

# Modeling Biology in Modelica: The Human Baroreflex

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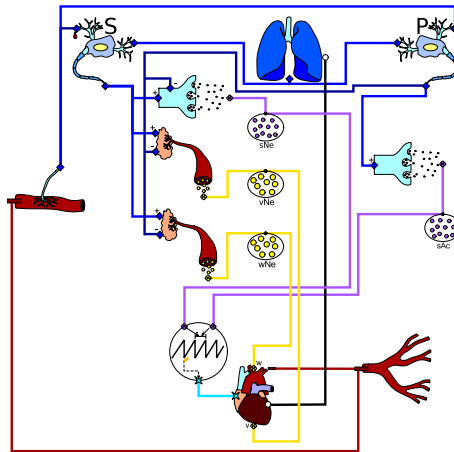
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Systems biology is a field that requires complex multi-scale models of systems that are evolved rather than engineered. No unifying theory exists for biology as it does for engineering domains. Thus, models appear in very diverse forms. Components can be genes, cells, organs, organisms or even whole ecosystems. These components can intuitively be represented as classes in an object-oriented language, making systems biology a perfect application for Modelica.

However, we still only see very few models from this domain. In an attempt to change this, we show that Modelica can exactly reproduce the simulation results of a reference implementation of the Seidel-Herzel model (SHM), an established biological model of the human baroreflex. The model can be seen in Figure 1. It features 30 mathematical equations that capture the essential functionality of the heart, the baroreceptors that measure our blood pressure, the autonomic nervous system, the lung and the windkessel arteries that dampen the blood pressure spike after a contraction. The model is able to realistically reproduce heart rate variability characteristics and can also be used to simulate disease conditions.

Our implementation highlights the strengths of Modelica like the event finding mechanism, which makes the model more precise compared to the original reference implementation. We also show that biological systems pose interesting modeling challenges. The interaction of complex rhythms in the contraction model leads to nontrivial conditions in when-equations that constitute a discrete equation system and the presence of non-uniform delays in the baroreceptors requires a convolution that cannot be implemented efficiently with conventional means. Both problems may point to areas where Modelica compilers or the language itself may be improved.



**Figure 1.** Diagram view of our Modelica implementation of the Seidel-Herzel model.