Hi Chris,  
  
Just to be clear, that we are talking about the iTRAQ experiments or proteomic experiments. Hence, the question is for a given protein, whether there is a differences in its protein abundance level between the treatment groups.   
  
The current write-up consists of the Phase 1 experiment is completely randomised design and Phase 2 experiment is row-column design.    
  
The Phase 1 experiment is the perturbation of the animals by the treatments, hence, the animals are the experimental units, and every observation has the same variance of \sigma\_A^2. The test between the treatment groups could have done here, but we cannot measure the protein abundance levels directly from each of these animals. Hence, the Phase 2 experiment consists of measuring the protein abundances of each animal.

The next step is to allocate the animals from Phase 1 experiment to Phase 2 experiment. To be able to estimate the variance components of between runs, we need to have technical replicates. For this write-up, I have kept the number of technical replicate to 2. I think this is where the \sigma^2 comes in, but it should really be in the Phase 2 not Phase 1 experiment.

The optimal design problem comes in at the Phase 2 experiment where we try to allocate the animals, from Phase 1 experiment, to the runs and tags. This is where we want to minimised the confounding of the animals with runs and tags, and this is also affect how the objective function is constructed. With some designs, some DF associated with animals effects can be in the between runs stratum, and the aim is trying to minimise that.

Thus, the Phase 2 design is just an optimal row-column design with consideration of the animals as the random effects, so there is between animals stratum when constructing this theoretical ANOVA table.