Code Readme

1. **Sensitivity Analysis**

i. DriverBasic\_sens.m – sens.mat and creates ranked sensitivities and time-varying sensitivities figures (Fig. S2A-B)

ii. Covariance.m – saves Correlations.mat

iii. SensHeatmap.m – creates heatmap figures (Fig. S2C-D)

1. **Optimization**
2. Individual Optimization

i. mainLogistic.m – optimizes 4 parameters for each patient, saved into PARS\_4vary.mat

ii. par\_boxplots.m – creates parameter boxplots (Fig. S3A)

iii. ModelvData.m – creates plot of model output versus data for all patients with 4 varying parameters (Fig. S3B)

1. Nested Optimization

i. NestedOpt.m – nested optimization for training set, saves PARS.mat and rhovarphi.mat

ii. mainLogistic.m – individual optimization for testing set patients using two uniform parameters in rhovarphi.mat

iii. PlotResults.m – plots individual fit for training (Fig. S4A-B) and testing (Fig. 1A-B) patients. Also plots stem cell proportions (Fig. S5)

ModelvData.m – plots model output versus data for patients in training set (Fig. S4C) and testing set (Fig. 1C)

iv. par\_boxplots.m – creates boxplots for ps and alpha for training (Fig. S4D) and testing (Fig. 1D) data sets

v. psvsalpha.m – Fits a curve through ps versus alpha for training (Fig. S4D) and testing (Fig. 1D) data sets

1. Cycle by Cycle Optimization

i. CycbyCycOpt.m – optimizes each cycle individually for each patient using two uniform parameters in rhovarphi.mat

ii. boxplot\_CyctoCyc.m – plots boxplot of ps changes from cycle to cycle for training patients (Fig. 8A)

1. **Forecast**

i. parCPD.m, parCPD\_2.m, parCPD\_3.m – creates cumulative probability distributions of changes in ps from cycle to cycle (Fig. 8B)

ii. mainLogistic.m – fits curves through ps versus alpha for each cycle, saves into psalphafit.mat

ConfidenceInt.m – plots ps versus alpha with fitted curve and 95% confidence interval (Fig. 8C)

iii. mainForecast.m – forecasts response for each patient, given a cycle number and plots the results (Fig. 2)

1. **Simulations**
2. No Induction

i. NoInductionSims.m – simulates IADT with and without induction, as well as continuous ADT. Saves time to progression (TTP) into TTP.mat and plots simulation results for each patient (Fig. 3G)

ii. SwimmerPlots.m – creates swimmers plot comparing time on treatment for each patient (Fig. 3A-D)

iii. KapMeier.m – plots Kaplan-Meier comparing TTP with and without induction and with continuous ADT (Fig. 3E)

iv. TTP\_Scatter.m – compares TTP between each of the simulations for all patients (Fig. 3F)

1. Alternative Thresholds

i. ThresholdSims – simulates IADT with alternative thresholds. Saves time to progression (TTP) into TTP.mat and plots simulation results for each patient (Fig. 4F)

ii. SwimmerPlots.m – creates swimmers plot comparing time on treatment for each patient (Fig. 4A-C) for each threshold

iii. KapMeier.m – plots Kaplan-Meier comparing Bruchovsky IADT protocol and alternative threshold IADT(Fig. 4D)

iv. TTP\_Scatter.m – compares TTP between each of the simulations for all patients (Fig. 4E)

1. Induction Docetaxel

i. DOCSims.m – simulates IADT with and without induction docetaxel for each patient (Fig. 5C-D)

ii. KapMeier.m – plots Kaplan-Meier comparing TTP Bruchovsky IADT protocol IADT with induction docetaxel (Fig. 5A)

iii. PlotTTP.m – compares TTP between IADT alone and IADT with induction docetaxel (Fig. 5B)

1. First Cycle Docetaxel

i. FirstCycDOCSims.m – simulates IADT with and without docetaxel after first cycle. Saves TTP into TTP.mat and plots simulations results for each patient (Fig. 6D)

ii. boxplot\_BenvNoBen.m – comparison of ps values between patients who do not benefit from docetaxel and those that do (Fig. 6A)

iii. KapMeier.m – plots Kaplan-Meier comparing IADT with and without docetaxel after the first cycle. Stratifies based on ps value (Fig. 6B)

iv. TTP\_Scatter.m – compares TTP between each of the simulations for all patients (Fig. 6C)

1. **Leave-One Out**
2. Leave-One Out

i. RunAll.m – runs leave-one out study for each patient individually

1. ROC Analysis

i. ROC.m – plots ROC curves for all patients simultaneously (individual ROC results saved in ROC.mat)