MelphPrototypeApp1 Checklist

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| Have any ideas for an application title? Currently it’s just **Melphalan** | We will update it later. |
| The presentation you showed us last week had some ANC simulations at different melphalan doses and the consequent duration in severe neutropenia. Take the patient characteristics you used and enter them into the Shiny app and see if you get the same profiles (for both patients and all tested doses). **See “Calculating Duration in Severe Neutropenia” below.** The application will let you compare up to three regimens for the same patient. I can add more if you like. | This prediction in the app is really awesome!!!!  However, duration seems much different from ours. ANC fluctuates up&down, so clinicians follow up patients until their ANC is above 0.5K for multiple days. Therefore, I calculated the duration when ANC falls below than 0.5K for the first time, and goes above 0.5K for the last time from 24hr-interval simulation in NONMEM.  Would you be able to code to calculate duration in this way? Could it be affected by the way if duration was calculated before or after simulation?  I attached the Excel and R codes how we calculated it. If it is not recovered, i.e. last time>30days, the last time could be set as the last time of simulation. |
| What **serum creatinine units** do you use? (in Australia we used micromol/L, but based on the Cockcroft-Gault equation you sent me, you seem to use different units!) | We used SCr (**mg/dL**) recorded in clinics  The denominator of the equation is ‘Scr\***72**’ for mg/dL unit. Would you correct it? |
| You can use the application to test the impact of your covariate effects. For some covariates you might find that when you change them, the ANC profile (and consequently duration of severe neutropenia) doesn’t significantly change. You may need to re-think the necessity of some of these covariates that don’t seem to make a clinical impact on your predictions. For example, gender? Let us know if you remove some covariates from your model – and what the updated model and model parameter values are. | All covariates were simulated after fixing others as median (please refer to the attached file). As you figured out, SEX could not make a difference. While I did further investigation, I found that 95% PI is quite big.  I simulated different SEX in the setting of medians for all covariates using NONMEM, and the result showed difference.  I think this is also because the calculation method for duration in the app is different from how we calculated here. |
| Layout and functionality? Were you able to work out how to use the application easily? Was everything easy to find? Did it all make sense? | Sure.  I would like to give more flexibility in dosing (5 instead of 10). And default dose level=200 in slider.  (Another thought is that melphalan may be given in the range of 100-300 mg/m2, so we would fix the slider according to it. – However, we may hold the decision till we discuss with physicians to check the range. This would be update later.)  Please separate out BSA so that clinicians can enter it by themselves. The calculation seems differently from what they calculated in clinics. BSA was provided by their hospital system. Their calculated BSA will be used to calculate standard dose in the other group. |
| Are there any other plots or summary statistics that you would like to add? | Can we add total amount in addition to dose level in the result or report? It will be helpful for them to precede the personalized regimen. |
| Would you like the application to print out results? For example save the plots, patient characteristics and dosing regimens to a word document for future reference? | Sure. It would be nicer if we add option to print out results, such as word or pdf form? |

### Other notes from Jess

**No Figure Legends**

I haven’t made any formal figure legends – but you’ll see the colours for the different regimen labels correspond with the colours that appear in the plots. The lines or circles in the plots refer to the “population predicted or PRED” and shaded ribbons or error bars are “individual predicted or IPRED” based on 50 randomly simulated individuals using your PPV estimates.

The ANC Profile plot is just simulated every 24 hours, and the Melphalan profile plot is just every half hour. If we add more time-points, the time it takes to update the plots from widget changes will significantly get slower.

**Calculating Duration in Severe Neutropenia**

The way I have calculated this is embedded in the model’s differential equations – as the differential equation solver calculates the amount in each compartment, it will also calculate the time spent in severe neutropenia. This way it can calculate the duration down to the “micro-minute” even though I may not have specified the time it enters and exits severe neutropenia in the original time sequence. If you calculated the duration in severe neutropenia after the simulation had finished, then we may have slightly different results for the same patient scenario.

**Sharing the Shiny Application**

As you can see, sending the application as R code is not friendly to people who have never used R – particularly clinicians. Shiny applications can be uploaded online and a URL can be entered into a web-browser to easily access the application, however this does not guarantee IP security! I can also package up the application and make it essentially a Windows program that can be installed on Windows computers (can’t do it for Mac just yet!). This is how I see the application being accessed in the future, but it’s not necessary to do just yet in the prototype stage.

**Making the Shiny Application Usable and Informative for Clinicians**

Rather than entering creatinine clearance and fat free mass, the application will calculate these automatically depending on “measurable” input such as age, total body weight, height and serum creatinine. Hopefully this may be more useful “clinically.”

Eventually I’ll add more tabs describing what this application is used for, how to use it and information about the model behind the predictions. This is something we will all work on towards the end – but will require you to draft some text about the model and patient population specifics.

### Other notes from Yu Kyoung and Mitch