Appendix A. ANOVA computation overview

The experiment in the main manuscript consisted of two experimental factors: PAIN and GENDER, each with two levels: (control, PFP) and (female, male). As detailed in the main manuscript the response variable of interest was a (1×100) scalar trajectory, and there were a total of 41 responses: 8 control females, 7 control males, 16 PFP females and 10 PFP males.

We can model these data using a general linear model (GLM):

$$\boldsymbol{Y} = \boldsymbol{X}\boldsymbol{\beta} + \boldsymbol{\varepsilon} \tag{A.1}$$

where $\boldsymbol{Y}$ is a (41×100) matrix of the experimentally measured responses, $\boldsymbol{X}$ is a (41×4) design matrix (Fig.A1), $\boldsymbol{\beta}$ is a (4×100) matrix of mean trajectories, and $\boldsymbol{\varepsilon}$ is a (41×100) matrix of residuals. Each column of $\boldsymbol{X}$ corresponds to a PAIN-GENDER pair, and the jth row contains a single one and three zeros, with the one appearing in the column corresponding to the jth subject's pain condition and gender.

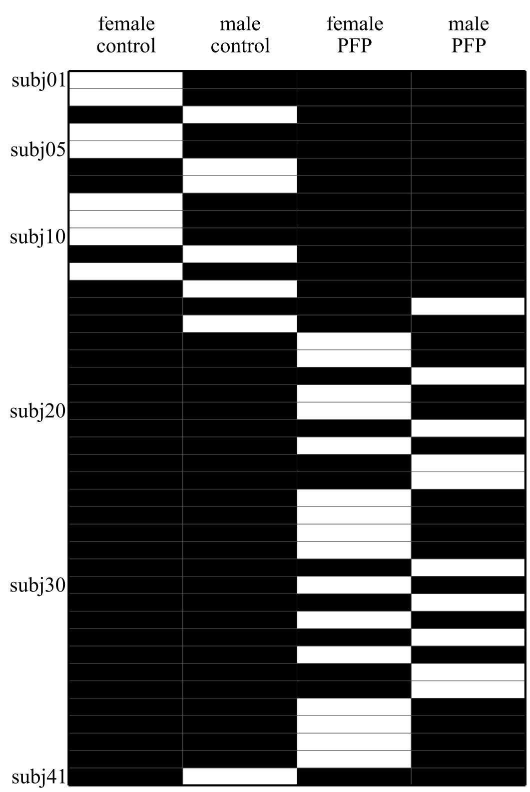

Figure A1: Experimental design matrix. White cells are ones and black cells are zeros.

The least-squares solution to Eqn.A.1 is:

$$\hat{\boldsymbol{\beta}} = (\boldsymbol{X}^{\mathrm{T}}\boldsymbol{X})^{-1}\boldsymbol{X}^{\mathrm{T}}\boldsymbol{Y} \tag{A.2}$$

and the model's residuals are:

$$\hat{\boldsymbol{\varepsilon}} = \boldsymbol{Y} - \boldsymbol{X}\hat{\boldsymbol{\beta}} \tag{A.3}$$

The fitted $\hat{\boldsymbol{\beta}}$ matrix is (4×100), containing one mean trajectory for each column of $\boldsymbol{X}$. The residuals matrix $\hat{\boldsymbol{\varepsilon}}$ is (41×100) and contains the differences between the original data $\boldsymbol{Y}$ and the relevant mean trajectory $\hat{\boldsymbol{\beta}}$. From the perspective of Random Field Theory (RFT), $\boldsymbol{\varepsilon}$ are assumed to be smooth, Gaussian random fields.

The entire fitted model may be visualized as a pseudo-color plot (Fig.A2). Note that each row of $\boldsymbol{Y}$, $\hat{\boldsymbol{\beta}}$ and $\hat{\boldsymbol{\varepsilon}}$ represents a single, temporally smooth trajectory.

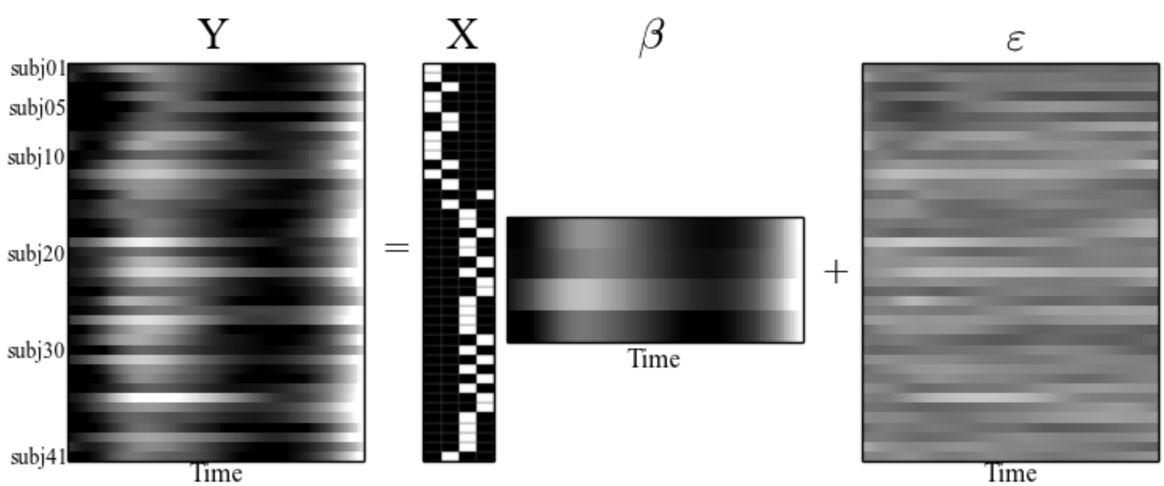

Figure A2: Statistical model (see Eqn.1). The time-normalized data (Y) are modeled as a set of mean trajectories (β) about which each subject's trajectory varies smoothly (varepsilon). The design matrix (X) is used to estimate the parameters (β) in a least-squares sense.

Since $\hat{\boldsymbol{\beta}}$ and $\hat{\boldsymbol{\varepsilon}}$ respectively embody mean and variance trajectories, it is clear that they can be combined to form test statistics in general, and F statistics in particular. Unfortunately the computational details are somewhat complex, so we leave this discussion with a conceptual, generalized summary:

Arbitrary biomechanics experiments (e.g. t tests, regression, ANCOVA, etc.) can be modeled using $\boldsymbol{X}$, and when the data can be assembled into a single response matrix $\boldsymbol{Y}$, the model parameters and variances can be rapidly computed using Eqns.A.2&A.3. Then test statistic fields can be constructed using combinations of $\hat{\boldsymbol{\beta}}$ and $\hat{\boldsymbol{\varepsilon}}$, and we can conduct statistical inference by comparing our observed test statistic field to the behavior of Gaussian fields which are funnelled through the same experimental design $\boldsymbol{X}$.

Readers interested in additional computational details, and a more thorough treatment of ANOVA theory may wish to consult Christensen (1996) and Friston et al. (2007).

References

Christensen, R. 1996. *Plane Answers to Complex Questions: The Theory of Linear Models*, Springer, New York.

Friston, K. J., Ashburner, J. T., Kiebel, S. J., Nichols, T. E., and Penny, W. D. 2007. *Statistical Parametric Mapping: The Analysis of Functional Brain Images*, Elsevier/Academic Press, Amsterdam.