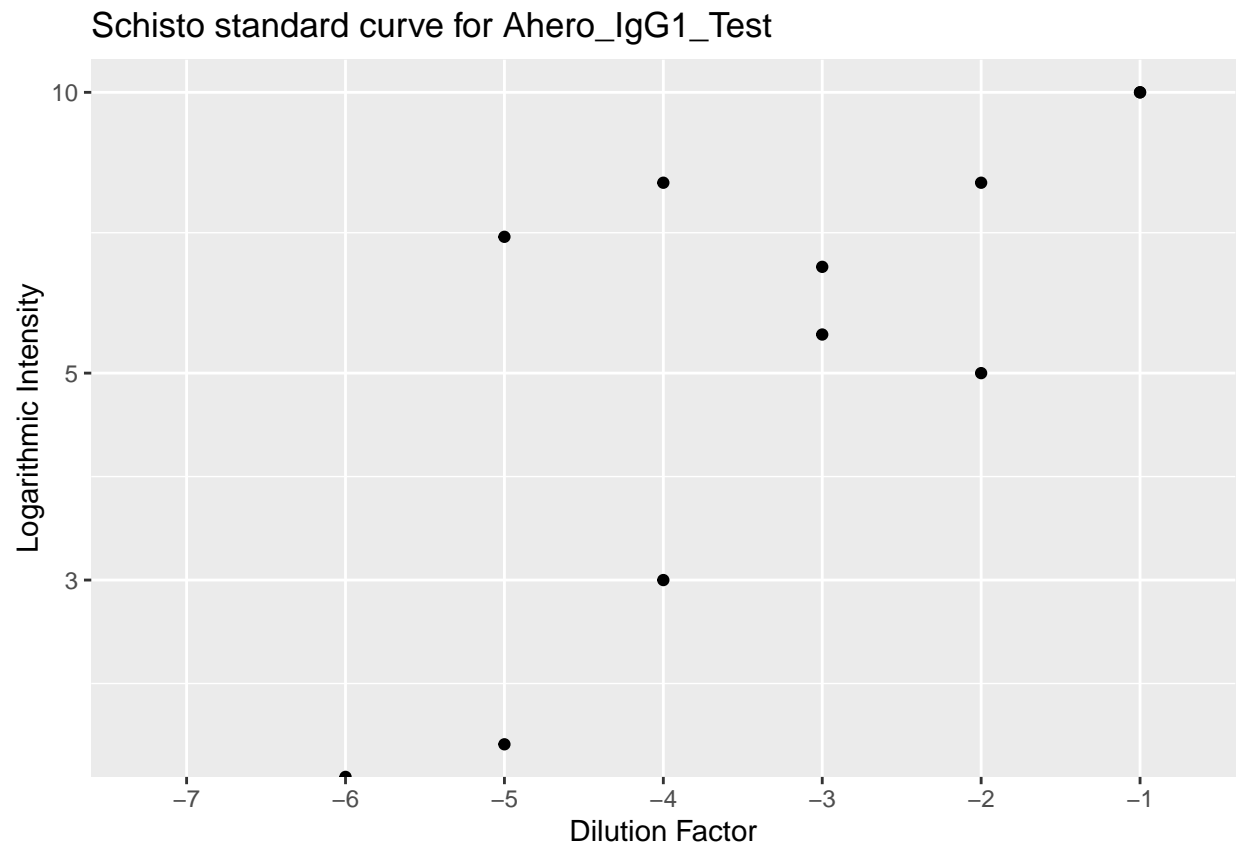


[[2]]

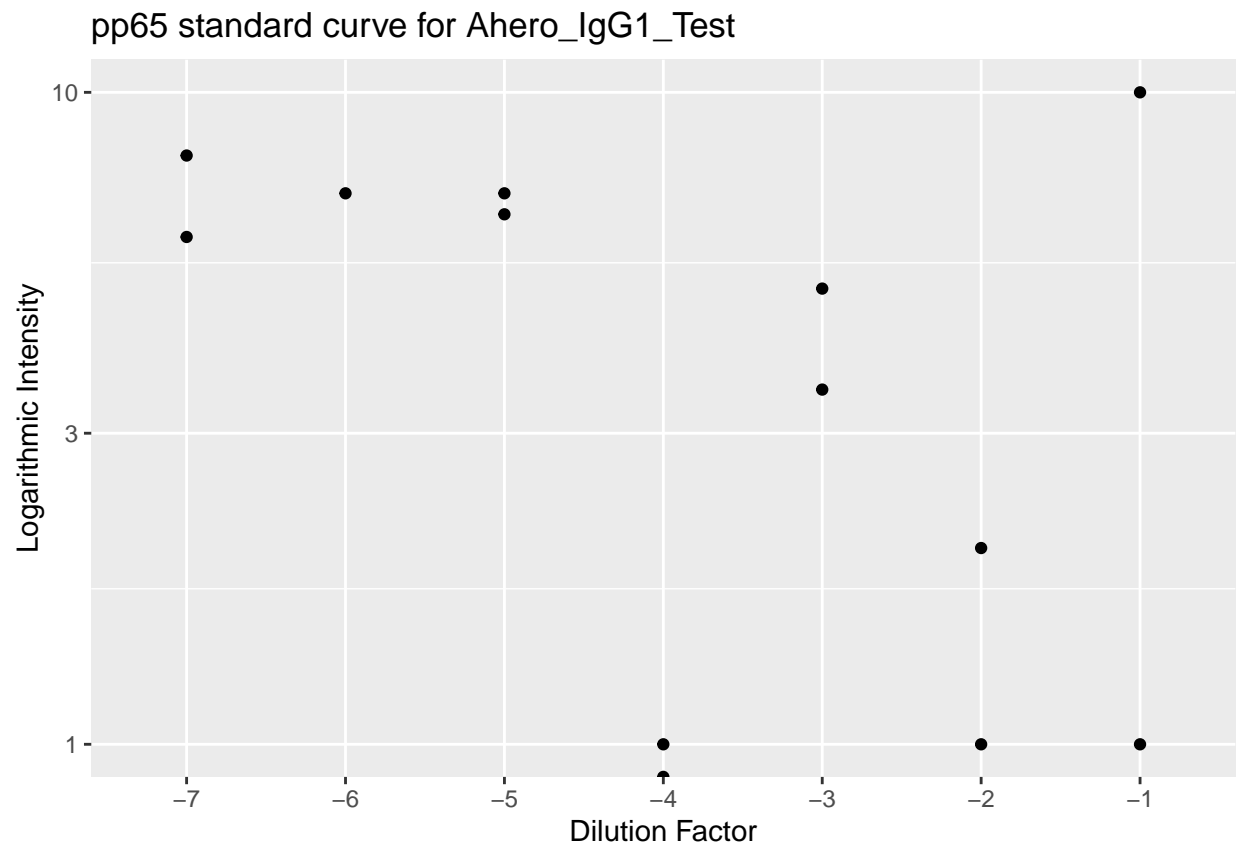
pp28 standard curve for Ahero_IgG1_Test



```
##  
## [[3]]
```

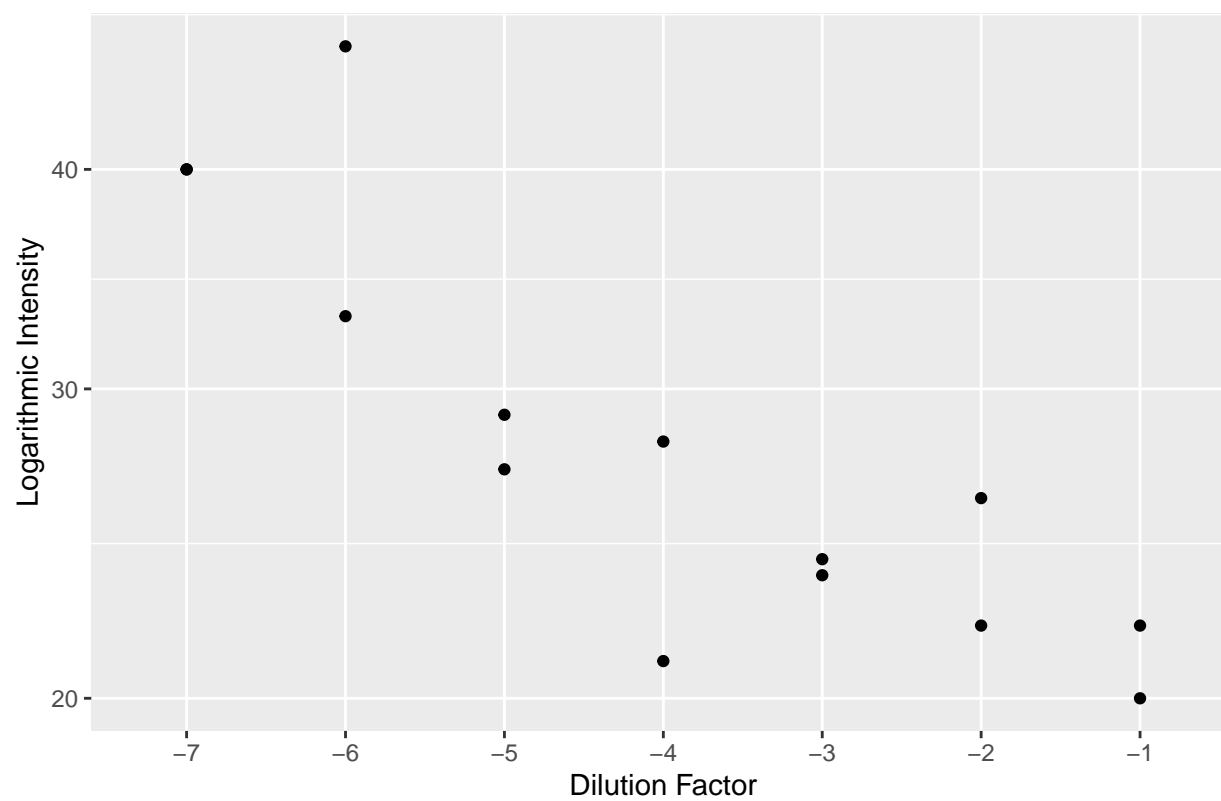


```
##  
## [[4]]
```

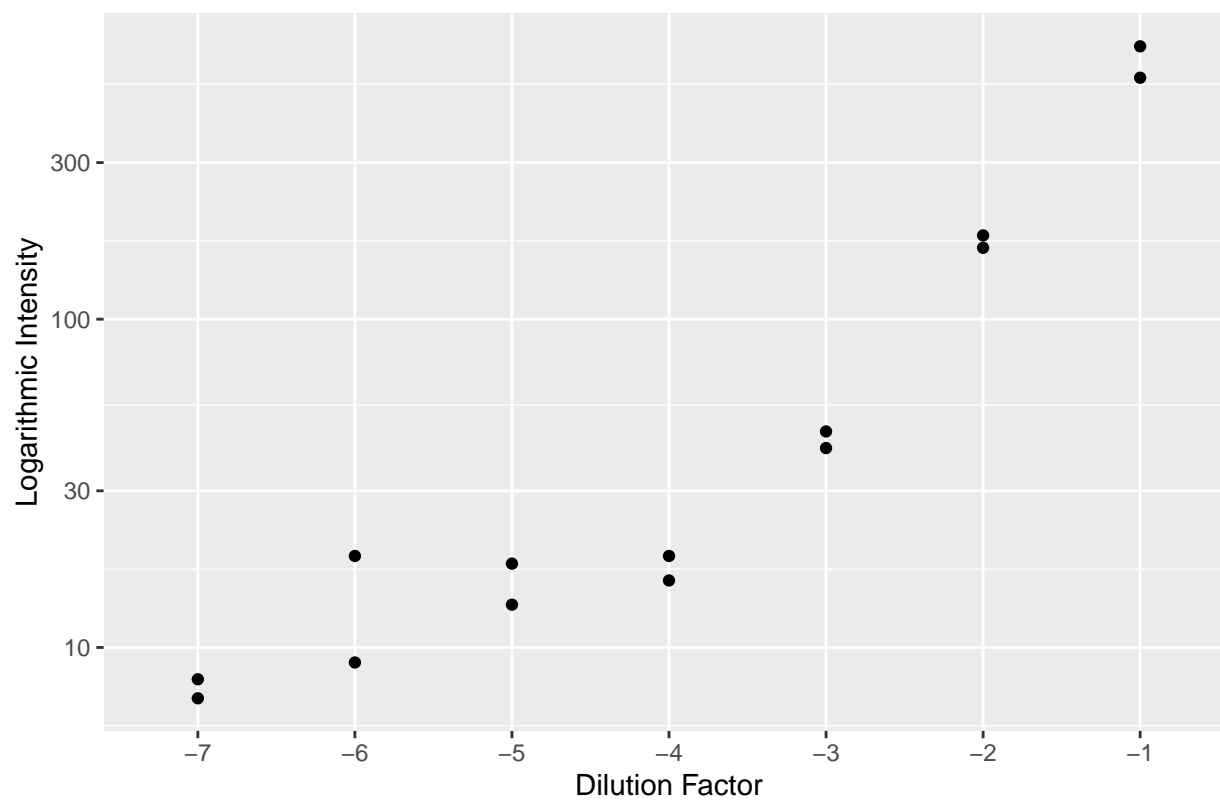
[[5]]

BSA standard curve for Ahero_IgG1_Test



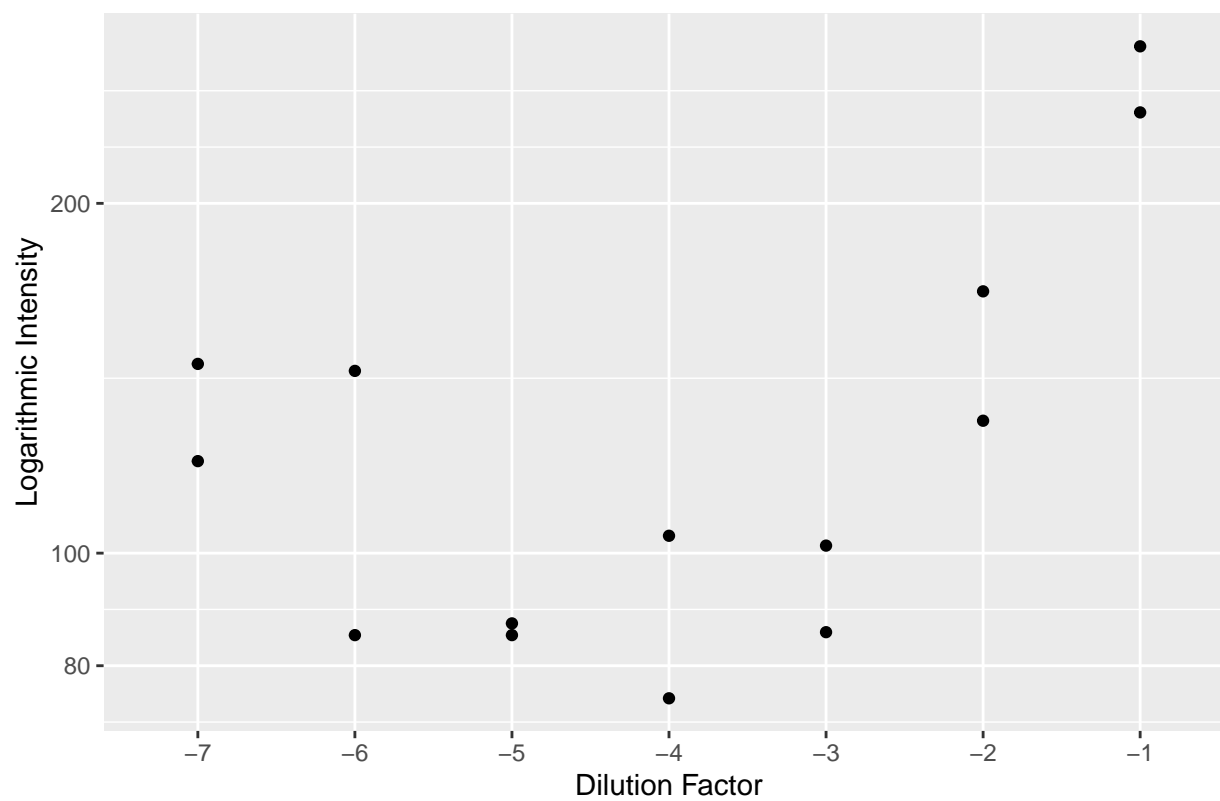
```
##  
## [[6]]
```

MSP1 standard curve for Ahero_IgG1_Test



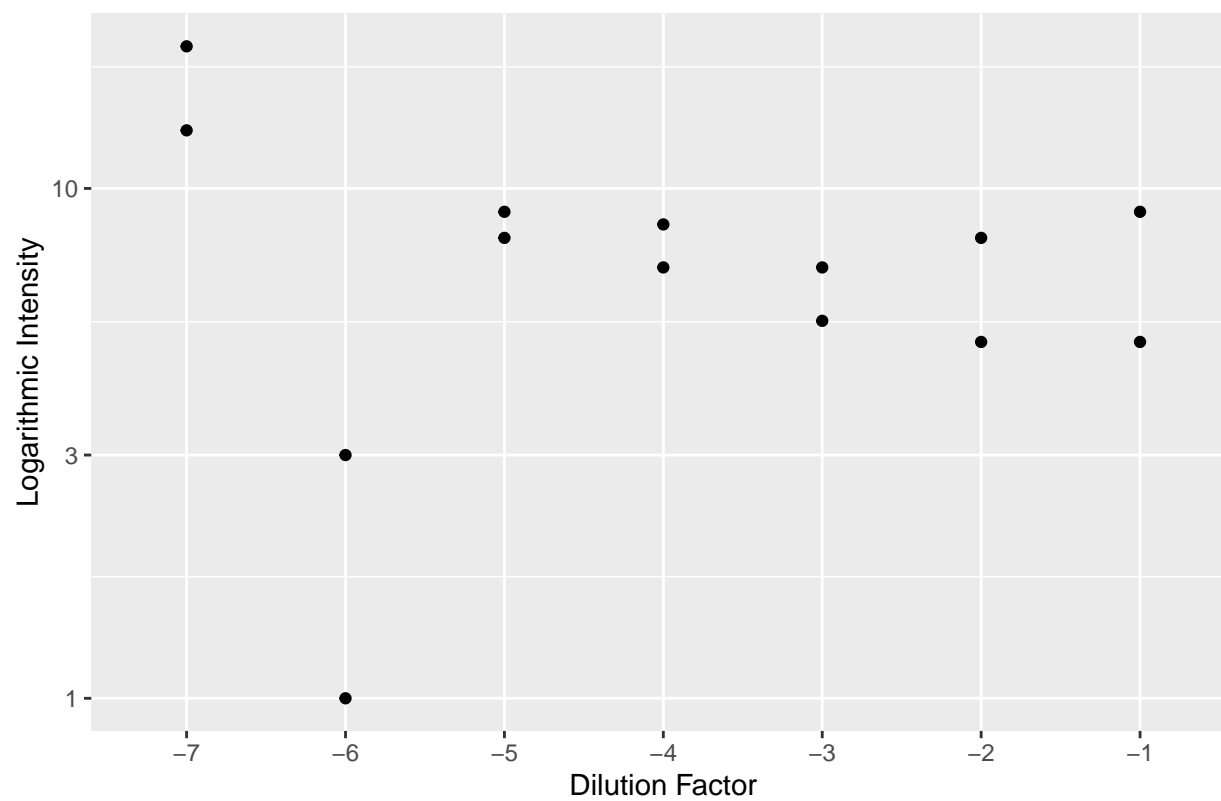
[[7]]

HRPII standard curve for Ahero_IgG1_Test

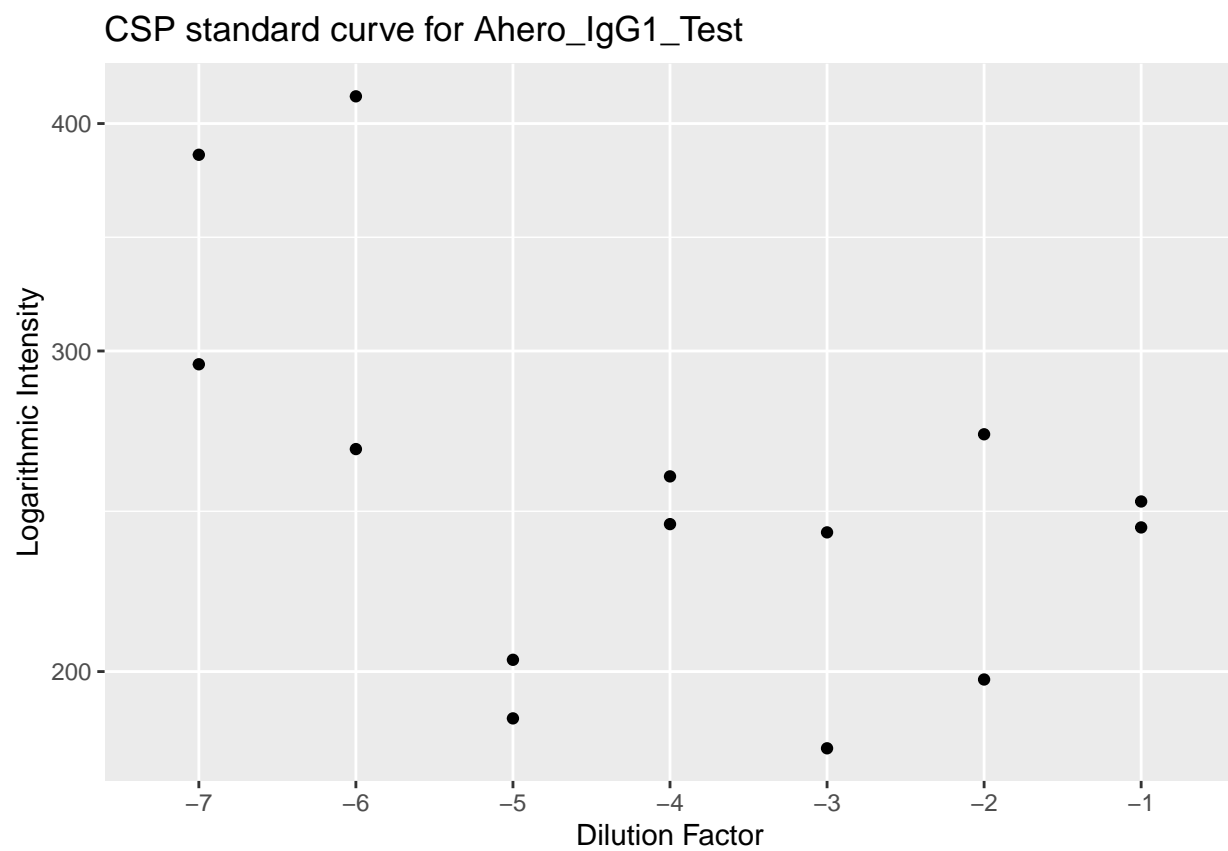


```
##  
## [[8]]
```

CellTos standard curve for Ahero_IgG1_Test



[[9]]



[[10]]

