Model Reduction for 'Large-scale' Compartmental Models

Thomas Heldt (George Verghese, Faisal Kashif)

Synopsis:

In efforts to improve 1) the representation of biological processes and 2) the fit of models to experimental data, mathematical models of physiological systems have undergone steady refinement over the past forty years. Along with this refinement has come an increase in the complexity of the model structures and in the number of parameters required to specify the models.

This situation is typical of domains (from biology to power systems) in which the component processes of a system are fairly well understood and mapped out mathematically. In such cases, the natural models for computation and simulation of the global behavior of the system comprise complex interactions of models for the component processes. However, the dynamics produced by such complex (possibly non-linear) models (containing perhaps hundreds or thousands of state variables and parameters) may look annoyingly similar to transients produced by a second-order model specified by just a few parameters! It is then natural to wonder whether the full complexity of the original model was needed.

Challenges:

Increasing the complexity of a model can significantly work against its usefulness in many respects:

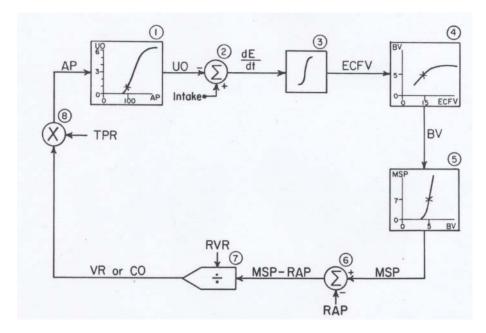
- 1. It becomes harder to pick (identify) parameter values reliably because many different parameter values can lead to responses (dynamics) that are essentially indistinguishable.
- 2. Simulation times are increased.
- 3. It becomes difficult to understand in a fundamental way what parts of a model are being exercised and how.

Toward Structured Model Reduction:

The mathematical representation of component processes tends to be a hardwon insight that often only emerges after lots of (usually very expensive and time-consuming) experimentation. In such cases, taking a black-box approach to modeling and identification ignores the mechanistic knowledge one has at one's disposal. Ideally, one would like a model reduction scheme that preserves the (mechanistic) model structure of component processes that contribute significantly to a particular phenomenon of interest, and collapses the representation of the minimally- to non-contributing processes into some lowerorder dynamics.

Example:

The 'Guyton Model' of cardiovascular dynamics (Guyton & Coleman 1967).



A somewhat refined version of the initial cardiovascular model:

| | NON-MUSCLE OXYGEN DELIVERY | MUSCLE BLOOD FLOW CONTROL AN | ND PO2 WASCULAR | KIDNEY C | THAMICS AND EXCRETION | THIRST AND DRINKING |
|---|--|------------------------------|--------------------|---------------|---|--|
| | | | | nim (Adda | 5-Figh | |
| | | | | | | La fai |
| | | | | | | |
| | | | | de la | 1645 | 1-2-2-2-2-2- |
| | A Sentine Len | | | | 한 한 한 한 한 | TO T |
| | | | | | | ANTIDURETIC HORMONE CONTROL |
| | | | 1 35 35 1 | . Pa | CAPILLARY MEMBRANE DYNAMICS | ····· |
| | Q-2-9-9-9-19 | | The second restant | - (3-5 ° A | | |
| | In State Contraction | | | | 19 Dec 5 | -\$*\$*\$*\$ |
| | | Contraction of the | | | POP DA | ANGIOTENSIN CONTROL |
| | NON-MUSCLE LOCAL BLOOD FLOW CONTROL | | | E. | | |
| | C. C. C. C. | | | : 2 | | |
| | | A STORES | | | | |
| | | | | | | ALDOSTERONE CONTROL |
| | 1 4 ANY DESCRIPTION AND 1 ANY 1 2014 (72) | | | 1 # | | |
| | | | A LAND | P. P. | T. Mr-3/111,200 ill | D - Carolingan |
| | TOTAL VILLE | | | | 1 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 2 | |
| | | | 酒 情 玉 | | | |
| | at the second se | | | \$- | | |
| Peresi kan line bio | P. P. P. S. | | | <u></u> | | The start |
| HEART RATE AND STROKE VOLIME PULMONIARY DYNAMICS RED CELLS MIGHT HYPERTROPHY LASS AND GEL ELECTROLYTES AND CELL MATER | HEART RATE AND STROKE VOLUME | | AND VISCOSITY OR | DETERIORATION | TISSUE FLUIDS, PRESSURES AND GEL | ELECTROLYTES AND CELL WATER |