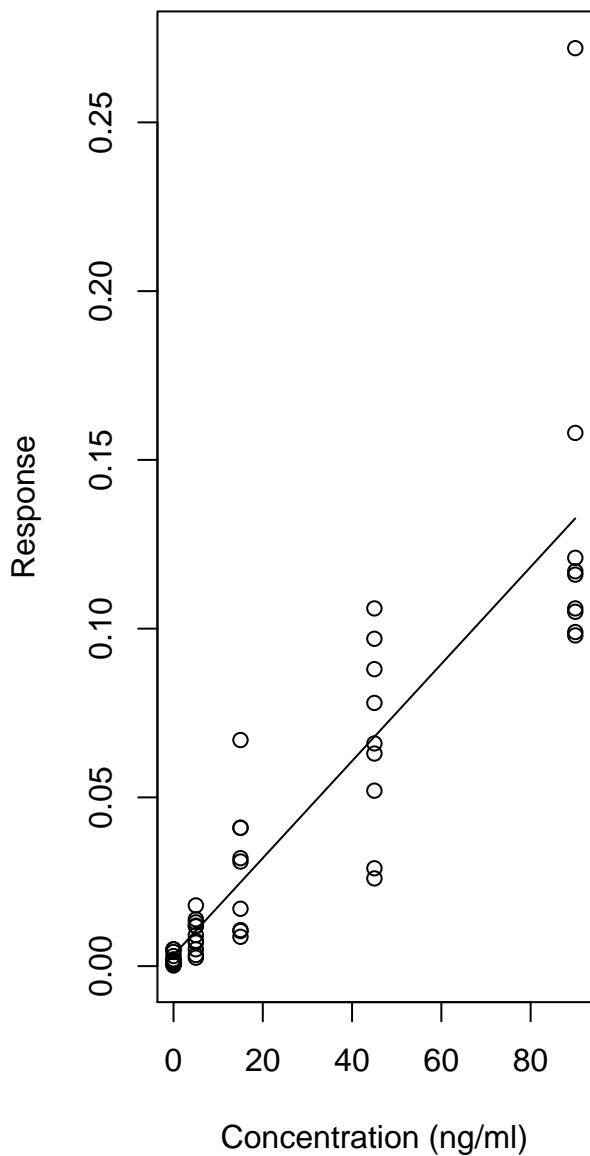
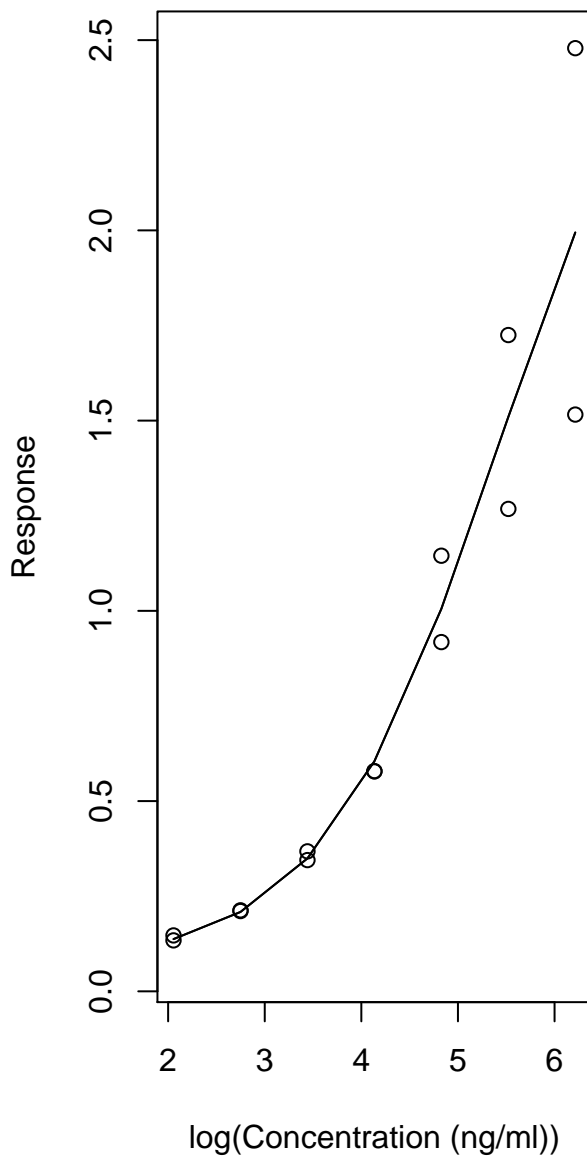


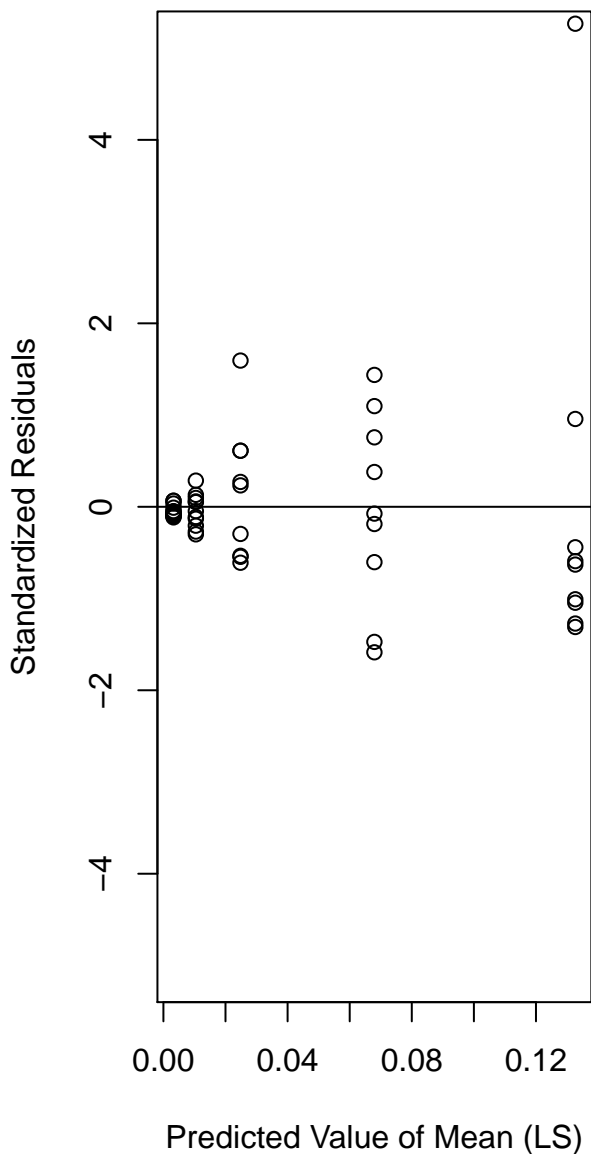
**HPLC data**



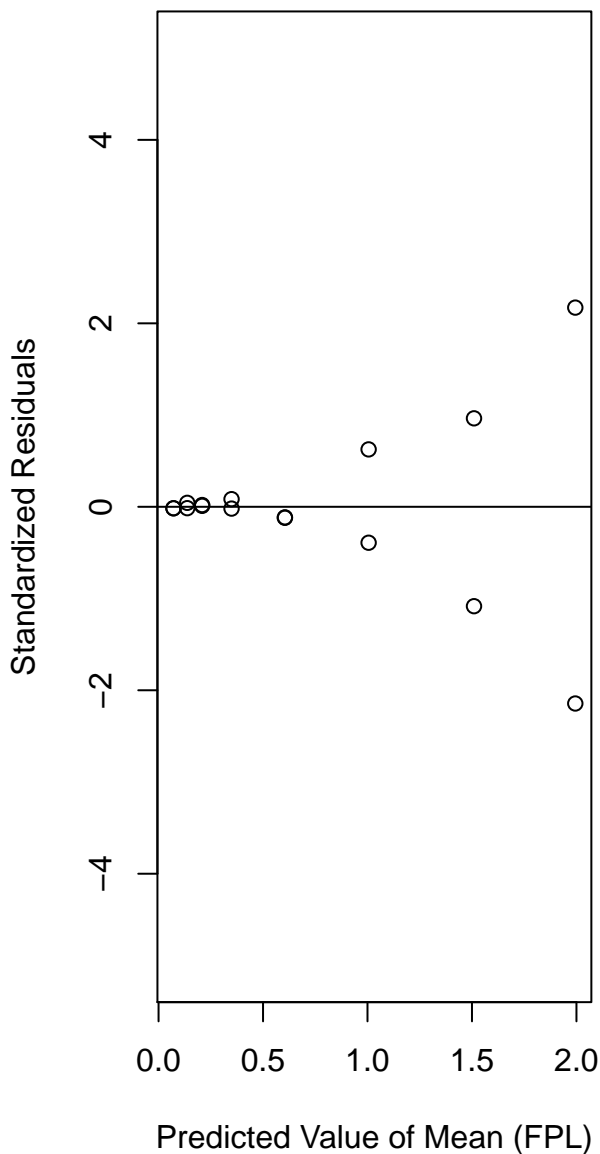
**ELISA data**

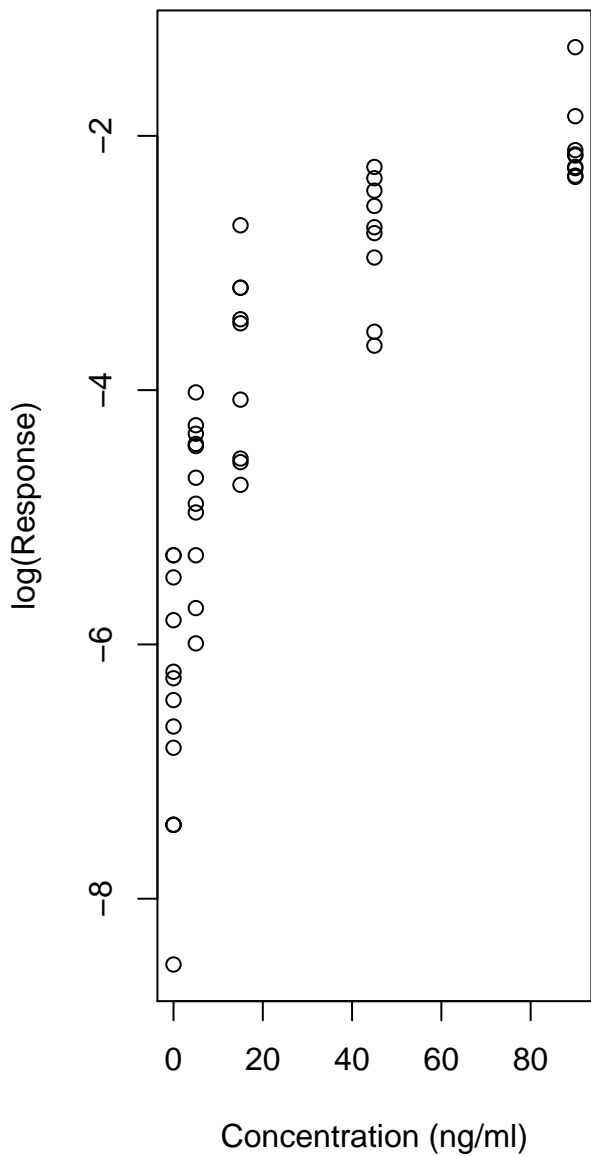


**HPLC data**

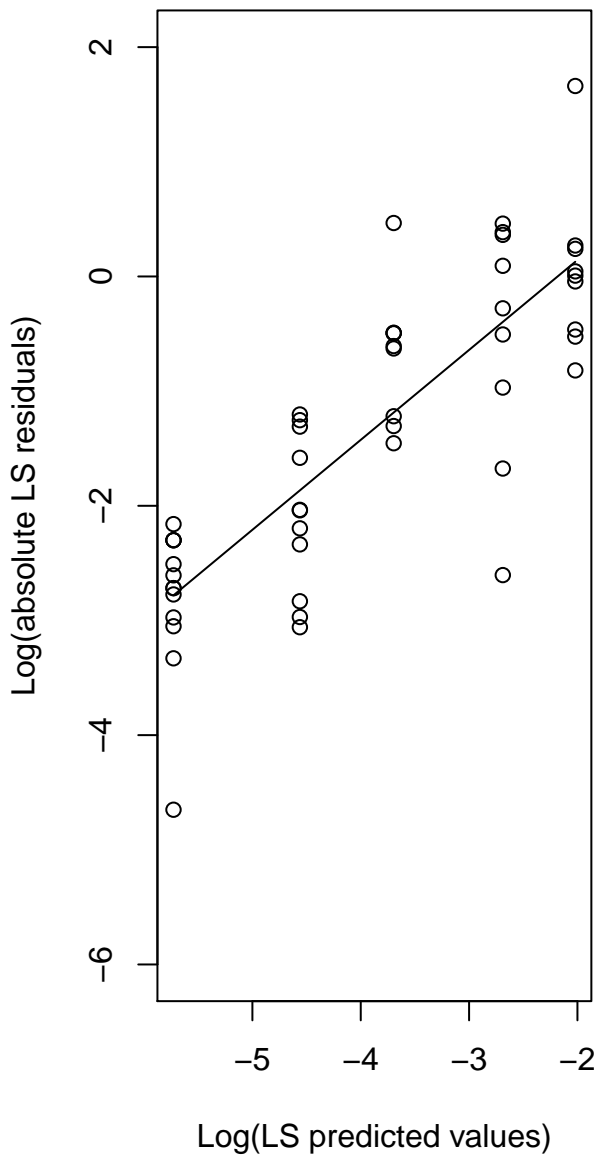


**ELISA data**





**HPLC data**

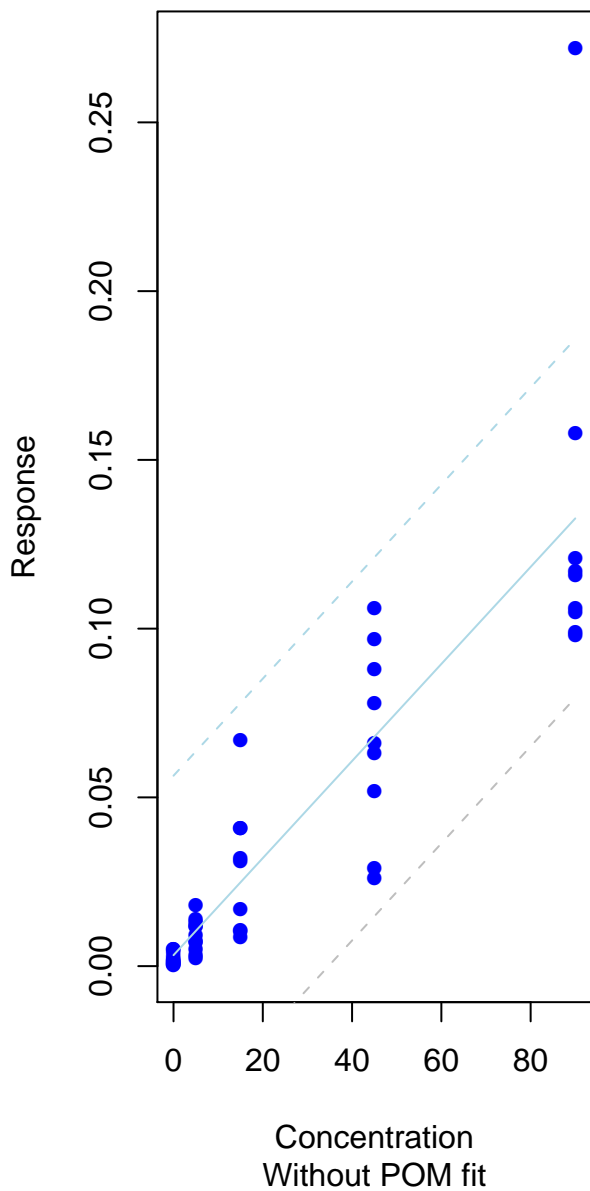


A scatter plot showing the relationship between the number of species ( $S$ ) and the number of samples ( $n$ ) for 1000 samples. The x-axis represents the number of samples ( $n$ ) and ranges from 0.00 to 0.12. The y-axis represents the number of species ( $S$ ) and ranges from 0 to 100. The data points are represented by open circles. The plot shows a general trend of increasing species richness with increasing sample size, with some outliers at higher species counts for smaller sample sizes.

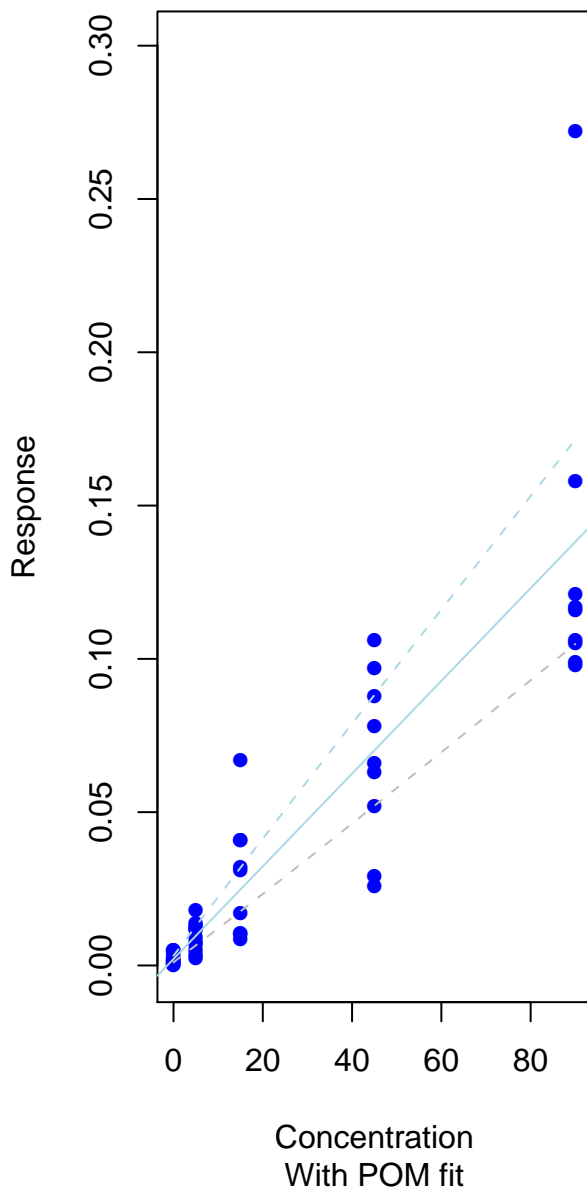
A scatter plot showing Standardized Residuals on the y-axis (ranging from -1.5 to 1.5) against Predicted Values on the x-axis (ranging from 0.0 to 2.0). The data points are represented by open circles. The residuals are mostly clustered between -0.5 and 0.5 for predicted values between 0.0 and 1.0. There are a few outliers with large positive residuals (around 1.7) at low predicted values and one with a large negative residual (around -1.6) at a low predicted value. At higher predicted values (around 1.5 and 2.0), the residuals are around -0.9 and 0.9 respectively.

Predicted Values	Standardized Residuals
0.05	-1.6
0.05	0.0
0.15	1.7
0.20	-0.25
0.25	0.0
0.35	-0.35
0.40	0.8
0.60	-0.4
0.65	-0.4
1.00	-0.6
1.00	1.2
1.50	-0.9
1.50	0.8
2.00	-1.1
2.00	0.9

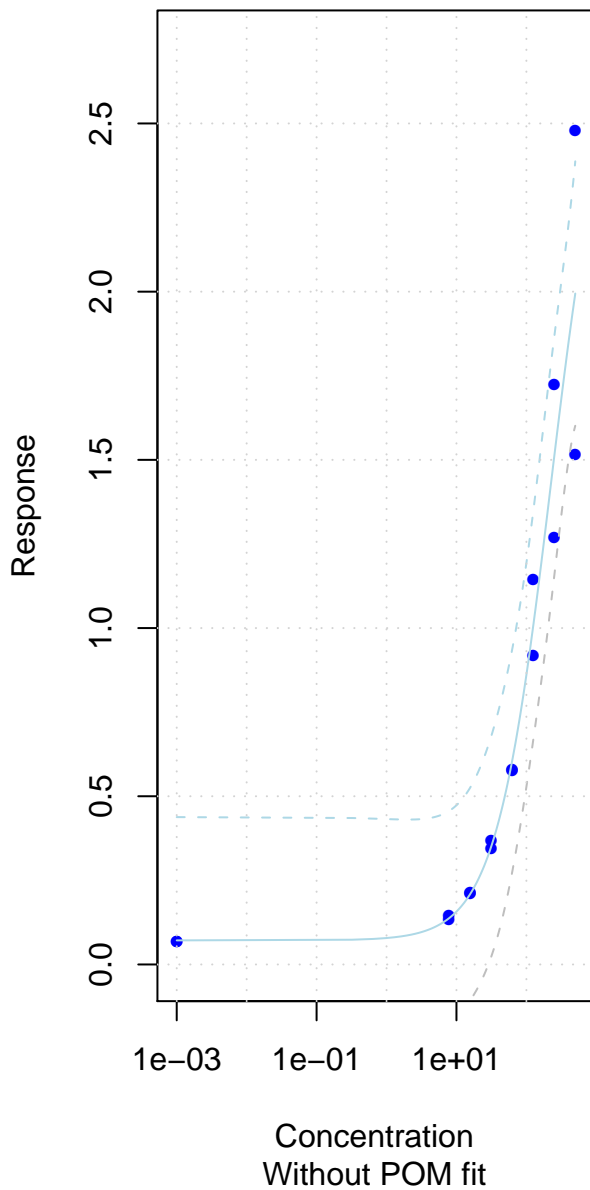
**HPLC data**



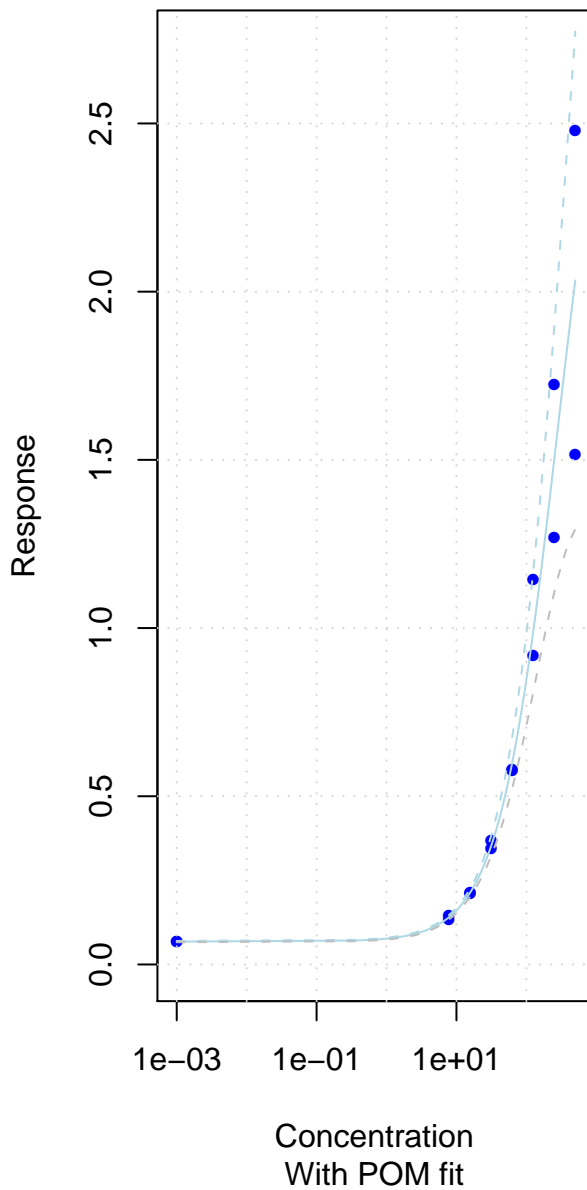
**HPLC data**



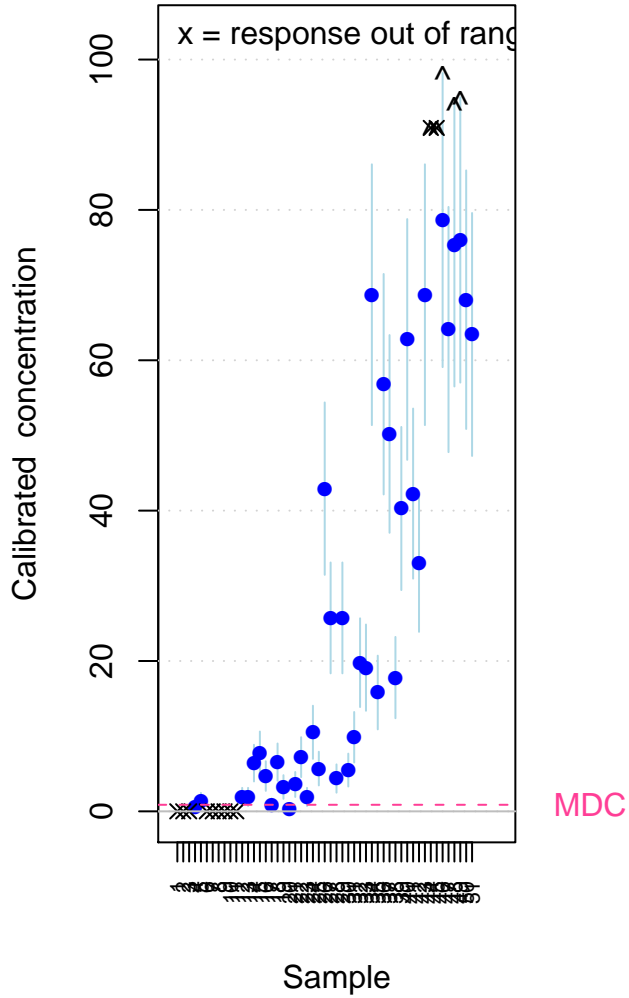
**ELISA data**



**ELISA data**

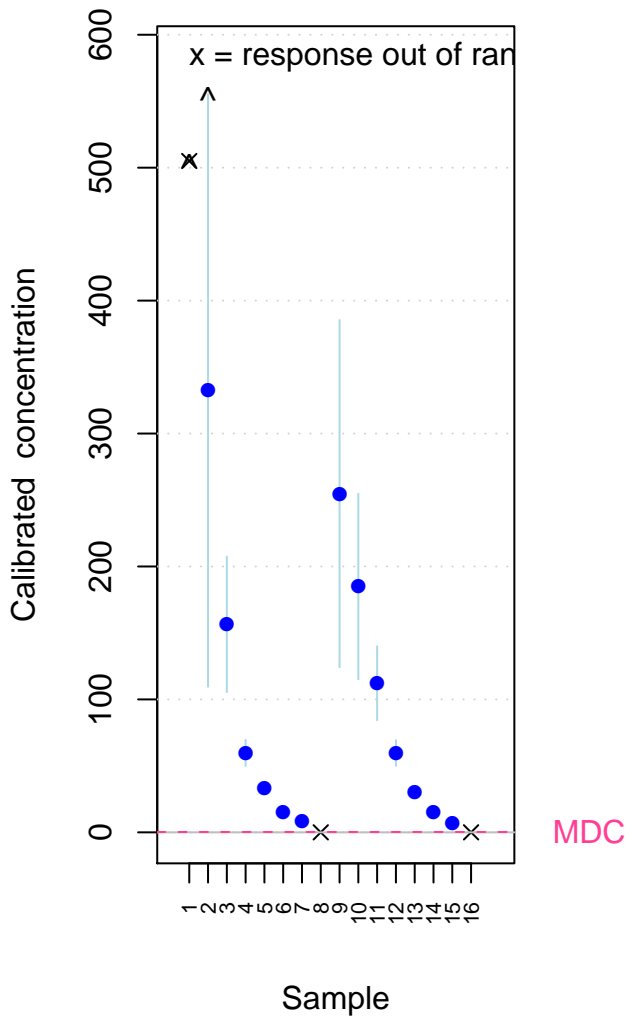


# HPLC data

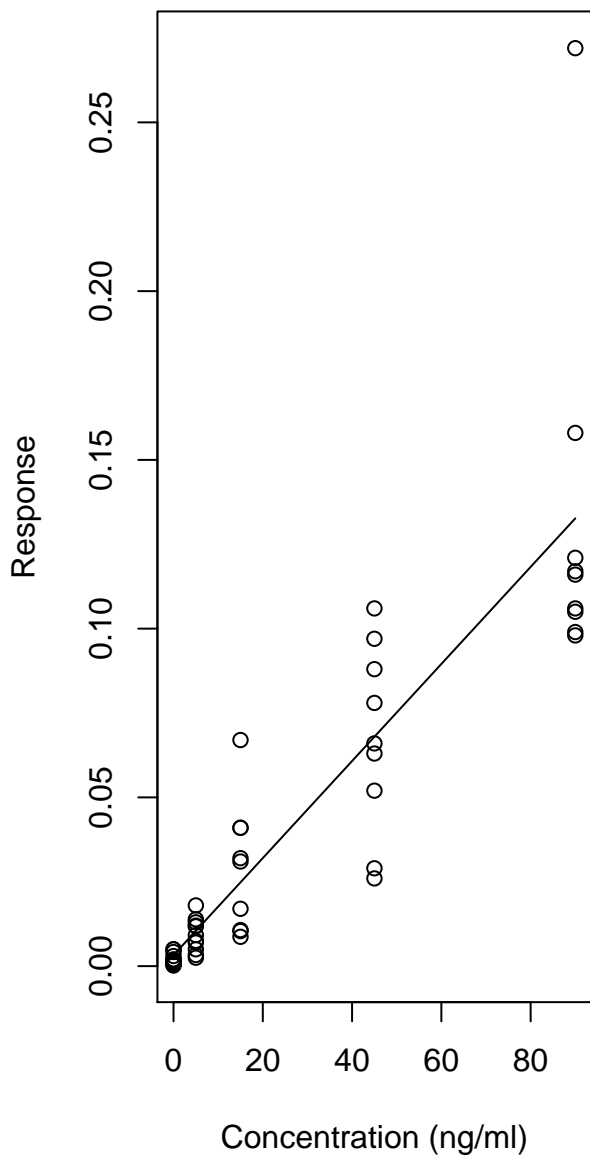




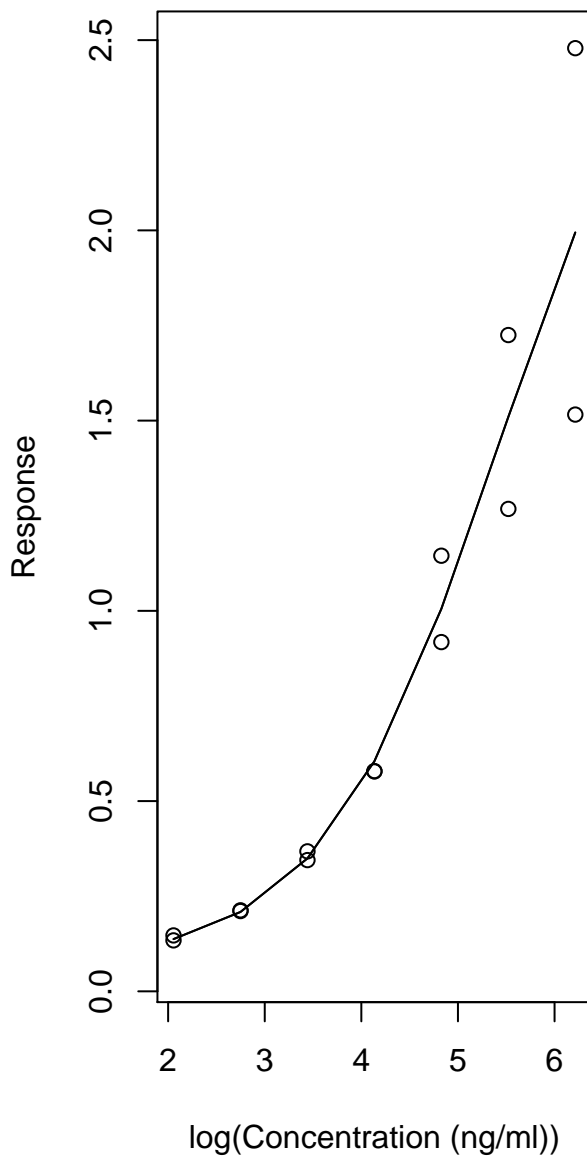
ELISA data



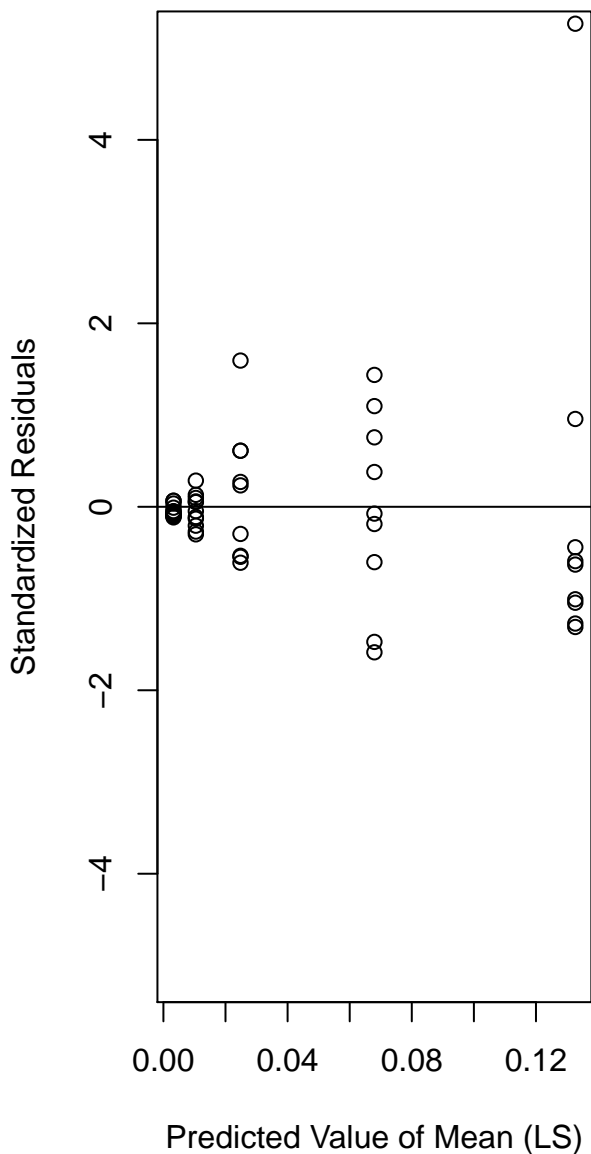
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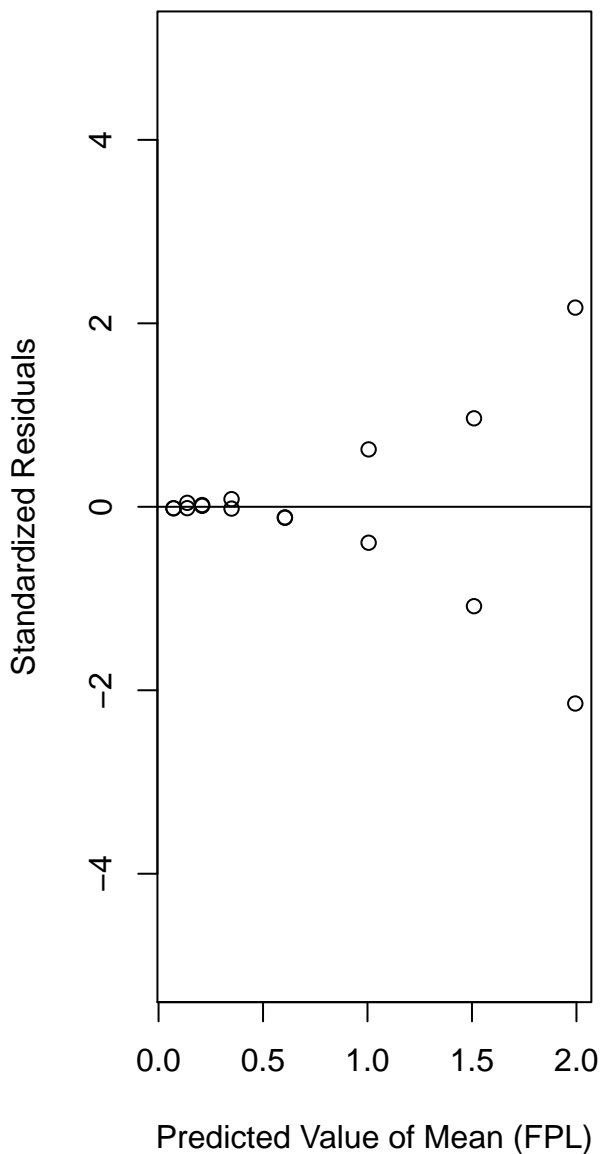
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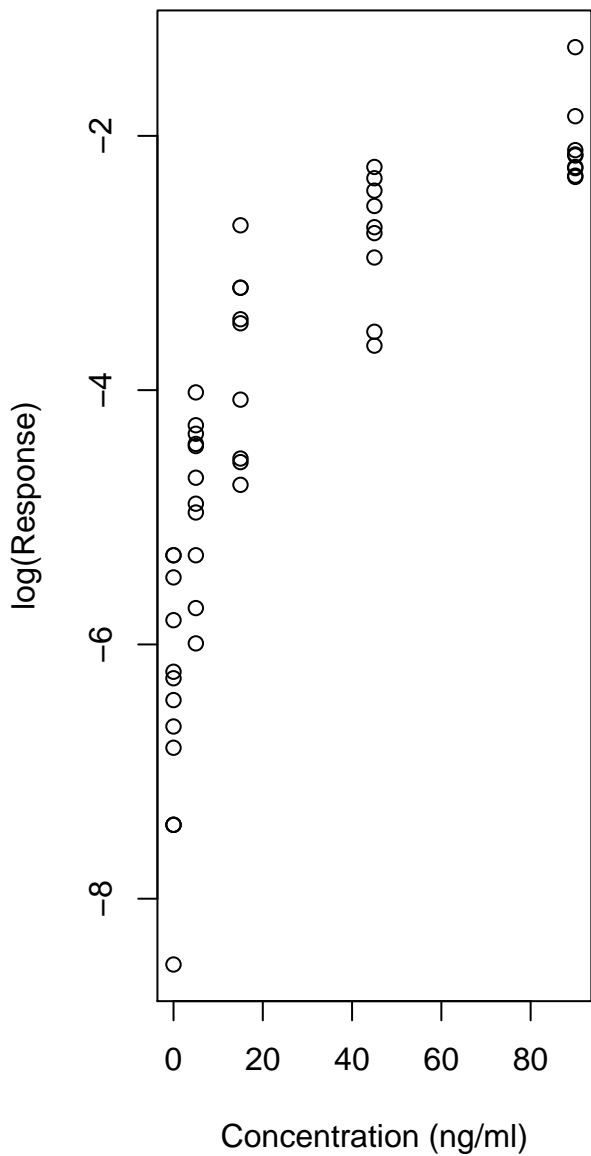


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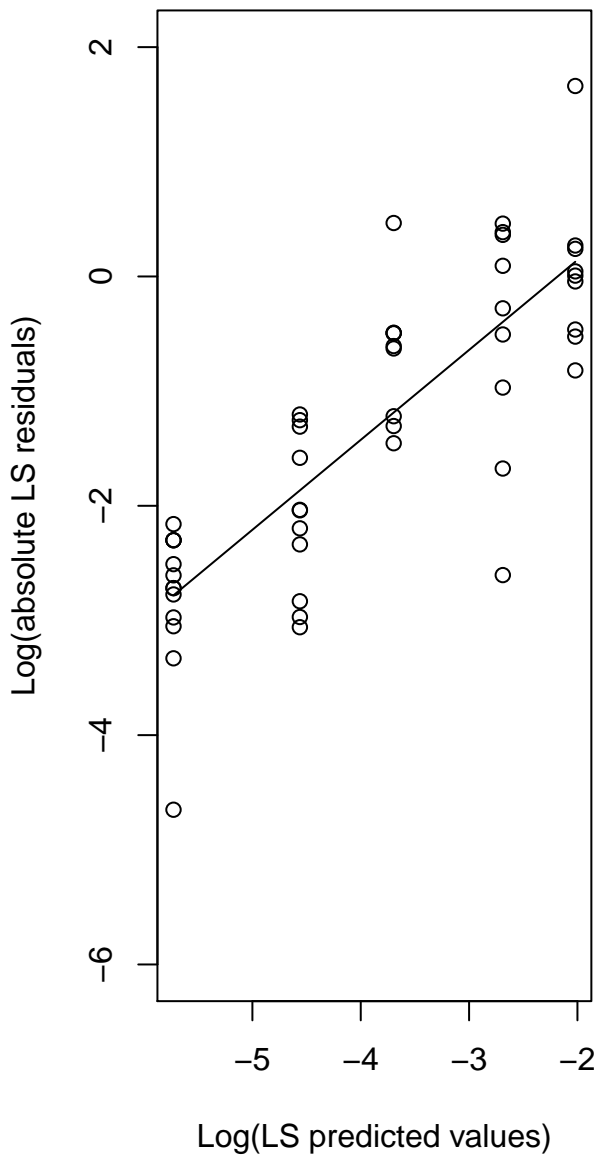


**ELISA data**





**HPLC data**

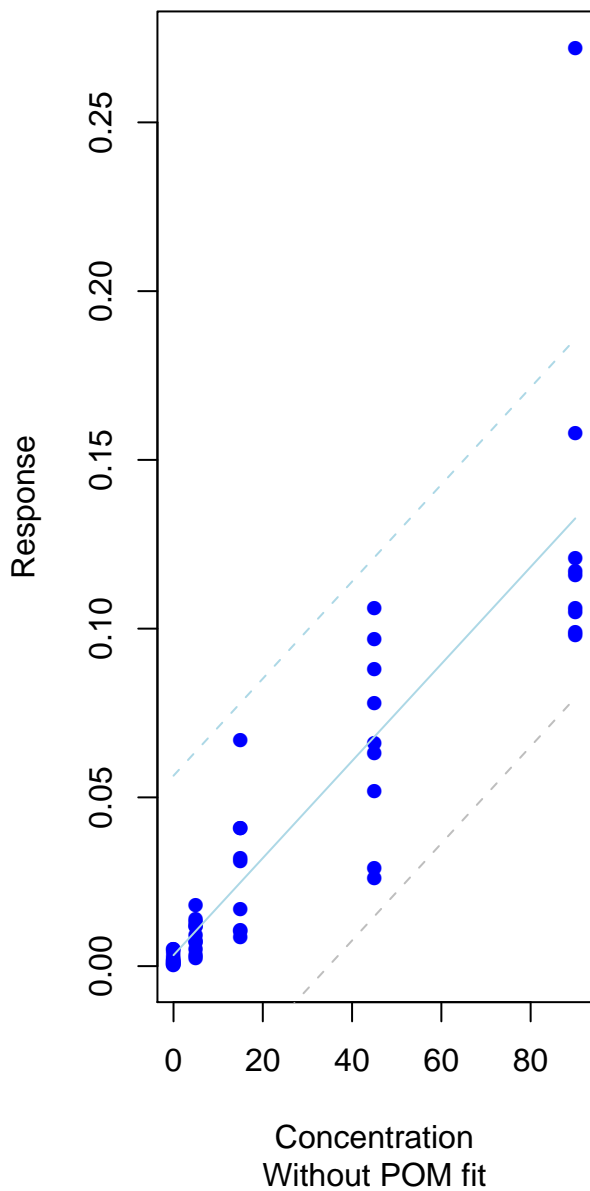


A scatter plot showing the relationship between the number of species ( $S$ ) and the number of samples ( $n$ ) for 1000 samples. The x-axis represents the number of samples ( $n$ ) and ranges from 0.00 to 0.12. The y-axis represents the number of species ( $S$ ) and ranges from 0 to 100. The data points are represented by open circles. The plot shows a general trend of increasing species richness with increasing sample size, with some outliers at higher species counts for smaller sample sizes.

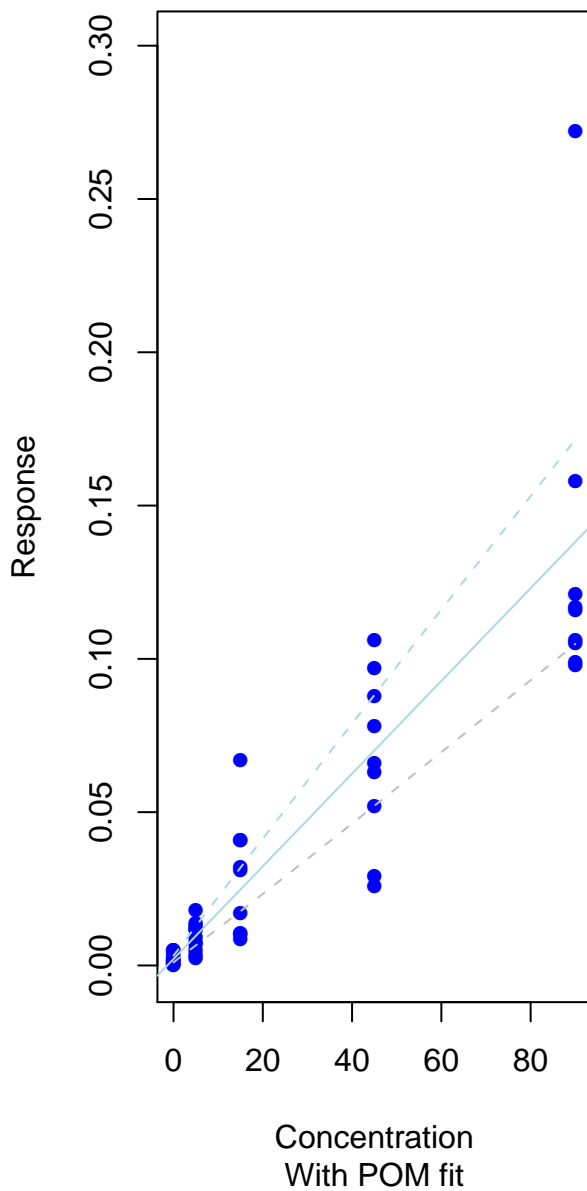
A scatter plot showing the relationship between Predicted Values (X-axis) and Standardized Residuals (Y-axis). The X-axis ranges from 0.0 to 2.0, and the Y-axis ranges from -1.5 to 1.5. The data points are represented by open circles. The residuals are scattered around zero, indicating a good fit of the model, but there is a slight downward trend as predicted values increase.

Predicted Values	Standardized Residuals
0.1	-1.6
0.1	0.0
0.2	1.7
0.2	-0.25
0.25	0.0
0.4	0.8
0.4	-0.35
0.6	-0.4
0.6	-0.4
1.0	1.2
1.0	-0.55
1.5	0.8
1.5	-0.9
2.0	0.95
2.0	-1.1

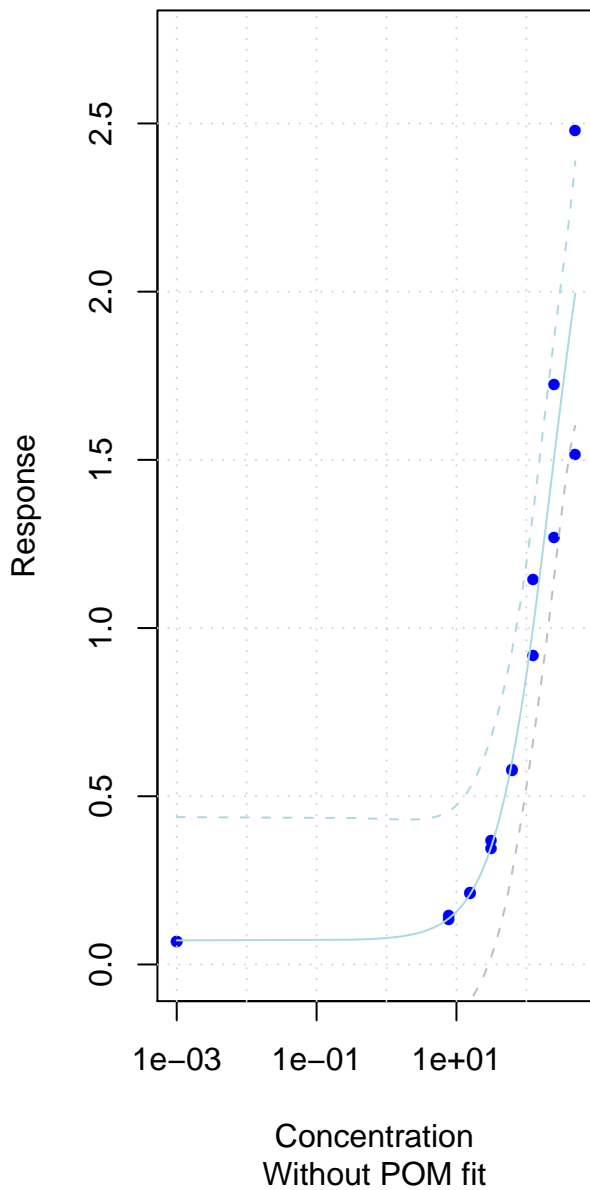
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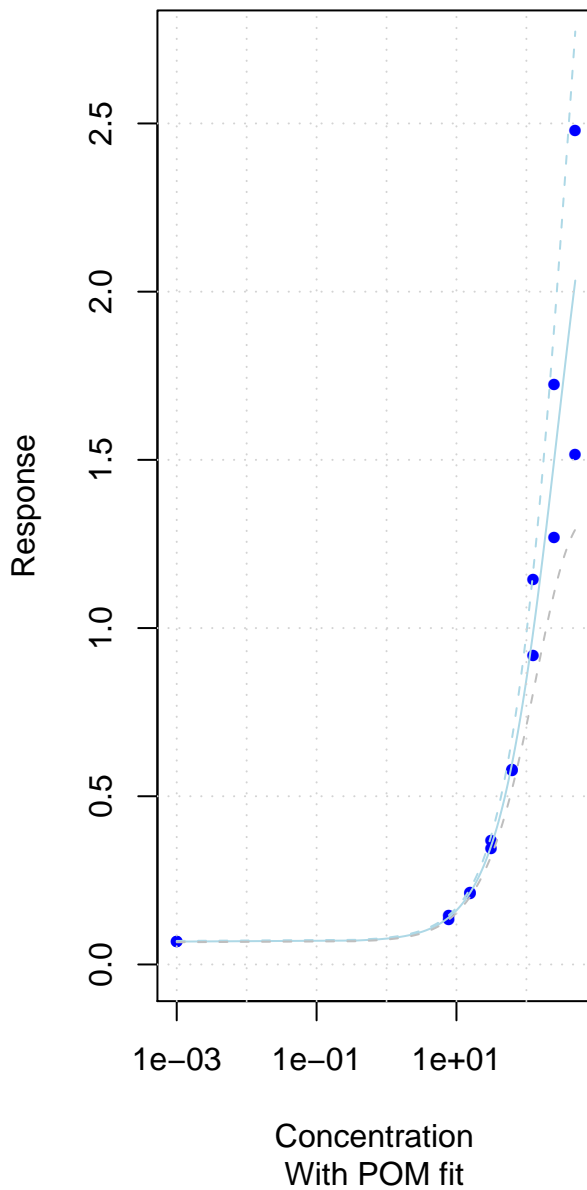
**HPLC data**



**ELISA data**

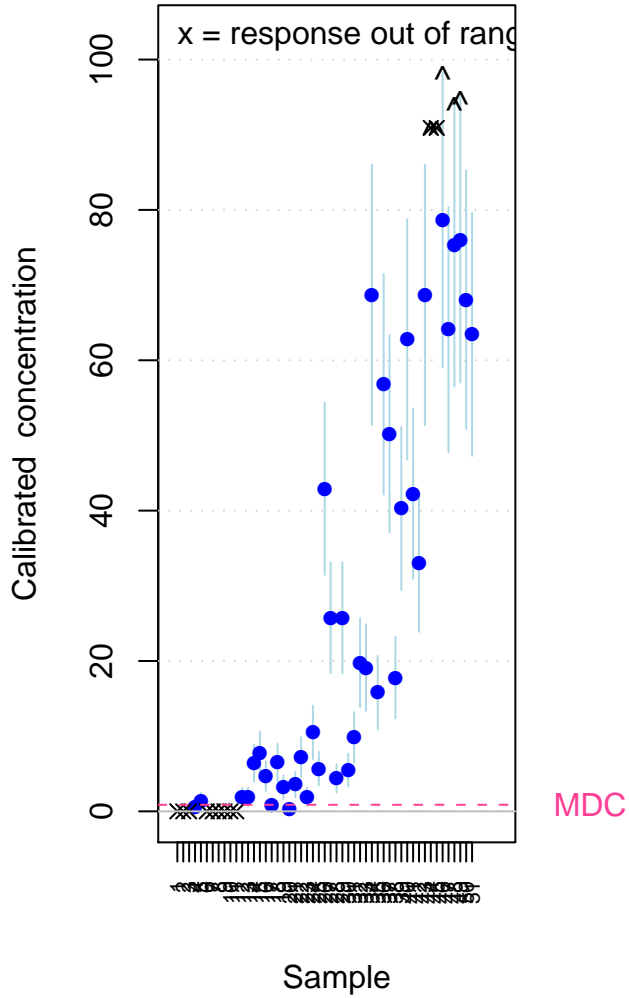


**ELISA data**





# HPLC data



ELISA data

