Appendices to: Functional Data Analysis of Dynamic PET Data

Yakuan Chen, Jeff Goldsmith and Todd Ogden

A Additional figures

The graph in Figure A.1 illustrates the one- and two-tissue compartment models. In this Figure, C_P $(kBq \cdot mL^{-1})$ is the concentration of the tracer in the arterial plasma and C_T $(kBq \cdot mL^{-1})$ is the concentration of the tracer in the target tissue. F, NS, SP represent the "free" tracer, tracer nonspecifically associated with other macromolecular components, and tracer specifically bound to the target protein, respectively. K_1 $((mL_{plasma}) \cdot min^{-1} \cdot (mL_{tissue})^{-1})$ is the plasma to brain transport constant; k_2 (min^{-1}) is the brain to plasma transport constant; k_3 (min^{-1}) is the first order association rate constant for specific binding; and k_4 (min^{-1}) is the disassociation rate constant for specific binding (Gunn *et al.*, 2001).

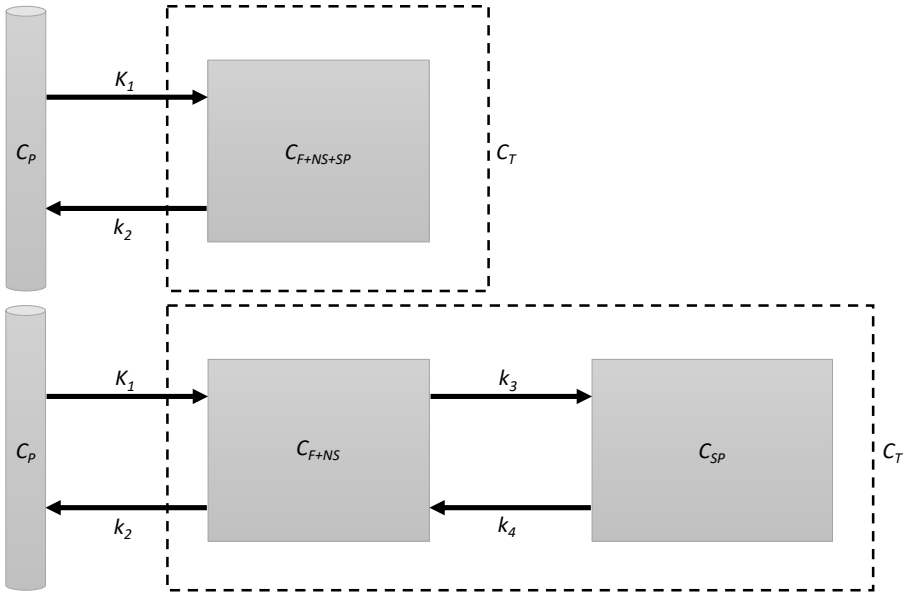

Figure A.1: An illustrative diagram of one-tissue compartment model (top) and two-tissue compartment model (bottom).

Figure A.2 shows fitted IRFs and group means produced in the analysis of the midbrain data using a one-tissue compartment model, a two-tissue compartment model, and the proposed non-parametric method. As in Figure 5, some differences in individual IRFs can be observed. Overall group means also differ somewhat, especially in the first half hour, due to the relative inflexibility of the mean structures in the parametric models.

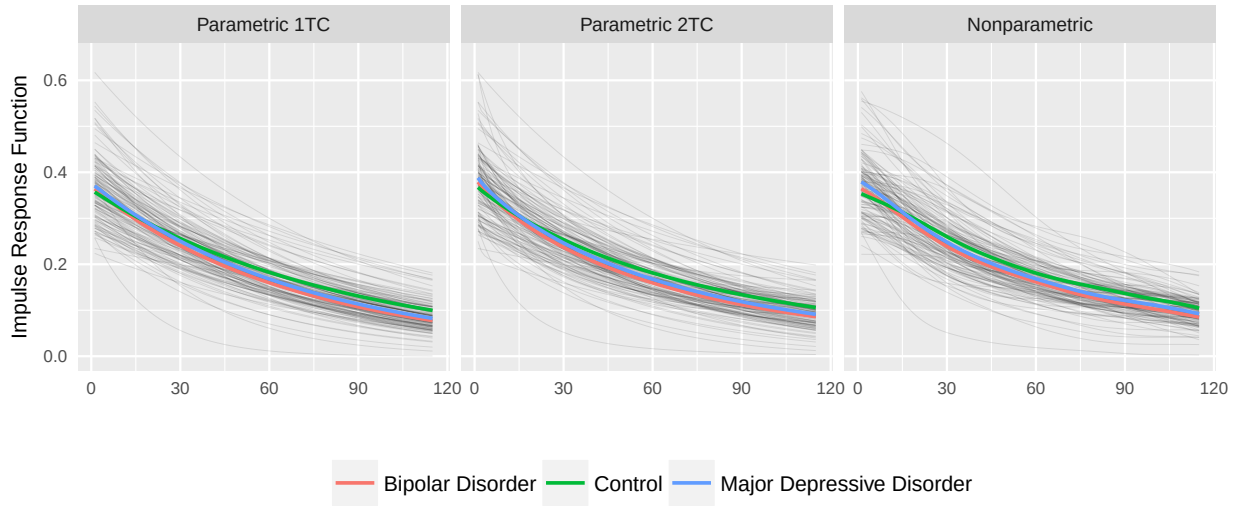

Figure A.2: Estimated group means (colored) and individual IRFs (gray) obtained using the 1TC model (left) , 2TC model (middle) and our method (right).

Figure A.3 shows the density of root integrated mean squared errors comparing observed TACs to the fitted values produced by each of three methods. The nonparametric model produces an RIMSE distribution with smaller overall values and fewer outliers than the compartment models.

Figure A.4 shows residuals obtained using both our nonparametric approach and the parametric methods. For all models, residuals are computed by convolving a subject's estimated IRF and input function to produce the fitted value for the TAC, and subtracting the fitted TAC from the observed TAC at every observation time. We show the distribution of errors at each observation time using boxplots; the residuals of our proposed method are centered at approximately zero, while the parametric models can miss trends in the data due to relatively inflexible mean structures.

Figure A.3: Densities of root integrated mean square errors of TACs of all 137 subjects.

Figure A.4: Box plots with residuals obtained using 1TC (left) and 2TC (middle) models and our proposed approach (right) by diagnosis group.