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Biological systems are not low order, linear, nor time invariant. But it is often useful to model them as such. Given the significant variability in biological systems, we want to fit models that are robust to biological “noise”—such as trial-to-trial variability, differences between individuals, sex differences, and parameter drift that may occur over time—but that nevertheless capture the system behavior in a parsimonious manner. Here, we present a straightforward approach for fitting low-order parametric transfer functions to frequency-domain data. Our goal is to produce a user-friendly set of tools based on model selection (e.g. AIC, BIC, cross validation) that will enable biologists to generate simple analytical expressions from necessarily nonlinear, time-varying, and infinite dimensional biological phenomena. Application to problems in sensorimotor control systems illustrate the approach. (Received January 24, 2014)