

# Serodynamics Analysis for Multiple Subjects

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## Introduction

This document demonstrates the full workflow using the **serodynamics** package. In this analysis, we run JAGS models for three different subjects:

- **sees\_npl\_128 (HlyE\_IgA)**
- **sees\_npl\_131 (HlyE\_IgA)**
- **sees\_npl\_133 (HlyE\_IgG)**

For each subject, we process the JAGS output to extract median parameter estimates and generate predicted antibody response curve plots.

## Run Models for Each Subject

```
# A tibble: 3 x 4
  Country id          antigen_iso visit_num
  <chr>   <chr>         <chr>         <int>
1 Nepal  sees_npl_128 HlyE_IgA         5
2 Nepal  sees_npl_131 HlyE_IgA         5
3 Nepal  sees_npl_133 HlyE_IgG         5
```

**Subject: sees\_npl\_128 (HlyE\_IgA)**

## Mapping Internal Subject to Original ID

```
# A tibble: 290 x 8
  Subject antigen_iso alpha shape t1    y0    y1 id
  <dbl>   <chr>         <dbl> <dbl> <dbl> <dbl> <dbl> <chr>
```

```

1      1 HlyE_IgA      0.00253    1.73  5.70  2.75  427. sees_npl_1
2      1 HlyE_IgG      0.00113    1.33  6.57  2.21  245. sees_npl_1
3      2 HlyE_IgA      0.000959   1.43  6.42  2.24  345. sees_npl_2
4      2 HlyE_IgG      0.00113    1.33  7.17  1.95  282. sees_npl_2
5      3 HlyE_IgA      0.00296    1.68  5.61  2.66  566. sees_npl_3
6      3 HlyE_IgG      0.000936   2.17  8.86  1.25  271. sees_npl_3
7      4 HlyE_IgA      0.00190    1.56  6.52  2.22  287. sees_npl_4
8      4 HlyE_IgG      0.00120    1.43  7.91  1.79  224. sees_npl_4
9      5 HlyE_IgA      0.00221    1.63  6.42  2.31  359. sees_npl_5
10     5 HlyE_IgG      0.00118    1.40  7.70  1.88  213. sees_npl_5
# i 280 more rows

```

### Display Specific MCMC Sample Parameters (1000 samples of sees\_npl\_128 (HlyE\_IgA))

```

# A tibble: 1,000 x 7
  Chain Iteration   alpha shape    t1    y0    y1
  <int>   <int>   <dbl> <dbl> <dbl> <dbl> <dbl>
1     1       1     0.00195  1.35  2.75  3.07  749.
2     1       2     0.00220  1.22  2.61  3.33 1311.
3     1       3     0.00168  1.36  3.14  3.09 1049.
4     1       4     0.00135  1.37  3.52  2.92 1271.
5     1       5     0.00147  1.28  3.69  3.06 1762.
6     1       6     0.00147  1.28  3.69  3.06 1762.
7     1       7     0.00147  1.28  3.69  3.06 1762.
8     1       8     0.00147  1.28  3.69  3.06 1762.
9     1       9     0.00116  1.39  2.42  3.07 2191.
10    1      10     0.00106  1.29  2.19  2.79 1912.
# i 990 more rows

```

## Plotting Predicted Antibody Response Curves

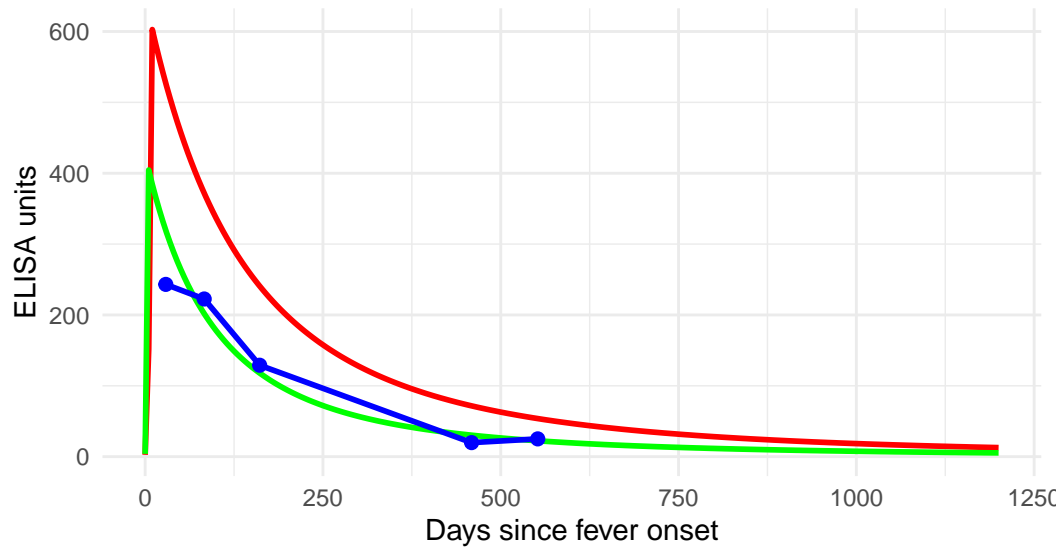
Below are three versions of the predicted antibody response curves:

- **plot**: A plot using median parameters from `param__medians__full` and partial parameters.
- **plot2**: A plot using full MCMC samples (without log scale).
- **plot3**: A plot using full MCMC samples with a log10 scale on the y-axis.

## Generate Plots

Below are three versions of the plot:

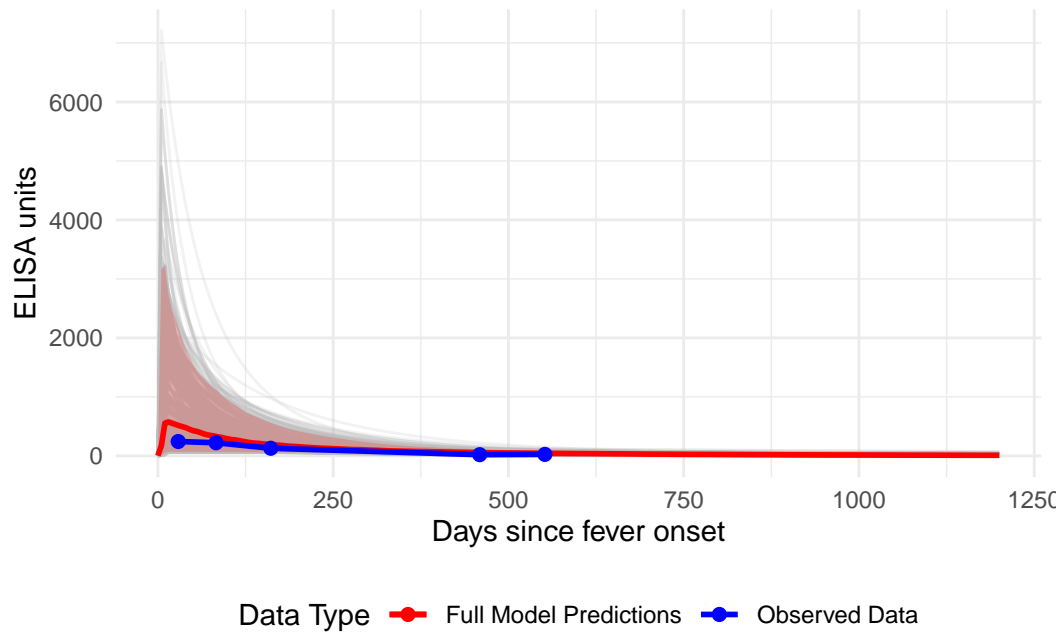
### Plot



Data Type    —●— Model Full Predictions    —●— Model Partial Predictions    —●— Observed Data

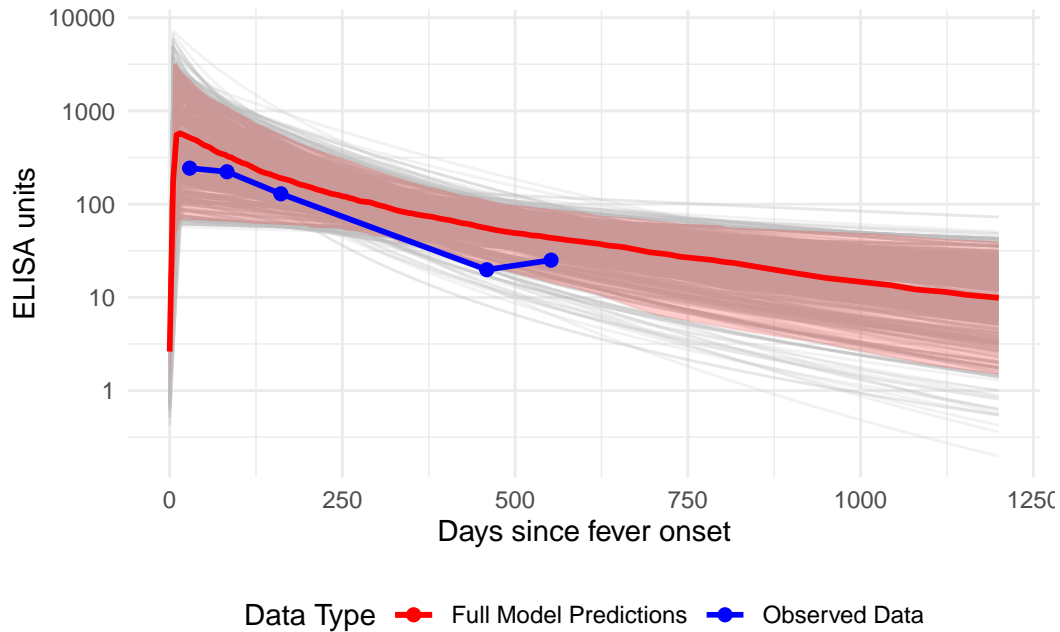
Shows the predicted curve using the median parameters from the full and partial processing.

**Plot2**



Displays the median curve along with the 95% credible interval (ribbon) derived from the full MCMC samples on a linear scale.

**Plot3**



The same as Plot2 but with a log10-transformed y-axis, which can help visualize differences when antibody levels span several orders of magnitude.

## Interpretation

In Plot3, the 95% credible band appears broad, particularly at later times, suggesting substantial uncertainty in long-term antibody decay—likely driven by parameters such as the decay rate ( ) and the shape parameter. This broad interval indicates that, given the data, a wide range of decay trajectories is plausible. However, a narrow credible band does not necessarily imply a good fit to the data. To properly assess model fit, we could use Bayesian goodness-of-fit metrics such as posterior predictive checks (which packages like ggs may already provide) to compare the observed data with data simulated from the model's posterior.