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Rapid Quantitative Pharmacodynamic Imaging with Bayesian Estimation

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We recently described rapid quantitative pharmacodynamic imaging, a novel method for estimating sensitivity of a biological system to a drug. We tested its accuracy in simulated biological signals with varying receptor sensitivity and varying levels of random noise, and presented initial proof-of-concept data from functional MRI (fMRI) studies in primate brain. However, the initial simulation testing used a simple iterative approach to estimate pharmacokinetic-pharmacodynamic (PKPD) parameters, an approach that was computationally efficient but returned parameters only from a small, discrete set of values chosen a priori. Here we revisit the simulation testing using a Bayesian method to estimate the PKPD parameters. This improved accuracy compared to our previous method, and noise without intentional signal was never interpreted as signal. We also reanalyze the fMRI proof-of-concept data. The success with the simulated data, and with the limited fMRI data, is a necessary first step toward further testing of rapid quantitative pharmacodynamic imaging.

Keywords: pharmacodynamics, PK-PD modeling, Bayesian parameter estimation, pharmacological imaging

INTRODUCTION

Measuring the sensitivity of an organ to a drug in vivo is a common, important research goal. The traditional approach is to independently measure biological responses to a range of different doses of drug. We recently described a novel method, rapid quantitative pharmacodynamic imaging (or QuanDyn™), for estimating sensitivity of a biological system to a drug in a single measurement session using repeated small doses of drug (Black et al., 2013). In that report, we tested QuanDyn™’s accuracy in simulated data with varying receptor sensitivity and varying levels of random noise. The initial simulation testing used a simple iterative approach to estimate pharmacokinetic-pharmacodynamic (PKPD) parameters including EC₅₀, the plasma concentration of drug that produces half the maximum possible effect Eₘₐₓ. The iterative approach was computationally efficient but could only select EC₅₀ from a short list of parameter values chosen a priori.

Here we revisit the simulation testing using a Bayesian method to provide continuous estimates of the PKPD parameters. The Bayesian approach also identifies data too noisy to produce meaningful parameter estimates (using a model selection package described below). Bayesian methods have been used successfully in other PKPD analyses (Lavielle, 2014, to cite but one example). For the present purpose we applied a Bayesian data analysis package specifically designed...
for efficient voxelwise analysis of 4-dimensional imaging data (Brethorst, 2014; Brethorst and Marutyan, 2014).

**METHODS**

**Simulated Data**

We used a standard sigmoid PKPD model (Holford and Sheiner, 1982) to create 6 time-effect curves that could reasonably represent biological signal from a pharmacological challenge study: one with no response to drug ($E_{\text{max}} = 0$) and five with varying sensitivities to drug: $E_{\text{max}} = 10$ and $EC_{50} \in \{0.25, 0.6, \sqrt{2}, \pi, 7.5\}$.

As in the previous work, the concentration of drug in plasma over time is modeled as

$$C(t) = \sum_{k=1}^{K} D_k \cdot u(t - t_s - t_k) \cdot 2^{-\frac{(t - t_s - t_k)}{t_{1/2}}}$$

where $K$ doses of drug, $D_k$, are given at times $t_k$, $u(t)$ is the unit step function, $t_s$ (for “time shift”) is a fixed delay between drug concentration and effect, and $t_{1/2}$ is the elimination half-life of drug from plasma (Black et al., 2013). Drug effect is modeled as

$$E(C) = \frac{E_{\text{max}}C^n}{(EC_{50})^n + C^n}$$

where $C$ is $C(t)$ from the previous equation and $n$ represents the Hill coefficient. Baseline non-quantitative signal drift was simulated by adding to each curve a quadratic function of time

$$B(t) = a_0 + a_1 t + a_2 t^2.$$  

The full model is then

$$B(t) + E(C(t)).$$

The test curves were generated using $K = 4$, $D_1 = D_2 = D_3 = D_4 = 1$ (arbitrary concentration units), $t_s = 0.5 \text{ min}$, $t_{1/2} = 41 \text{ min}$, $n = 1$, $a_0 = 1000$, $a_1 = 2/(40 \text{ min})$, and $a_2 = 0$. The 6 resulting curves are shown in Figure 1.

Finally we added Gaussian noise to each time point. This was done 1000 times for each of the 6 curves above and for each of 8 noise levels from $SD = 0.01E_{\text{max}}$ to $2E_{\text{max}}$, resulting in 48,000 noisy time–signal curves plus the original 6 “clean” curves (see Supplemental Data).

**Testing the Method Using the Simulated Data**

In the simulated data described above, each of the 48,006 time courses were analyzed using the “Image Model Selection” package from the Bayesian Data-Analysis Toolbox (Brethorst, 2014; Brethorst and Marutyan, 2014). The Toolbox computes the posterior probability for the set of models (Brethorst, 1988) given a 4d data set. A Markov chain (Gilks et al., 1996) is used to draw samples from the joint posterior probability for all of the parameters including the choice of model. The Markov chain Monte Carlo simulation included the full model $B(t) + E(C(t))$, the baseline model $B(t)$, and a “no signal” model. Each model has equal prior probability, or more precisely we specify that the conditional probability of any model, given the supplied prior probabilities for the parameters relevant to that model, is equal to that of any other model (see Brethorst, 2014, section 22.1, at equation 22.6). Monte Carlo integration is then used to obtain samples from the posterior probability for each model and from the posterior probability for each parameter given the model. For the present analysis we specified 2500 samples at each step (50 samples run in parallel, repeated 50 times). Simulated annealing is used to minimize the risk of convergence to a non-global local maximum (see Brethorst, 2014, appendix B, for details). If the posterior probability for the model
indicated the full model, $B(t) + E(C(t))$, was preferred, the package also returned values for $EC_{50}$, $t_s$, $E_{\text{max}}$, $a_0$, $a_1$, and $a_2$. The software returns both the mean parameter values and the values from the simulation with maximum likelihood; the present report uses the latter. This analysis was repeated for each of the 48,006 time courses.

To provide more even sampling of parameter space across the conventional logarithmic abscissa for concentration-effect curves, $EC_{50}$ was coded as $10^q$, where $q = \log_{10} EC_{50}$, and a uniform prior probability was assumed for $q$ with range $[-3, 1.3]$, corresponding to a wide range of $EC_{50}$ values from 0.001 to 20.0. A uniform prior with range $[0, 1]$ min was used for the time shift parameter $t_s$. The Hill coefficient $n$ and the drug’s elimination half-life—parameters that for biological data could be estimated separately, from a typical PK study—were fixed at $n = 1$ and $t_1/2 = 41$ min. $E_{\text{max}}$ and the coefficients of the signal drift function $a_0 + a_1 t + a_2 t^2$ were marginalized.
Since tissues with high values of $EC_{50}$ respond less to a given dose of drug, i.e., $E \ll E_{\text{max}}$, the ratio $SD/E_{\text{max}} \ll SD/E$ underestimates the effect of noise relative to the observed effect. Therefore, we computed a signal-to-noise ratio (SNR) to simplify comparisons across the various input values of $EC_{50}$ and noise. We defined “signal” as the maximum value of $E$($C(t)$), without added noise, for $0 \leq t \leq 40$ min, i.e., the local maximum of the modeled signal shortly after the last dose of drug, less the input linear drift at that same time point. In Figure 1 this value can be appreciated near the right side of the plot and ranges from about 3 for $EC_{50} = 7.5$ to about 9 for $EC_{50} = 0.25$. We define SNR as the ratio of this signal to the standard deviation of the added noise.

**Testing the Method On In vivo Data**

We tested the model described above using the same pHfMRI (pharmacological fMRI) data we analyzed previously with the iterative method, namely, regional BOLD-sensitive fMRI time-signal curves from midbrain and striatum in each of two animals (Black et al., 2013). These studies were approved by the Washington University Animal Studies Committee (protocols # 20020085, 20050126). Each animal was studied twice, at least 2 weeks apart, producing 8 regional time-signal curves. On each day a total of 0.1 mg/kg of the dopamine $D_1$ agonist SKF82958 was given intravenously, divided into 4 equal doses on one day and into 8 equal doses on the other day (see Table 4 and Figure 10 in Black et al., 2013).

The iterative analysis had allowed only values of 5 or 30 min for the half-life of drug disappearance from the blood during the scan session; here we used a uniform prior probability over [2, 60] min for $t_{1/2}$. Prior probabilities for all other parameters were the same as described above for the simulated data.

### RESULTS

**Simulated Data Example**

Figure 2 provides an example result from one time course, to orient the reader to the following summary. Note that the parameter estimates are (approximately) the best estimates for the provided noisy data, even though they differ slightly from the input values used to produce the data.

**Sensitivity: prob(model) with Signal**

The full PKPD model explained the data better than a simpler model, i.e., prob(model) >0.5, except when signal was low (higher $EC_{50}$) or noise was substantial (Figures 3, 4).

**FalsePositives: prob(model) with Noise Only**

For the data sets containing no intentional signal, i.e., noise added to the $E_{\text{max}} = 0$ line, the Toolbox never returned $p > 0.5$ for any of the 8000 curves. In other words, there were no false positives.

**Accuracy**

Accuracy of the $EC_{50}$ estimate was considered for time courses with prob(model) >0.5. Figure 5 shows the mean estimated $EC_{50}$ as a function of the input $EC_{50}$; as expected, accuracy is best with higher SNR. Figure 6 shows the ratio of estimated $EC_{50}$ to input $EC_{50}$ in terms of SNR. Perfect accuracy would produce a ratio of 1.0, and values >1.0 indicate overestimation of $EC_{50}$, i.e., underestimation of the sensitivity to drug.

**In vivo Data**

The full PKPD model was selected for 6 of the 8 regional time-signal curves (see Table 1). The data and selected model curves are shown in Figure 7.

### DISCUSSION

**Simulation Testing**

Bayesian parameter estimation for the QuanDyn™ quantitative pharmacodynamic imaging method produced excellent results in simulated data: first, the Model Select method very accurately identified time courses with a meaningful drug-related signal,
FIGURE 7 | Time-signal curves from in vivo data from a phMRI study, in red, with the selected model in dark blue. (A–D) 4-dose experiments. (E–H) 8-dose experiments. Left column, midbrain. Right column, striatum. See Table 1 for further details.
until noise overwhelmed signal, i.e., when SNR < about 3.5. The Bayesian Data-Analysis Toolbox successfully avoided false positives, correctly refraining from identifying a signal in every noise-only time course, even where sensitivity was 100%. In time courses with a signal, mean accuracy was reasonable even in the face of low SNR, as shown in Figures 5, 6. Furthermore, the errors were conservative, with EC$_{50}$ usually erring on the high side (Figure 6). Said differently, the most likely quantitative error was to report slightly lower sensitivity to drug, especially when sensitivity is in fact low.

**Limitations**

This simulation used a simple noise model that may be best suited to a temporally stable, quantitative outcome measure, such as positron emission tomography, arterial spin labeling, or quantitative BOLD. However, because the PKPD model $E(t)$ is simply added to the baseline model $B(t)$, the latter can be replaced with a more complex signal, if needed, for non-quantitative imaging methods. For instance, Fourier series have been used to model typical BOLD-sensitive fMRI data over long time intervals. The baseline model $B(t)$ could be optimized further to best suit a specific scanner, tracer or sequence, or to other experimental design choices.

Similar comments hold for the signal as well as for noise: the QuanDyn$^\text{TM}$ quantitative pharmacodynamic imaging method will perform less well if the PKPD model does not realistically model the data. However, prior to initiating an expensive imaging study, one would determine the appropriate family of PKPD models for the drug to be tested, based on traditional dose-response experiments. We discuss this point further in Black et al. (2013). The choice of imaging method also affects the signal characteristics; for instance, typical BOLD implementations may not provide adequately linear responses to biological signal. On the other hand, using a more traditional phMRI design, the magnitude of the acute BOLD response to a single dose of drug per imaging session did increase monotonically with larger doses (Miller et al., 2013).

**In vivo Data**

Even with the relatively simple signal and noise models adopted for this initial testing, the tested method appeared to handle reasonably the in vivo data from a BOLD phMRI study (Figure 7). Further validation will require a larger set of similar multi-dose phMRI data, and comparison data from a more traditional dose-response study design.

The QuanDyn$^\text{TM}$ method described here has several potential advantages compared to the traditional approach to quantifying a drug effect, which is to estimate the population EC$_{50}$ by sampling a wide range of doses, one dose per subject and several subjects per dose. That approach is an excellent choice when the population under study is homogeneous (e.g., an inbred rodent strain), but does not apply well to single human subjects. One might adapt the traditional approach by repeatedly scanning a single subject, one dose per scan session, but that option brings its own complications, including scientific concerns such as sensitization or development of tolerance with repeated doses in addition to the practical and ethical consequences of repeated scanning sessions in each subject. That option, like the population method, would also require that subjects receive doses substantially higher than the EC$_{50}$, which may often be inappropriate in early human studies. Specifically, to estimate EC$_{50}$, traditional population PKPD studies require drug doses that produce effects of at least ~ 95% $E_{\text{max}}$ (Dutta et al., 1996). For all these reasons, the QuanDyn$^\text{TM}$ method may prove to be a better choice when single-subject responses are important, such as for medical diagnosis or individualized treatment dosing. We elsewhere discuss potential challenges related to moving this approach into humans (Black et al., 2013).

**DATA DEPOSITION**

The following information was supplied regarding the deposition of related data: The simulated data sets (1000 time courses for each set of parameter values and noise level) are available at the journal web site as Supplementary Data.

**AUTHOR CONTRIBUTIONS**

JK performed the experiments, analyzed the data, contributed analysis tools, reviewed and critiqued the manuscript. MV performed the experiments, analyzed the data, reviewed and critiqued the manuscript. GB contributed analysis tools, reviewed and critiqued the manuscript. KB conceived and designed the experiments, performed the experiments, analyzed the data, wrote the paper.

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**SUPPLEMENTARY MATERIAL**

The Supplementary Material for this article can be found online at: http://journal.frontiersin.org/article/10.3389/fnins.2016.00144
REFERENCES


Conflict of Interest Statement: Authors KB and JK have intellectual property rights in the QuanDyn\textsuperscript{TM} method (U.S. Patent #8,463,552 and patent pending 13/890,198, "Novel methods for medicinal dosage determination and diagnosis."). KB is an Associate Editor for the Brain Imaging Methods section of Frontiers in Neuroscience.

The other authors declare that the research was conducted in the absence of any commercial or financial relationships that could be construed as a potential conflict of interest.

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