

Stats 201B Project due Monday Noon (3/17/2014)

Data were from experiments that studied a biological system with Herpes simplex virus type 1 (HSV-1) and six antiviral drugs: Interferon-alpha (*A*), Interferon-beta (*B*), Interferon-gamma (*C*), Ribavirin (*D*), Acyclovir (*E*), and TNF-alpha (*F*). The experiments were performed in batches. A batch or experiment tested up to 32 drug combinations in 32 wells. Cell culture was prepared before each experiment. Virus and drugs were added simultaneously to 32 wells during the experiment manually. The output, **readout**, was the percentage of infected cells after the combination drug treatment. Within each batch, an extra well was used as positive control, which had viral infection and no drug treatment. A batch used 33 wells, which were the experimental units.

The file `hsv4model.txt` contains 6 batches of experiments, and has 182 rows and 9 columns. (Note 10 observations have been removed from these 6 batches.) The variables *A–F* were the actual dosages (in ng/mL) used for each combination. The variable **pc** was the readout of the positive control.

The file `hsv4predict.txt` contains 10 drug combinations which were part of the experiments but I removed the output, readout. Your task is to build a model with `hsv4model.txt` and then use your model to predict the readout for the 10 drug combinations in `hsv4predict.txt` and give standard errors.

Instruction on your report: The report should be typed (in **font size 12pt**) and include your name, methods, results and discussions. **The report is limited to maximum 2 pages.** You can include an appendix of figures or R outputs/codes if you like, but **the appendix is limited to maximum 4 pages.** Do not include a cover page or an introduction. Focus on describing your analysis strategy/procedure and how (or why) you come up with your final model. State your final model and report your predictions and standard errors. Discuss any interesting findings.

Email me your prediction results (10 predicted readouts and 10 standard errors) for the 10 drug combinations in `hsv4predict.txt`. Use **201B project** as the subject and format your prediction results in one line as

`Lastname.Firstname p1 p2 ... p10 se1 se2 ... se10`

where *p1* to *p10* are your predicted readouts and *se1* to *se10* are the standard errors of your predictions. Round up your numbers by 2 decimals, for example,

`Xu.Hongquan 1.11 2 3 4 5 6 7 8 9 10 1.1 1.2 1.3 1.4 1.5 1.6 1.7 1.8 1.9 2.00`

Turn in your report to me (in MS 8955) and email me your predictions **by Monday noon**. If you cannot come to my office, email me your predictions and report (in PDF).

Hint: If you make a transformation on the response, remember to do an inverse transformation on your predictions and standard errors.

You should complete the project by yourself. No discussion with others. No help of any kind from anyone else.