**Predicting amyloid burden to accelerate recruitment of secondary prevention clinical trials**

**Supplemental Material**

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| **Supplemental Figure 1.** Predictors such as age, *APOEε*4 dose, and Clinical Function Instrument (CFI), both participant (“Pt”) and study partner (“SP”), were assumed to have monotonic relationship with amyloid PET SUVR. |

Table 1 - Model fitting algorithm steps

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| **Algorithm** XGBoost – Bayesian optimization |
| 1:  | Generate an initial search space of the hyper-parameters $x$ |
| 2: | Fit XGBoost $x$hyper-parameters using CV |
| 3: | Return out-of-fold predictions for each of the training data |
| 4: | Query summary metric to obtain $y$ |
| 5: | Augment data $D=(x, y)$ |
| 6: | Fit Gaussian Process Model using $D$ |
| 7: | **For** $b=1, 2, …., B$ **do** |
|  | Select new $x\_{b+1}=arg max\_{x }α(x, D\_{b})$ |
| 9: | Fit XGBoost model $x\_{b+1}$hyper-parameters using CV |
| 10: | Return out-of-fold predictions for each of the training data |
| 11: | Query summary metric to obtain $y\_{b+1}$ |
| 12: | Augment data $D\_{b+1}=(D\_{b}, \left(x\_{b+1}, y\_{b+1}\right))$ |
| 13: | Update Gaussian Process Model using $D\_{b+1}$ |
| 14: | Fit XGBoost model using hyper-parameters such that $x\_{optim}=arg max\_{x }(y)$ |
| 15: | Fit XGBoost quantile models using hyper-parameters $x\_{optim}$ |