Appendix B. SPM vs. PCA

Statistical Parametric Mapping (SPM) and Principal Component Analysis (PCA) have emerged relatively recently in the Biomechanics literature. The primary difference between the two is that SPM is a hypothesis testing technique and PCA is a dimensionality reduction technique. This Appendix aims to explain this difference conceptually, as applicable to the analysis of experimental 1D trajectories.

To start, let us revisit the general linear model (Eqn.A.1), which is replicated here for convenience:

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

The variables in this equation emerge, in chronological order, as follows:

1. $\boldsymbol{X}$: experimental design, set by an investigator prior to conducting an experiment.
2. $\boldsymbol{Y}$: experimental data, measured during the experiment.
3. $\boldsymbol{\beta}$: computed regression parameters, usually the least-squares map between the design $\boldsymbol{X}$ and the data $\boldsymbol{Y}$.
4. $\boldsymbol{\varepsilon}$: computed model residuals, representing the experimental variability about the parameters $\boldsymbol{\beta}$.

Note that this model is applicable to all experimental designs including: t tests, regression, ANOVA (as detailed in Appendix A) and more complex designs like MANCOVA. For t tests and ANOVA the $\boldsymbol{\beta}$ parameters are mean trajectories (one per group), and we shall limit subsequent discussion to this case.

SPM and PCA are equivalent up until the end of Step #2: both involve analysis of $\boldsymbol{Y}$ as measured during some experiment $\boldsymbol{X}$. SPM proceeds to Step #4, and then asks a conceptually simple question: *what is the probability that the effects embodied in* $\boldsymbol{\beta}$ *could be produced by random 1D trajectories like those embodied in* $\boldsymbol{\varepsilon}$? In a two-sample t test, for example, the two rows of $\boldsymbol{\beta}$ represent the two groups' mean trajectories, and those two trajectories are generally different. Difference itself is scientifically uninteresting because a variety of factors including measurement error ensure that mean trajectories are never precisely equivalent. Probabilities associated with trajectory differences are much more relevant: if random trajectories would frequently produce trajectory differences as large or larger than the observed mean trajectory differences, then the null hypothesis (of no difference) has successfully predicted the experimental result. On the other hand, if random trajectories would produce the observed difference relatively infrequently, then the null hypothesis failed to predict the experimental result and can be rejected. Formally, SPM quantifies such probabilities using Random Field Theory, which

analytically describes the frequency with which trajectory differences are expected to emerge when Gaussian random fields are routed through the experimental design $\boldsymbol{X}$. Like all 0D parametric hypothesis testing procedures, SPM regards the residual trajectories $\boldsymbol{\varepsilon}$ as independent and normally distributed, but these assumptions can easily be relaxed with non-parametric forms of SPM.

In contrast, PCA asks the following question: *what trajectories represent the most variance in* $\boldsymbol{Y}$? Some of the resulting PCs may be similar to the sample means ($\boldsymbol{\beta}$), but in general are different. Since PCA does not compute $\boldsymbol{\beta}$ directly, it effectively ignores the experimental design $\boldsymbol{X}$. This approach allows one to powerfully probe trends in $\boldsymbol{Y}$ irrespective of $\boldsymbol{X}$, but by doing so one loses the ability to ask probabilistic questions which pertain to $\boldsymbol{X}$. The probabilistic meaning of PCA results only emerges when tested on independent datasets using one or more validation procedures, as described in the machine learning literature (Bishop C. M., 2007).

In summary, whereas SPM establishes a probabilistic link amongst all four model elements (Eqn.B.1), PCA instead analyzes the variability in $\boldsymbol{Y}$ in isolation. The consequences are that SPM results generalize beyond the analyzed dataset, and that PCA results must be validated on independent datasets to establish generalizability. Most concisely: SPM is a hypothesis testing technique and PCA is a dimensionality reduction technique.

The practical implications are as follows: if one wishes to formally test *a priori* hypotheses regarding whole 1D trajectories, then SPM is a good choice. If, however, one wishes to describe the sources of variability within a particular dataset, then PCA is a good choice. The important scientific distinction is that, whereas SPM generates probability values corresponding to the given experimental dataset, PCA results can only adopt probabilistic meaning when validated on independent datasets. Interested readers may wish to consult machine learning textbooks (e.g. Bishop, 2007), which clarify the role of PCA and other dimensionality reduction techniques in the broader spectrum of probability computations.

References

Bishop C. M. 2007. *Pattern Recognition and Machine Learning*, Springer, New York.