Note on Kate's Rotation Project

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For the linear mixed-effects model to fit the parabolas, we can consider

$$\boldsymbol{y} = \boldsymbol{X}(\boldsymbol{\beta} + \boldsymbol{b} + \boldsymbol{\Gamma}(\boldsymbol{\alpha}'\boldsymbol{x})) + \boldsymbol{\epsilon}.$$

The goal is to find a vector $\boldsymbol{\alpha}$ that gives the best "purity" when clustering. $\boldsymbol{X}$ will be the design matrix for the orthogonal polynomials; $\boldsymbol{b}$ the vector of random effects; $\boldsymbol{\Gamma}$ a vector (of the same dimension of $\boldsymbol{\beta}$) of fixed-effects.

Actually, we can fit a model separately for the drug and placebo treatments

$$\boldsymbol{y}_1 = \boldsymbol{X}(\boldsymbol{\beta}_1 + \boldsymbol{b}_1 + \boldsymbol{\Gamma}_1(\boldsymbol{\alpha}'\boldsymbol{x})) + \boldsymbol{\epsilon}_1 \ \text{ and } \ \boldsymbol{y}_2 = \boldsymbol{X}(\boldsymbol{\beta}_2 + \boldsymbol{b}_2 + \boldsymbol{\Gamma}_2(\boldsymbol{\alpha}'\boldsymbol{x})) + \boldsymbol{\epsilon}_2.$$

My intuition says to find $\boldsymbol{\alpha}$ that leads to big differences in $\boldsymbol{\Gamma}_1$ and $\boldsymbol{\Gamma}_2$ as well as differences between $\boldsymbol{\beta}_1$ and $\boldsymbol{\beta}_2$. If we choose $\boldsymbol{\alpha}$ and then fit the model, that will determine $\hat{\boldsymbol{\Gamma}}_1, \hat{\boldsymbol{\Gamma}}_2, \hat{\boldsymbol{\beta}}_1$ and $\hat{\boldsymbol{\beta}}_2$.