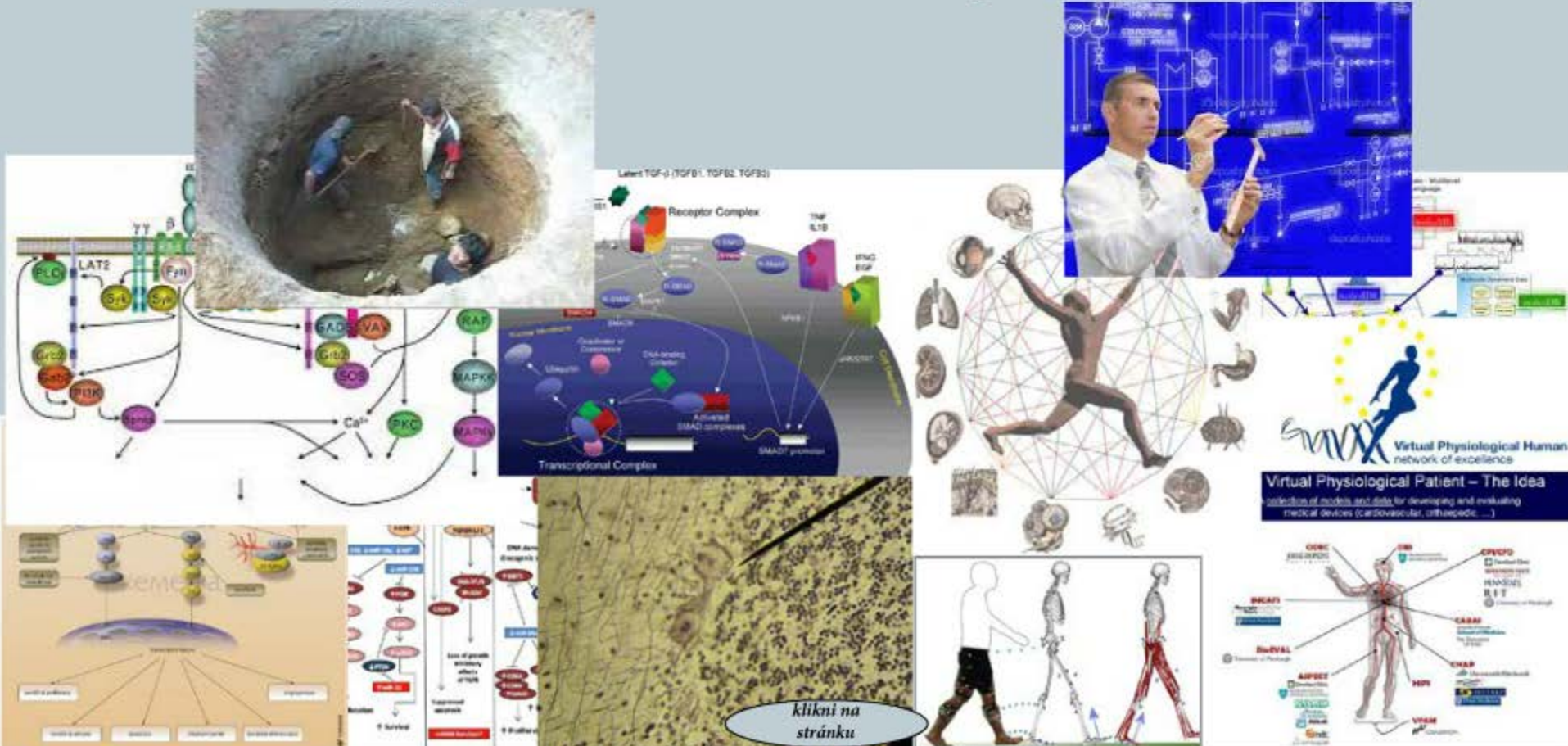




# Dva základní směry lékařsko-biologického výzkumu

*Stále detailnější výzkum  
mechanismů řízení  
biologických systémů na  
nitrobuněčné a molekulární  
úrovni*

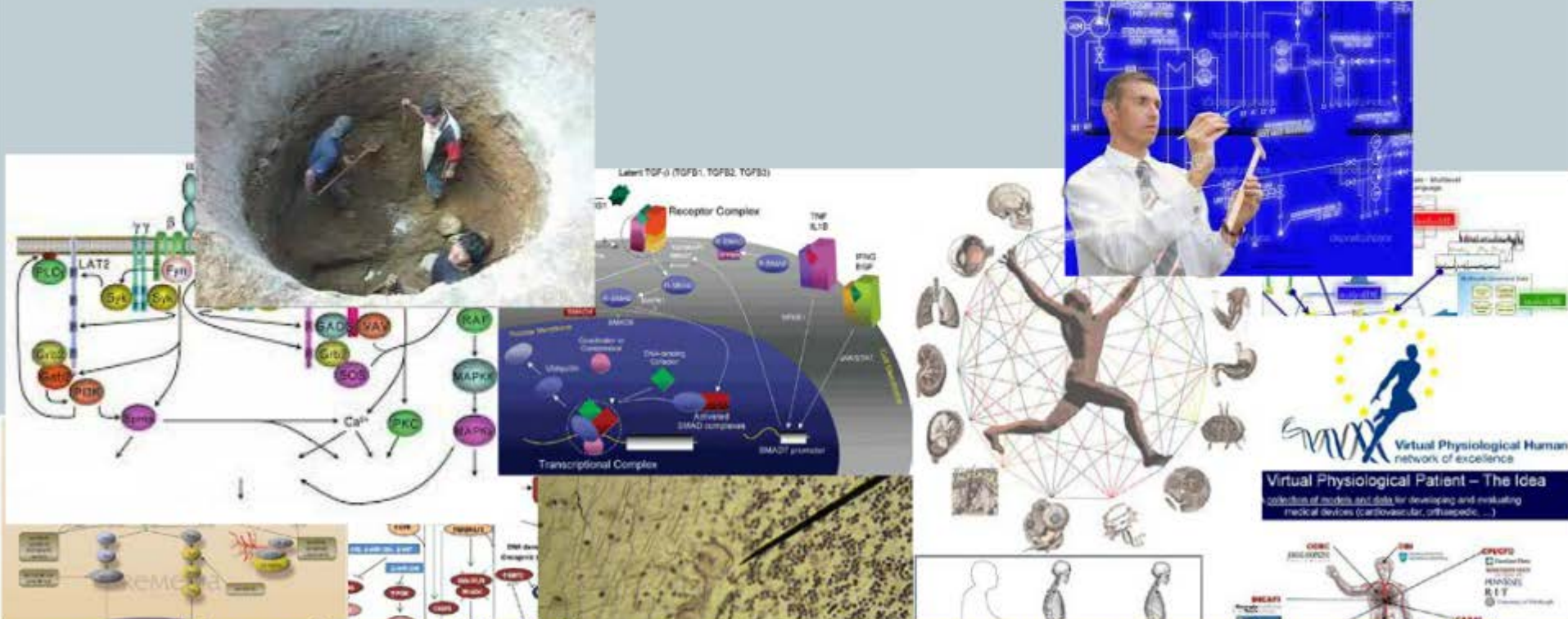
*Integrace poznatků s cílem  
porozumění, jak to funguje  
dohromady jako systém  
(integrativní fyziologie,  
systémová biologie)*



# Dva základní směry lékařsko-biologického výzkumu

*Stále detailnější výzkum  
mechanismů řízení  
biologických systémů na  
nitrobuněčné a molekulární  
úrovni*

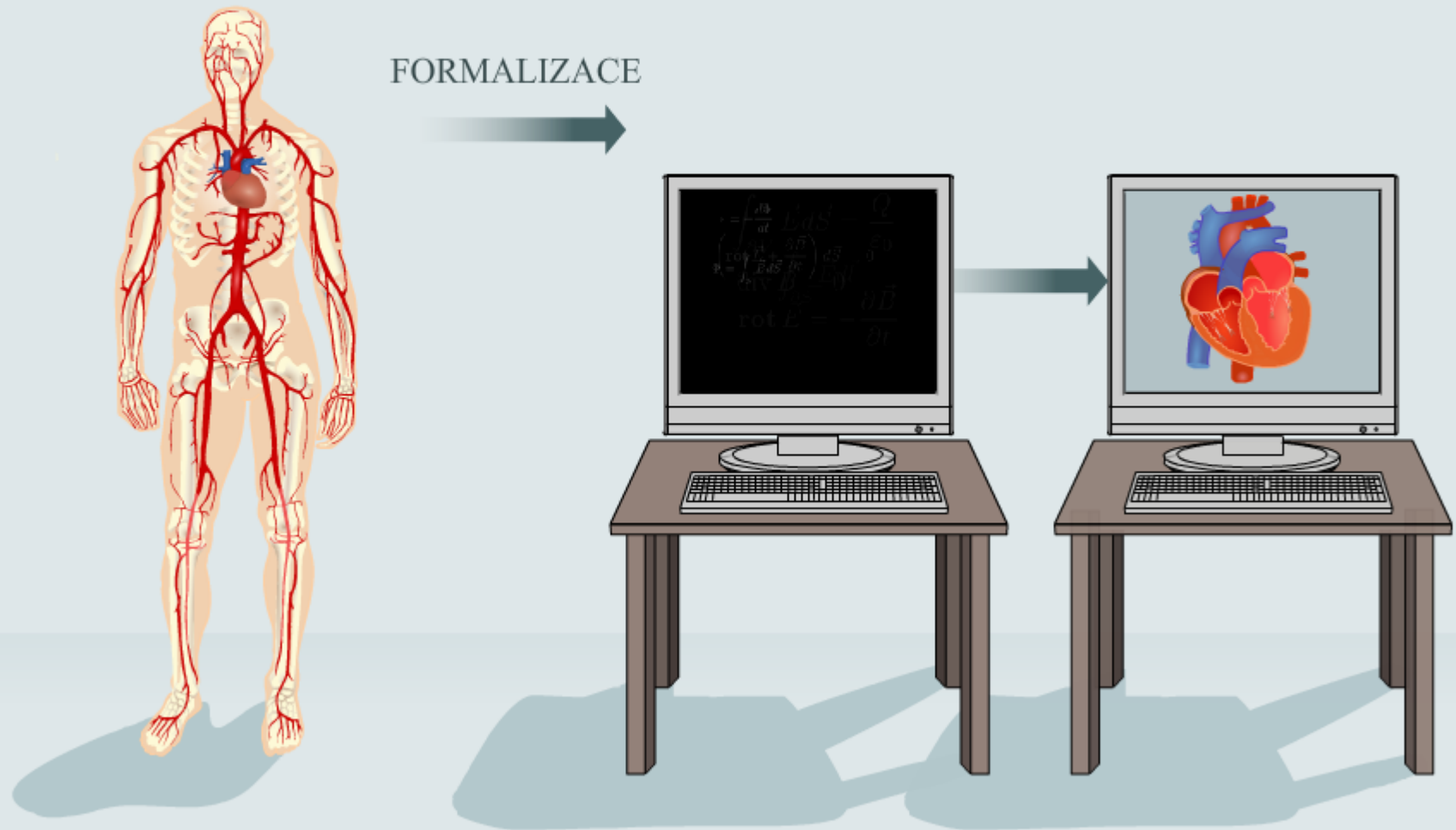
*Integrace poznatků s cílem  
porozumění, jak to funguje  
dohromady jako systém  
(integrativní fyziologie,  
systémová biologie)*



*Experimentální data*

*Integrace experimentálních  
poznatků*

# Formalizace v biologii a v medicíně



# Formalizace v biologii a v medicíně

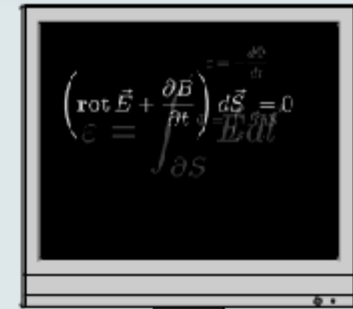
EXPERIMENTÁLNÍ  
FYZIOLOGIE



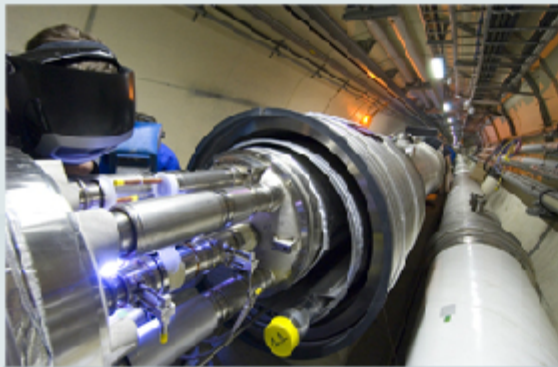
FORMALIZACE



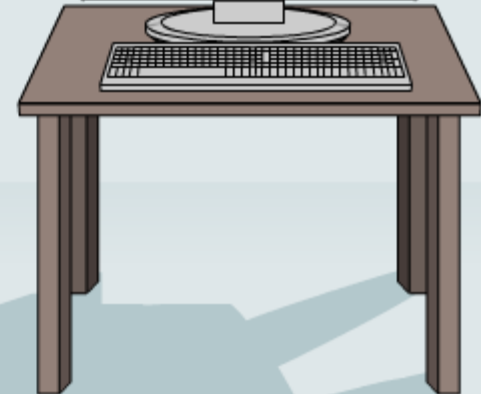
TEORETICKÁ FYZIKA



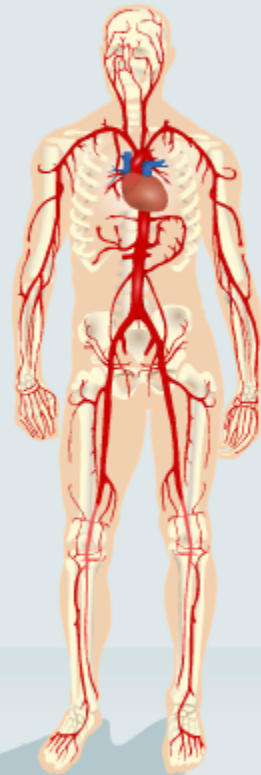
EXPERIMENTÁLNÍ  
FYZIKA



FORMALIZACE



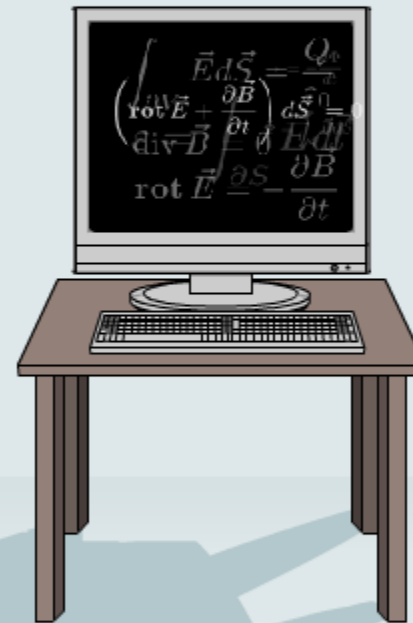
EXPERIMENTÁLNÍ  
FYZIOLOGIE



FORMALIZACE



INTEGRATIVNÍ  
FYZIOLOGIE



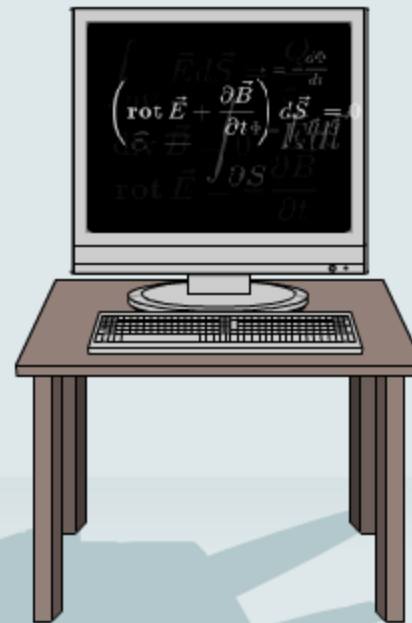
EXPERIMENTÁLNÍ  
FYZIOLOGIE



FORMALIZACE



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FYZIOLOGIE



IUPS Physiome Project



PHYSIOME (IUPS Physiome Project),  
Virtual Physiological Human (EU VPH Project)



Virtual Physiological Human  
network of excellence



[Home](#) [About](#) [Models](#) [JSim](#) [Links](#) [Search](#)

## Welcome to the NSR Physiome Project!

The Physiome Project is the worldwide effort of several loosely connected research groups to [define the physiome](#) via databasing and the development of integrated quantitative and descriptive modeling. This work will help determine the future of medicine, change the way we think about human physiology, and strengthen the fabric of international scientific collaboration across political allegiances.

### Recent Publications

NSR, the National Simulation Resource at the University of Washington Department of Bioengineering, provides the following tools in support of the Physiome Project:

### The JSim Modeling System

- [Home Page](#) (Getting started with JSim)
- [Downloads](#)

### Physiological Model and Tutorial Repository

- [NSR Physiome Models and Information](#)
- [Tutorials list](#)
- [Reproducible modeling and model standards](#)
- [JSim Consolidated Model Database](#)

### Collaborative modeling and software efforts

- [The Virtual Physiological Rat Project](#): Modeling the physiological characteristics of the rat.
- [Systems Biology Workbench \(SBW\)](#): SBW enables applications (potentially running on separate, distributed computers) to communicate via a simple network protocol.

### Courses in Physiological Systems Modeling

- No courses currently scheduled.
- Archived course materials are available via the [NSR Course Archives](#).

The Physiome Commission of the International Union of Physiological Sciences, [IUPS](#), provides leadership to the Physiome Project through its satellite and central meetings and through the [University of Auckland's IUPS Physiome Website](#). Please take advantage of the information provided by the IUPS and this website to learn more about the project.

[NSR Local User Information](#) (NSR user account holders only)

### The Physiome Project Provides

#### Databasing of information

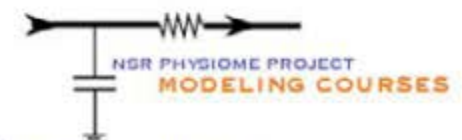
- genome, proteome, morphome
- functional behavior of molecules and biological systems
- observations of intact cellular systems, organs, and intact organisms

#### Integration and consilience of knowledge

- schema of interactions (descriptive models)
- quantitative descriptions of relationship (casual, statistical, mechanistic)
- computer models of small and large systems
- parameter sets for different cells, tissues, and species

#### Network access to databases and models

- **platform-independent** networked search engines
- **platform-independent** web operation of models
- access to databases from descriptive and computational models





# Physiome project


www.physiome.org

Webpages: x

www.physiome.org/Links/

Aplikace Garden - Memrise Kalendář Google Seznam Slovník - on... Physiology for the 2... Překladáč Google Oxford Dictionaries ... get Ostatní záložky

Served by Glon



Home About Models JSim Links Search

## Websites:

- [Physiome Projects](#)
- [Physiome Sites with Models Displayed or Available for Download](#)
- [Physiome Markup Languages](#)
- [Simulation Software and Modeling Environments](#)
- [Ontologies](#)
- [Enzyme-Genome-Proteome Databases](#)
- [Other Related Links](#)

## Physiome Projects

### Asia

- [Computational Bioengineering Laboratory](#): National University, Singapore
- [Institute for Advanced Biosciences E-cell Project](#): Keio University, Tokyo, Japan
- [Kitano Symbiotic Systems Project](#): Tokyo, Japan
- [Center for Advanced Medical Engineering and Informatics](#): Osaka University, Osaka, Japan

### Australasia

- [IUPS Physiome Project](#): University of Auckland, Auckland, New Zealand

### Europe

- [BIOMED Town](#): Biomedical Research & Technology, Biomedical Industry and Clinical Practice
- [Oxford Cardiac Electrophysiology Group](#): Dr. Denis Noble, Oxford University, Oxford, UK
- [COR \(Cellular Open Source\)](#): Dr. Alan Gamy, Cardiac Electrophysiology Group
- [European Bioinformatics Institute](#): Cambridge, United Kingdom
- [Renal Physiome Project](#): Randy Thomas, Evry, France
- [Quantitative Kidney Database \(QKDB\)](#): Necker Hospital, Paris, France

### International

- [The Living Human Project](#): International
- [Giome.com](#): Asia, Europe, North America
- [Harvey Project](#): International

### North America

- [Biological Network Modeling Center](#): California Institute of Technology, Pasadena, California, USA

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National Simulation Resource  
Department of Bioengineering  
University of Washington



You are here: [Home](#)

## The CellML project

The CellML language is an open standard based on the XML markup language. CellML is being developed by the Auckland Bioengineering Institute at the University of Auckland and affiliated research groups.

The purpose of CellML is to store and exchange computer-based models. CellML allows scientists to share models even if they are using different modelling tools. It also enables them to reuse components from one model to another, thus accelerating model development. [Read more...](#)

### About CellML

Find out about the CellML language; what it can be used for, its history, and future directions.

### Getting started

New to CellML? This section contains information about CellML that will help get you up and running with CellML.

### Tools and API

The CellML community is committed to providing freely available tools for creating, editing, and using CellML models.

### Model repository

The model repository is a central place where modelers can collaborate with each other to build and share models with the rest of the world.

### Specifications

Read the CellML specifications - core language and a variety of metadata specifications are available.

### Community

CellML is built around open science and software. This website is a community hub for things CellML.

## 9th International CellML Workshop

## News

Announcing the 9th International

The screenshot shows the CellML Model Repository website. The browser address bar displays <https://models.physiomeproject.org/cellml>. The website features a navigation menu with [Models Home](#), [Exposures](#), and [Documentation](#). The main content area is titled "CellML Model Repository" and includes a "Main Model Listing" section. Below this, there is a "Browse by category" list with the following items: Calcium Dynamics, Cardiovascular Circulation, Cell Cycle, Cell Migration, Circadian Rhythms, Electrophysiology, Endocrine, Excitation-Contraction Coupling, Gene Regulation, Hepatology, Immunology, Ion Transport, Mechanical Constitutive Laws, Metabolism, Myofilament Mechanics, Neurobiology, pH Regulation, PKPD, Signal Transduction, and Synthetic Biology. A "Searching" section at the bottom states: "Searching of models can be done anywhere on the site using the search box on the upper right hand corner." The footer contains the copyright notice: "© 2001-2014 - EPRS Physiome Project."



# Nástroje a repozitáře modelů - cellML



Models Home Exposures Documentation

You are here: Home / Exposures / Bondarenko, Szigeti, Bett, Kim, Rasmusson, 2004 / Computer model of action potential of

## Model Metadata

### CellML Model Authorship

**Title:**  
Computer model of action potential of mouse ventricular myocytes (Septal Cell Description)

**Author:**  
Penna Inácio

**Organisation:**  
Department of Physiology, Anatomy & Genetics, Oxford University

### Citation

**Authors:**

- Bondarenko, B E
- Szigeti, G P
- Bett, G C
- Kim, S I
- Rasmusson, R L

**Title:**  
A Computer Model for the Action Potential of Mouse Ventricular Myocytes

**Source:**  
American Journal of Physiology Heart and Circulatory Physiology

**Identifier:**  
ajpcell.2004.287.H1403



Models Home Exposures Documentation

You are here: Home / Exposures / Bondarenko, Szigeti, Bett, Kim, Rasmusson, 2004 / Computer model of

## Model Mathematics

Component: environment

Component: membrane

$$I_{stim} = \begin{cases} stim\_amplitude & \text{if } time \geq stim\_start \wedge time \leq stim\_end \wedge time - stim\_start - 0 \\ 0 & \text{otherwise} \end{cases}$$

$$\frac{d}{dt}(V) = -\frac{1}{C_m} (I_{CaL} + I_{pCa} + I_{NaCa} + I_{CaB} + I_{Na} + I_{NaB} + I_{NaK} + I_{KtoI} + I_{stim})$$

Component: calcium\_concentration

$$\frac{d}{dt}(Ca) = BI \left( J_{leak} + J_{xfer} - \left( J_{up} + J_{trpn} + \frac{(I_{CaL} + I_{pCa} - (B_{NaCa})_{AnpCa})}{BV_{myo}} \right) \right)$$

$$\frac{d}{dt}(CaSR) = BI_{SR} \left( \frac{J_{up} V_{SR}}{V_m} - \left( \frac{J_{off} V_{myo}}{V_m} + \frac{I_{CaL} AnpCa}{2V_{myo}} \right) \right)$$

$$\frac{d}{dt}(CaJSR) = BI_{JSR} (J_{tr} - J_{rel})$$

$$\frac{d}{dt}(CaNSR) = \frac{(J_{up} - J_{leak}) V_{myo}}{V_{NSR}} - \left( \frac{J_{off} V_{myo}}{V_{NSR}} \right)$$

$$BI = \left( 1 + \frac{C_{MERS} (dR_{Ca} - C_{MERS})}{(R_{Ca} - C_{MERS})^2} \right)^{-1}$$



Models Home Exposures Documentation

You are here: Home / Exposures / Bondarenko, Szigeti, Bett, Kim, Rasmusson, 2004 / Computer model of action potential of mouse ventricular myocytes (Septal Cell Description)

## Computer model of action potential of mouse ventricular myocytes (Septal Cell Description)

A Computer Model for the Action Potential of Mouse Ventricular Myocytes

### Model Status

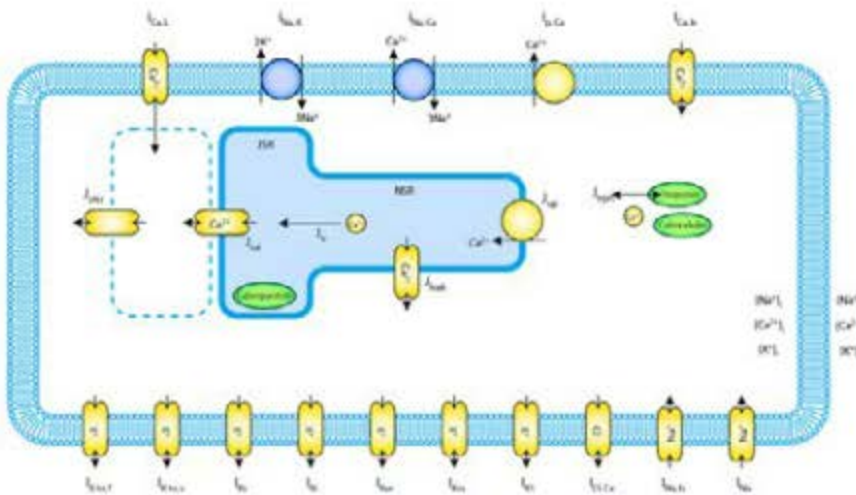
This CellML model runs in both OpenCell and COR to reproduce the the action potential traces from Figure 16 of the publication. This model represents the SEPTAL CELL variant as described in Bondarenko et al.'s 2004 paper.

### Model Structure

**ABSTRACT:** We have developed a mathematical model of the mouse ventricular myocyte action potential (AP) from voltage-clamp data of the underlying currents and Ca<sup>2+</sup> transients. Wherever possible, we used Markov models to represent the molecular structure and function of ion channels. The model includes detailed intracellular Ca<sup>2+</sup> dynamics, with simulations of localized events such as sarcoplasmic Ca<sup>2+</sup> release into a small intracellular volume bounded by the sarcolemma and sarcoplasmic reticulum. Transporter-mediated Ca<sup>2+</sup> fluxes from the bulk cytosol are closely matched to the experimentally reported values and predict stimulation rate-dependent changes in Ca<sup>2+</sup> transients. Our model reproduces the properties of cardiac myocytes from two different regions of the heart: the apex and the septum. The septum has a relatively prolonged AP, which reflects a relatively small contribution from the rapid transient outward K<sup>+</sup> current in the septum. The attribution of putative molecular bases for several of the component currents enables our mouse model to be used to simulate the behavior of genetically modified transgenic mice.

The original paper reference is cited below:

Computer model of action potential of mouse ventricular myocytes, Vladimir E. Bondarenko, Gyula P. Szigeti, Glenn C. L. Bett, Song-Jung Kim, and Randall L. Rasmusson, 2004, *American Journal of Physiology*, 287, H1378-H1403. PubMed ID: 15142845



Search Site

Log in

### Model Curation

Curation Status ★ ★ ★  
 JSim ★ ★ ★  
 COR ★ ★ ★  
 OpenCell ★ ★ ★

### Source

Derived from workspace Bondarenko, Szigeti, Bett, Kim, Rasmusson, 2004 at changeset c1192956599b.

### Collaboration

To begin collaborating on this work, please use your mercurial client and issue this command:

```
hg clone http://models.physioamerp
```

### Downloads

- Complete Archive as .tgz
- Download This File

### Views Available

- Documentation
- Model Metadata
- Model Curation
- Mathematics
- Generated Code
- Cite this model
- Source View
- Simulate using OpenCell

### License

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### Navigation

Computer model of action potential of mouse ventricular myocytes (Apical Cell Description)

Computer model of action potential of mouse ventricular myocytes (Septal Cell Description)

# Nástroje a repozitáře modelů - cellML

OpenCell

File View Tools Help

Traces: Channel / Exchanger / Pump Currents (picoA/picoF) & Fluxes (mM/ms) vs Time (ms)

| Type | Value    | Units          |
|------|----------|----------------|
| V    | -82.4202 | millivolt      |
| Cm   | 1        | microF_per_cm2 |
| Vmyo | 25.84e-6 | microlitre     |
| VJSR | 0.12e-6  | microlitre     |
| VNSR | 2.090e-6 | microlitre     |
| Vss  | 1.405e-9 | microlitre     |
| Acap | 1.534e-4 | cm2            |
| Ko   | 5400     | micromolar     |
| Nao  | 140000   | micromolar     |
| Cao  | 1800     | micromolar     |

Basic settings | Advanced settings

Start time point: 0 (millisecond)

Point density<sub>max</sub>: 10000 (points/graph)

End time point: 1000 (millisecond)

Maximum step size: 0.1 (millisecond)

Algorithm: BDF 1-5 with solve

Integrate

Electrophysiological Cell Diagram: Click elements to toggle traces on graph above

Zoom | Reset View

Script Message: No fluxes displayed

# Nástroje a repozitáře modelů - cellML

The screenshot displays the cellML software interface, which is used for simulating biological models. The interface is divided into several panels:

- Models Panel (Left):** Shows a list of models. The selected model is "beeler\_reuter\_1977".
- Properties Panel (Middle-Left):** Displays the configuration for the selected model. It includes:
  - Type:** A list of components such as "time\_dependent\_o...", "slow\_inward\_curre...", "membrane, stimulu...", "environment, stimu...", and "membrane, leak\_c...".
  - Component 1:** membrane
  - Component 2:** leak\_current
  - Variable Mapping:** Variable 1 is "i\_leak" and Variable 2 is "i\_leak".
  - Units:** "ms" is Derived and "per\_ms" is Derived.
- Basic settings Panel (Bottom-Left):** Contains simulation parameters:
  - Start time point: 0 (ms)
  - Point density<sub>max</sub>: 10000 (points/graph)
  - End time point: 10000 (ms)
  - Maximum step size: 0.1 (ms)
  - Algorithm: RKF 1-5 with solve
- Plot Panel (Right):** Shows a graph of membrane potential (V) over time (ms). The y-axis ranges from -80 to 30 mV, and the x-axis ranges from 0 to 100 ms (scaled by  $\times 10^2$ ). The plot displays a series of action potentials (spikes) that reach approximately 30 mV and then rapidly decay back to a resting potential of about -80 mV.
- Legend Panel (Bottom-Right):** A table showing the data series plotted:
 

| Model              | Y      | X         | Type  |
|--------------------|--------|-----------|-------|
| beeler_reuter_1977 | V (mV) | time (ms) | Lines |
| Link Selected      | V (mV) | time (ms) | Lines |

At the bottom of the window, a status bar indicates: "Clicked point was (1282.7090080536525, 67.31792017712208)." The "Export CSV" button is visible at the bottom center.

# Nástroje a repozitáře modelů - JSim (MML)

PHYSIOME PROJECT

Home About Models JSim Links Search

# JSim

## JSim Home Page

- What's new?
- Download and installation
- Running JSim
- Writing JSim models
- Citing JSim
- Model archives
- Instructional videos
- Glossary
- JSim Development
- Bibliography of JSim related work
- Acknowledgements
- Confused? Contact us.

[This page was last modified 22Oct14, 10.49 am.]

Model development and archiving support at physiome.org provided by the following grants: NIH/NIDIB DC08407 Software Integration, JSim and SBW 6/1/09-5/31/13; NIH/NIDIB T15 HL80516-

JSim is a Java based simulation system for building quantitative numeric models and analyzing them with respect to experimental reference data. JSim's primary focus is in physiology and biomedicine, however its computational engine is quite general and applicable to a wide range of scientific domains. JSim models may intermix ODEs, PDEs, implicit equations, integrals, summations, discrete events and procedural code as appropriate. JSim's model compiler can automatically insert conversion factors for compatible physical units as well as detect and reject unit unbalanced equations. JSim also imports and exports model archive formats SBML and CellML.

JSim downloads are available as [precompiled binaries](#) (Linux, Macintosh, Windows) or [source code](#). JSim can also [run as an applet](#) within your web browser. JSim is provided free for non-commercial use as a public service by the [National Simulation Resource](#) at the University of Washington.

**NEW** JSim 2.15 released (22 Oct 2014): [release notes](#) / [download](#)

### Getting oriented:

- [JSim overview](#) : what JSim does and how it is structured.
- [Introduction to the JSim GUI](#) : an step-by-step introduction to using the JSim graphic user interface.
- [Introductory Survey of MML](#) : writing models with JSim's Mathematical Modeling Language.

### Related software:

- [J4](#): Java-based quantitative medical imaging system.
- [I4](#): J4's predecessor imaging system.
- [XSIM](#): JSim's predecessor simulation
- [Systems Biology Workbench \(SBW\)](#): An open source framework connecting model simulation and analysis tools
- [SemGen](#): Software for automating the modular composition and decomposition of biosimulation models.
- [More](#)

# Nástroje a repozitáře modelů - JSim (MML)

The screenshot shows a web browser window with the URL [www.physiome.org/jsim/docs/MMLhtml](http://www.physiome.org/jsim/docs/MMLhtml). The page features a navigation menu on the left with links for Home, About, Models, JSim, Links, Search, FAQ, Contact, and Feedback. The main content area is titled "MML - Mathematical Modeling Language" and includes sections for "Writing JSim Models", "Basic MML", "Specific MML Topics", "Reference guides", "Connecting JSim to other software products", "RTML", and "Example Models". A footer section provides information about model development and archiving support at [physiome.org](http://physiome.org).

**PHYSIOME PROJECT**

Home About Models JSim Links Search

## Writing JSim Models

This page is for the current JSim version 2.0. Click [here](#) for the earlier JSim 1.6 version.

The documents below provide information on how to write JSim models. JSim models are written in JSim's own Mathematical Modeling Language (MML), an easy-to-read text-based language. MML models are most often expressed in terms of mathematical equations (for example, ordinary or partial differential equations), but formulation via discrete events and function calls to Java, C and Fortran are also available. MML is constructed so that model writers may intermix mathematics, events and procedural code as needed.

### Basic MML

- [Introductory Survey](#)
- [Physical units](#)

### Specific MML Topics

- [Built-in constants, operators & functions](#)
- [Ordinary differential equations](#)
- [Partial differential equations \(PDEs\)](#)
- [Integrals & Summations](#)
- [Implicit Equations](#)
- [Delay Lines](#)
- [Variable Functions](#)
- [Events \(discrete state changes\)](#)
- [Functions & Procedures \(embedded Java, C, Fortran, Matlab\)](#)
- [Templates \(reusable model components\)](#)
  - [MFAX templates](#)
  - [XSIM templates](#)
- [Miscellaneous short topics](#)

### Reference guides

- [MML Reference Manual](#)
- [MFAX Reference Manual](#)
- [Debugging guide](#)
- [Glossary](#)

### Connecting JSim to other software products

- [Antimony](#)
- [Matlab](#) **new**
- [SBML](#)
- [CellML](#)
- [MathML](#)
- [XSIM](#)
- [XXML](#)

### RTML

RTML is a graphic description language used to customize the appearance of models in the JSim GUI

- [Introduction](#)
- [Reference Manual](#)

[JSim Home Page](#)

Comments or Questions?  
[Give feedback](#)

[This page was last modified 06Jul12, 3:17 pm.]

Model development and archiving support at [physiome.org](http://physiome.org) provided by the following grants: NIH/NIDIB BE08407 Software Integration, JSim and SBW 6/1/09-5/31/13; NIH/NHLBI T15 HL08516-01 Modeling for Heart, Lung and Blood: From Cell to Organ, 4/1/07-3/31/11; NSF BES-0506477 Adaptive Multi-Scale Model Simulation, 8/15/05-7/31/08; NIH/NHLBI R01 HL073598 Core 3: 3D Imaging and Computer Modeling of the Respiratory Tract, 9/1/04-8/31/09; as well as prior support from NIH/NCRR P41 RR01243 Simulation Resource in Circulatory Mass Transport and Exchange, 12/1/1980-11/30/01 and NIH/NIDIB R01 EB001973 JSim: A Simulation Analysis Platform, 3/1/02-2/28/07.

# Nástroje a repozitáře modelů - JSim (MML)

JSim Model Archives

www.physiome.org/jsim/models/index.html

Home About Models JSim Links Search

## JSim Model Archives

This page provides links to archives of JSim runnable models. Models may be MML, SBML or CellML format.

### Available archives

- [NSR Physiome WebModel Database \(330 MML models\)](#)
- [JSim Consolidated Model Database \(73,000+ models\)](#)
- [NSR Physiome model repository](#)
- [Biomodels archive \(366 SBML models\)](#)
- [JWS models database \(68 SBML models\)](#)
- [Kegg pathways database \(72,000+ SBML models\)](#)
- [CellML archive \(910 CellML models\)](#)
- [FPack archive \(legacy XSim models\) \(9 MML models\)](#)
- [MML examples \(90 MML models\)](#)
- [NSR Modeling Course Materials Archive](#)

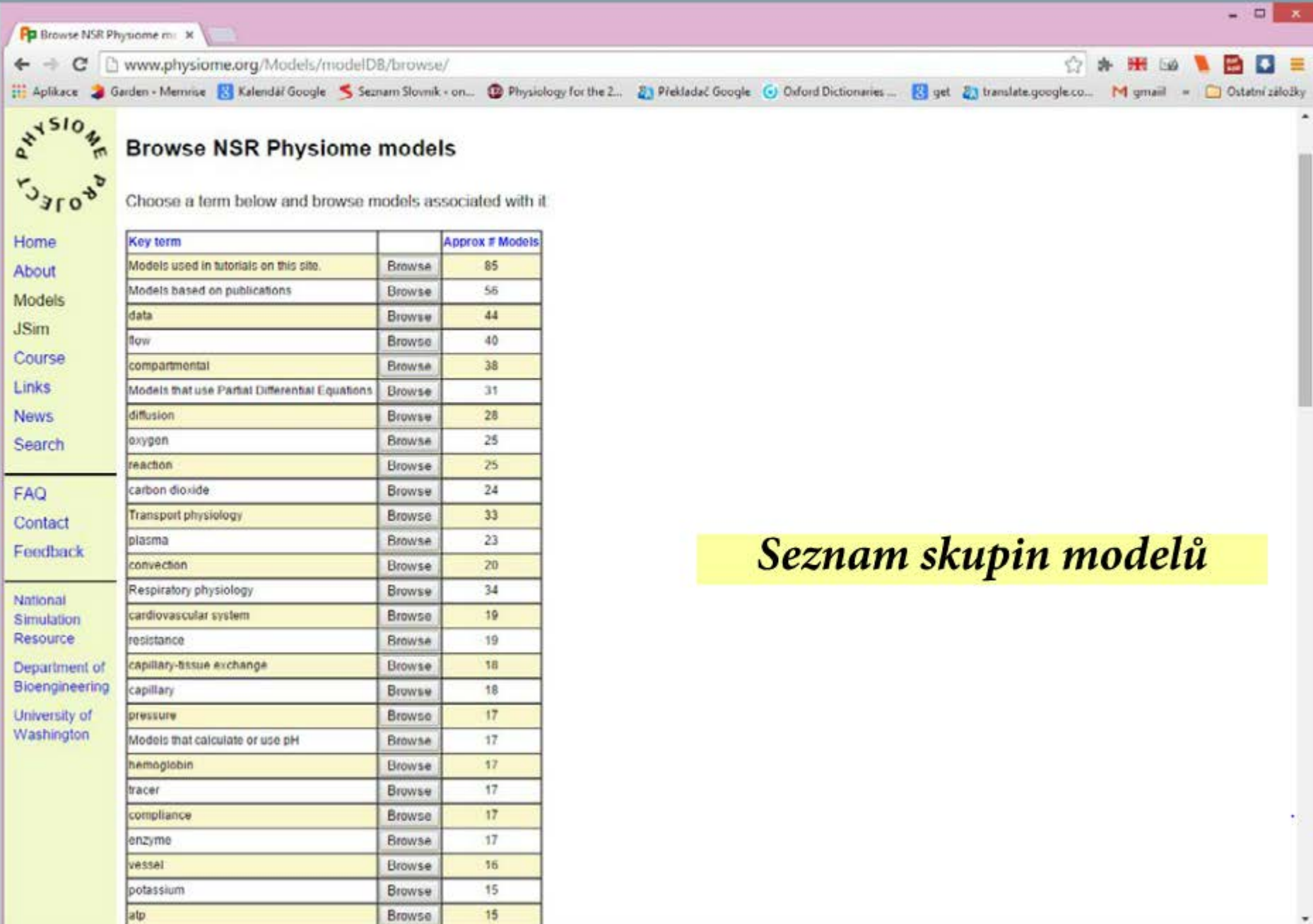
[This page was last modified 23Sep14, 1:39 pm.]

**Model development and archiving support at physiome.org provided by the following grants:** NIH/NIBIB BE08407 Software Integration, JSim and SBW 6/1/09-5/31/13; NIH/NHLBI T15 HL88516-01 Modeling for Heart, Lung and Blood: From Cell to Organ, 4/1/07-3/31/11; NSF BES-0506477 Adaptive Multi-Scale Model Simulation, 8/15/05-7/31/08; NIH/NHLBI R01 HL073598 Core 3: 3D Imaging and Computer Modeling of the Respiratory Tract, 9/1/04-8/31/09; as well as prior support from NIH/NCRR P41 RR01243 Simulation Resource in Circulatory Mass Transport and Exchange, 12/1/1980-11/30/01 and NIH/NIBIB R01 EB001973 JSim: A Simulation Analysis Platform, 3/1/02-2/28/07.

National Simulation Resource  
Department of Bioengineering  
University of Washington



# Nástroje a repozitáře modelů - JSim (MML)



The screenshot shows the Physiome.org website interface. The browser address bar displays 'www.physiome.org/Models/modelDB/browse/'. The page title is 'Browse NSR Physiome models'. Below the title, there is a navigation menu on the left with links for Home, About, Models, JSim, Course, Links, News, Search, FAQ, Contact, Feedback, National Simulation Resource, Department of Bioengineering, and University of Washington. The main content area features a table with three columns: 'Key term', 'Browse', and 'Approx # Models'. The table lists various key terms and their corresponding model counts. A yellow highlight box on the right side of the page contains the text 'Seznam skupin modelů'.

**Browse NSR Physiome models**

Choose a term below and browse models associated with it:

| Key term                                       | Browse                 | Approx # Models |
|--|------------------------|-----------------|
| Models used in tutorials on this site.         | <a href="#">Browse</a> | 85              |
| Models based on publications                   | <a href="#">Browse</a> | 56              |
| data   | <a href="#">Browse</a> | 44              |
| flow   | <a href="#">Browse</a> | 40              |
| compartmental                                  | <a href="#">Browse</a> | 38              |
| Models that use Partial Differential Equations | <a href="#">Browse</a> | 31              |
| diffusion                                      | <a href="#">Browse</a> | 28              |
| oxygen   | <a href="#">Browse</a> | 25              |
| reaction                                       | <a href="#">Browse</a> | 25              |
| carbon dioxide                                 | <a href="#">Browse</a> | 24              |
| Transport physiology                           | <a href="#">Browse</a> | 33              |
| plasma   | <a href="#">Browse</a> | 23              |
| convection                                     | <a href="#">Browse</a> | 20              |
| Respiratory physiology                         | <a href="#">Browse</a> | 34              |
| cardiovascular system                          | <a href="#">Browse</a> | 19              |
| resistance                                     | <a href="#">Browse</a> | 19              |
| capillary-tissue exchange                      | <a href="#">Browse</a> | 18              |
| capillary                                      | <a href="#">Browse</a> | 18              |
| pressure                                       | <a href="#">Browse</a> | 17              |
| Models that calculate or use pH                | <a href="#">Browse</a> | 17              |
| hemoglobin                                     | <a href="#">Browse</a> | 17              |
| tracer   | <a href="#">Browse</a> | 17              |
| compliance                                     | <a href="#">Browse</a> | 17              |
| enzyme   | <a href="#">Browse</a> | 17              |
| vessel   | <a href="#">Browse</a> | 16              |
| potassium                                      | <a href="#">Browse</a> | 15              |
| atp  | <a href="#">Browse</a> | 15              |

**Seznam skupin modelů**

# Nástroje a repozitáře modelů - JSim (MML)

www.physiome.org/Models/modelDB/browse/browse.php?key\_term=respiratory

Home About Models JSim Links Search

## Seznam modelů respiračního systému

Model results for *respiratory* search:

[Return to Model browse](#)

Y: Model from a Published paper. Y: Model contains data.

| Model # | Model Name   | Pub | Data | Model Description  |
|---------|--|-----|------|--|
| 0038    | Athanasiaides_2000                                 | Y   |      | This model is based on Athanasiaides et al. energy analysis of a nonlinear model of the normal human lung. J Biol Sys. 8(2):115-39, 2000.  |
| 0071    | Air_Blood_ExchangeNetwork                          |     |      | Model represents a network of multilayer segments for pulmonary air-blood exchange.  |
| 0072    | Airway_bronchiole_alveolus                         |     |      | This model represents an inertial flow in a rigid airway, compliant bronchiole, compliant bronchiolus and a compliant alveolus.  |
| 0073    | Alveoli_Bronchi_2comp                              |     |      | Airflow from atmosphere to Bronchi to Alveoli modeled with 2 compartments.   |
| 0120    | Comp_four_gen_weibel_lung                          |     |      | This model represents four generations of the bipodial human lung or the Weibel lung. The lengths and diameter of the airways are based on the Weibel lung geometry. The airways are assumed compliant.                            |
| 0121    | Compliant1Comp                                     |     |      | Simple one compartment model with pressure source and constant compliance.   |
| 0122    | Compliant_bifurcating_airway                       |     |      | This model represents a bifurcating compliant airway that could be used as a building block for constructing a network of airways. You could use the model to simulate flow in rigid airway bifurcation.                           |
| 0124    | Compliant_bifurcating_bronchiole_compliant_alveoli |     |      | This model represents a bifurcating compliant bronchiole with two compliant alveoli.   |
| 0125    | Compliant_bronchiole_compliant_alveolus            |     |      | This model represents a compliant bronchiole with a compliant alveolar sac. The driving force for this model is a pressure gradient which represents the difference in the alveolar and the pleural pressures.                     |
| 0129    | Co-vsCounter-CurrentExchange                       |     |      | Steady state air-blood exchange for two geometric configurations.  |
| 0142    | FourSeg_wPleuralPress                              |     |      | Four segment (larynx, trachea, bronchi, alveoli) pressure-flow model represents the respiratory system and it is driven by pleural pressure.   |
| 0144    | Gas_Exch   |     |      | Recirculation of O2 and CO2 between a 2-compartment lung and 2-compartment body.   |
| 0145    | GasExch_Lu_2001                                    | Y   |      | Model for O2, CO2, and N2 in airways and O2, CO2 in blood of circulating system. Lu et al 2001.  |
| 0162    | Lung_RC_P  |     |      | Single compliant tank driven by pleural pressure. This is the simplest lung model possible.  |
| 0180    | Pleural_vs_ExternalPress                           |     |      | Two different ways of expressing breathing, one as if using a ventilator at the mouth and the other one as human pleural muscle generating pressure gradient against external pressure. Three models used to compare differences.  |
| 0182    | PulmonMech_andGasConc                              |     |      | This model is based on Lutchen et al. A nonlinear model combining pulmonary mechanics and gas concentration dynamics. IEEE Trans. Biomed. Eng. 29: 629-641, 1982   |
| 0187    | Rigid_four_gen_weibel_lung                         |     |      | This model represents four generations of the bipodial human lung. The lengths and diameter of the airways are based on the weibel model. The compliance of the airway was considered to be negligible to represent rigid airways. |
| 0188    | Rigid_bifurcating_bronchiole_compliant_alveolus    |     |      | This model represents a bifurcating rigid bronchiole with two compliant alveoli.   |

# Nástroje a repozitáře modelů - JSim

The screenshot shows a web browser window with the URL [www.physiome.org/jsim/models/webmodel/NSR/Two\\_Compartment\\_Lung/](http://www.physiome.org/jsim/models/webmodel/NSR/Two_Compartment_Lung/). The page title is "Two\_Compartment\_Lung". The navigation menu includes Home, About, Models, JSim, Links, and Search. The main content area has a yellow highlight with the text: "Popis modelu, včetně odkazu na publikované články o modelu". Below this, the model number is 0213. There is a "Run Model:" section with a "Run applet" button and a link to "Help running a JSim model". The "Description" section contains text about the model's two compartments and flow characteristics. Another yellow highlight is present in the "Equations" section with the text: "Popis modelu, včetně odkazu na publikované články o modelu". The governing equations are listed, including  $\frac{\partial V_2}{\partial t} = P_2 - P_1$ ,  $P_2 = \frac{(P_{air} - P_2)}{R_{2a}}$ , and a piecewise function for  $P_2$  based on the relationship between  $V_2$  and  $V_{r2}$ .

*Popis modelu, včetně odkazu na publikované články o modelu*

*Popis modelu, včetně odkazu na publikované články o modelu*

## Two\_Compartment\_Lung

Airway is one tank, alveolus a second. Both are c

Model number: 0213

**Run Model:**  [Help running a JSim model](#)

(Java model applet may take 10-20 seconds to load )

### Description

This model demonstrates two compartments with a pressure source and some initial amount of mass of compound C contained in the two tanks. The mass of compound C inside the two tanks decreases if we assume that the concentration of C in the incoming air is zero. Two mass balance equations and the periodic nature of flow driven by a pressure source cause the total mass of compound C to reach values close to zero after some time. We assume that pressure drops are proportional to the flow rate. Pressure-volume relationships are defined in a similar way as in one-tank-switched model. Rate of change of volume is equal to the difference of inflow and outflow (see Equations). We defined two switches to model the fact that the amount of compound C in the two flow streams depends on the directions of flows. The switch for flow direction has condition such that Switch = if (Flow > 0) 1 else 0. We applied a switch in the compound balance equation to change the concentration of inflow or outflow of each compartment based on the actual direction of flow.

### Equations

The governing equations are:

$$\frac{\partial V_2}{\partial t} = P_2 - P_1$$

$$P_2 = \frac{(P_{air} - P_2)}{R_{2a}}$$

$$P_2 = \begin{cases} \frac{(V_2 - V_{r2})}{C_{om2}} & \text{for } V_2 > V_{r2} \\ \left[ 1 - \left( \frac{V_{r2}}{V_2} \right)^\beta \right] \frac{V_{r2}}{\beta C_{om2}} & \text{for } V_2 \leq V_{r2} \end{cases}$$

$$\frac{\partial C_2}{\partial t} = (P_1 / (1 - \text{switch}_1) - C_2 \cdot \text{switch}_1) + P_2 (C_{air} \cdot \text{switch}_2 + C_2 (1 - \text{switch}_2))$$

# Nástroje a repozitáře modelů - JSim (MML)

JSim version 2.13: Project C:\Users\jirka\Downloads\Two\_Compartment\_Lung.proj

Project airway2compartm... pars\_1

airway2compartment: ParSet Pages Run All Runs Help

Domain t

|        |      |               |
|--------|------|---------------|
| Lmin   | 0    | sec           |
| Lmax   | 100  | sec           |
| LCT    | 1801 | dimensionless |
| Ldelta | 0.1  | sec           |

Model Inputs

|            |        |               |
|------------|--------|---------------|
| Pzero      | 0      | mmHg          |
| Pamp       | 10     | mmHg          |
| R12        | 2      | mmHg*sec/ml   |
| R2a        | 2      | mmHg*sec/ml   |
| Com1       | 5      | ml/mmHg       |
| Com2       | 5      | ml/mmHg       |
| Vr1        | 5      | ml            |
| Vr2        | 5      | ml            |
| C10        | 2      | mmol/ml       |
| C20        | 0      | mmol/ml       |
| Cair       | 0      | mmol/ml       |
| beta       | 1      | dimensionless |
| Paource(t) | fgen 1 | dimensionless |

*Vstupy, výstupy, a parametry modelu*

|         |            |               |
|---------|------------|---------------|
| P1(t)   | -0.33953   | mmHg          |
| P2(t)   | -1.5248    | mmHg          |
| Pair(t) | 0          | mmHg          |
| V1(t)   | 3.7327     | ml            |
| V2(t)   | 1.9803     | ml            |
| F1(t)   | -0.59266   | ml/sec        |
| F2(t)   | .76242     | ml/sec        |
| x21(t)  | 0          | dimensionless |
| xa2(t)  | 1          | dimensionless |
| V2x(t)  | 1.3551     | ml/sec        |
| V1x(t)  | -0.59266   | ml/sec        |
| Q2x(t)  | 3.7955E-4  | mmol/sec      |
| Q1x(t)  | -3.7955E-4 | mmol/sec      |

Message Plot pages (5)

Flow: File View Zoom Help

XY plot update after run

Data airway2compartment F2 Curve 2 show

X-Expr

Y Log Autoscale Min Max

Flow vs Time

1: F1 ml/sec  
2: F2 ml/sec

17X114 05:55

Graph Text

line 1 terminated normally

# Nástroje a repozitáře modelů - JSim (MML)

JSim version 2.13: Project C:\Users\jirka\Downloads\Two\_Compartment\_Lung.proj

Project: airway2compartm... pars\_1

airway2compartment: File Edit Compile Help

```
real P2(t) mmHg; // Transmural pressure in vessel 2
real Pair(t) mmHg; // pressure in external air

real V1(t) ml; // Volume of vessel 1
real V2(t) ml; // Volume of vessel 2
// Flows are out of phase because of compliance
real F1(t) ml/sec; // Flow from vessel 2 to vessel 1 (positive or F
real xa2(t); //switches for P2 = P air->2 positive or

//INITIAL CONDITIONS:
when (t<t.min) { V1 = Vr1+0.25*Com1*Pamp; V2 = Vr2+0.375*Com2*Pamp;
Q1 = C10*Vr1; Q2 = C20*Vr2;}

// EQUATIONS: // Switches for flow direction:
x21 = if (F1 > 0) 1 else 0; // The switches set windows of 0 or
xa2 = if (F2 > 0) 1 else 0; // used in the solute transport equa
// the direction of flow
Pair = Pzero + Pamp*#source; // Respirator pressure using in gene

real beta = 1.0 dimensionless;
V2:t = F2 - F1; // flow, volume, pressure equations
F2 = (Pair - P2) / R2a;
P2 = Pzero + (if (V2 > Vr2) (V2 - Vr2) / Com2 else (1.0 - (V2 / Vr2) ^ beta) * V

V1:t = F1; // flow, volume, pressure equations
F1 = (P2 - P1) / R1a;
P1 = Pzero + (if (V1 > Vr1) (V1 - Vr1) / Com1 else (1.0 - (V1 / Vr1) ^ beta) * V
// Equations for solute carried by
Q2:t = (F1 * (-C1 * (1 - x21) - C2 * x21) + F2 * (Cair * xa2 + C2 * (1 - xa2)));
C2 = Q2 / V2;
Q1:t = (F1 * ((C2 * x21) + C1 * (1 - x21)));
C1 = Q1 / V1;

/* Check on numerics for flows:
real fmean1(t) ml/s, fmean10 = 0 ml/s, tauF1 = 100 s; when (t - t.min)
fmean1:t = (1 / tauF1) * (F1 - fmean1); //should be zero average after
```

**Zdrojový text modelu**

Message Plot pages (6)

Flow: File View Zoom Help

XY plot update after run

Data: airway2compartment F1 Curve 2 show

X Expr

Y Log Autoscale Min 0 Max 1

Flow vs Time

17X014 05:35

Graph Text

Source Run time Browser Debug Loops

Sensitivity Optimizer Monte Carlo Notes Images Memory

line 1

# Nástroje a repozitáře modelů - JSim (MML)

Systemic\_Circulation\_Olansen\_et\_al\_2000

A lumped-parameter model of the systemic circulation. A chopped-sine left ventricle produces a textbook pressure profile throughout the circulation and a total cardiac output

Model number: 0224

Run JSim model Applet: [Run applet](#) [JSim Tutorial](#)

**Description**

This is a lumped-parameter model of the systemic circulation based on Olansen et al system. Seven windkessel compartments in series represent the peripheral circulatory element alone. The arterial, venous and Vena cava segments are each characterized single compliance value. The resistance of the arterial and Vena cava segments are produce a textbook pressure profile throughout the circulation and a total cardiac output

JSim version 2.13: Project C:\Users\jirka\Downloads\Systemic\_Circulation\_Olansen\_et\_al\_2000.prj

Project: syscirc example1

Domain t

|       |       |               |
|-------|-------|---------------|
| tmin  | 0     | sec           |
| tmax  | 10    | sec           |
| Lc1   | 1.001 | dimensionless |
| Ldola | .01   | sec           |

Model Inputs

|         |       |                  |
|---------|-------|------------------|
| Rav     | .001  | mmHg*sec*ml^-1   |
| Rcv     | 28    | mmHg*sec*ml^-1   |
| Rcrb    | 2.3   | mmHg*sec*ml^-1   |
| Rtaop   | .08   | mmHg*sec*ml^-1   |
| Raop    | 17.5  | mmHg*sec*ml^-1   |
| Riaod   | .04   | mmHg*sec*ml^-1   |
| Raad    | .013  | mmHg*sec*ml^-1   |
| Rsad    | .56   | mmHg*sec*ml^-1   |
| Rsc     | .22   | mmHg*sec*ml^-1   |
| Rsv     | .2    | mmHg*sec*ml^-1   |
| Caop    | .35   | ml*mmHg^-1       |
| Caod    | .9    | ml*mmHg^-1       |
| Csad    | 2.65  | ml*mmHg^-1       |
| Cvc     | 1.0   | ml*mmHg^-1       |
| Cvc     | 0     | ml*mmHg^-1       |
| Laop    | .0015 | mmHg*sec^2*ml^-1 |
| Laod    | .008  | mmHg*sec^2*ml^-1 |
| Kc      | 17.3  | mmHg             |
| Do      | 50    | ml               |
| Vsa_0   | 210   | ml               |
| Vsa_max | 250   | ml               |
| Kp1     | .03   | mmHg             |
| Kp2     | .2    | mmHg*ml^-2       |
| Kr      | .04   | mmHg*sec*ml^-1   |
| tau_p   | .1    | ml^-1            |
| Kv      | 26    | mmHg             |
| Vmax_sv | 3500  | ml               |
| D1      | 0     | mmHg             |
| D2      | -5    | mmHg             |

Model Outputs

|          |           |    |
|----------|-----------|----|
| Rvc(t)   | .02662    | mm |
| Rsa(t)   | .34826    | mm |
| Paop1(t) | 1.5516    | mm |
| Paop2(t) | 78.50063  | mm |
| Paop(t)  | 78.58043  | mm |
| Paod(t)  | 78.59336  | mm |
| Psa_a(t) | 1.44942   | mm |
| Psa_p(t) | 12.22904  | mm |
| Psa(t)   | 78.58523  | mm |
| Psad(t)  | 68.1191   | mm |
| Psc(t)   | 20.0764   | mm |
| Psv(t)   | 15.61460  | mm |
| Pvc(t)   | 1.833     | mm |
| fav(t)   | 0         | ml |
| Faop(t)  | -0.70912  | ml |
| Faad(t)  | 27.12103  | ml |
| Ftaop(t) | -10.84686 | ml |
| Fiaod(t) | -27.83096 | ml |
| Fsa(t)   | 30.05223  | ml |
| Ftsa(t)  | -2.9304   | ml |
| Fsad(t)  | 66.48475  | ml |
| Ftsad(t) | -38.43252 | ml |
| Fsc(t)   | 69.42258  | ml |
| Ftsc(t)  | -2.9370   | ml |
| Fsv(t)   | 68.90822  | ml |
| Ftsv(t)  | -51436    | ml |
| Fvc(t)   | 68.85209  | ml |
| Ftvc(t)  | .05613    | ml |
| Fcort(t) | 2.8045    | ml |

Message Pressures Volumes Flows

XY plot update after run

Data: syscirc /rav Curve 6 show [x]

X Expr: [ ]

Log [ ] Asc [ ] Min 0 Max 1.35.2

Systemic circulatory pressures

Graph Text

# Nástroje a repozitáře modelů - SBML

The screenshot shows a web browser window displaying the SBML.org website. The browser's address bar shows 'sbml.org/Main\_Page'. The website header features the SBML.org logo and the title 'The Systems Biology Markup Language'. A navigation menu includes links for News, Documents, Downloads, Forums, Facilities, Community, Events, and About. A search bar is also present.

The main content area is divided into several sections:

- Welcome to the portal for the Systems Biology Markup Language (SBML),** a free and open interchange format for computer models of biological processes. SBML is useful for models of metabolism, cell signaling, and more. **It continues to be evolved and expanded** by an international community.
- For the curious:** What is SBML? Read our [introduction](#), then perhaps browse the [mailing lists](#), the [FAQ](#), and the [SBML Level 3 package activities](#) to glimpse what's happening with SBML today.
- For modelers:** Looking for software that supports SBML? Our [software guide](#) lists over 250 systems. Are you instead looking for models? Visit [BioModels Database](#), where you can find hundreds!
- For software developers:** Want to support SBML in your software? Read our [intro](#) and then the [specifications](#) to understand SBML in depth, then check our [libraries](#), [test resources](#), and also [3rd-party software](#).

No matter how you use SBML, we invite you to sign up for news updates either through our [RSS feed](#), our [Twitter feed](#), or one of the [mailing lists](#), and get involved with [community efforts](#) to help improve SBML. You can also call attention to your project's support of SBML by displaying the [SBML logo](#).

SBML would not have been possible without support from [many agencies and organizations](#), as well as contributions from many motivated individuals, including the [major contributors](#) who are shaping SBML Level 3.

At the bottom of the main content area, there is a Google+ badge showing 41049 recommendations and a SourceForge badge with the text 'Visit SBML on SF.net'.

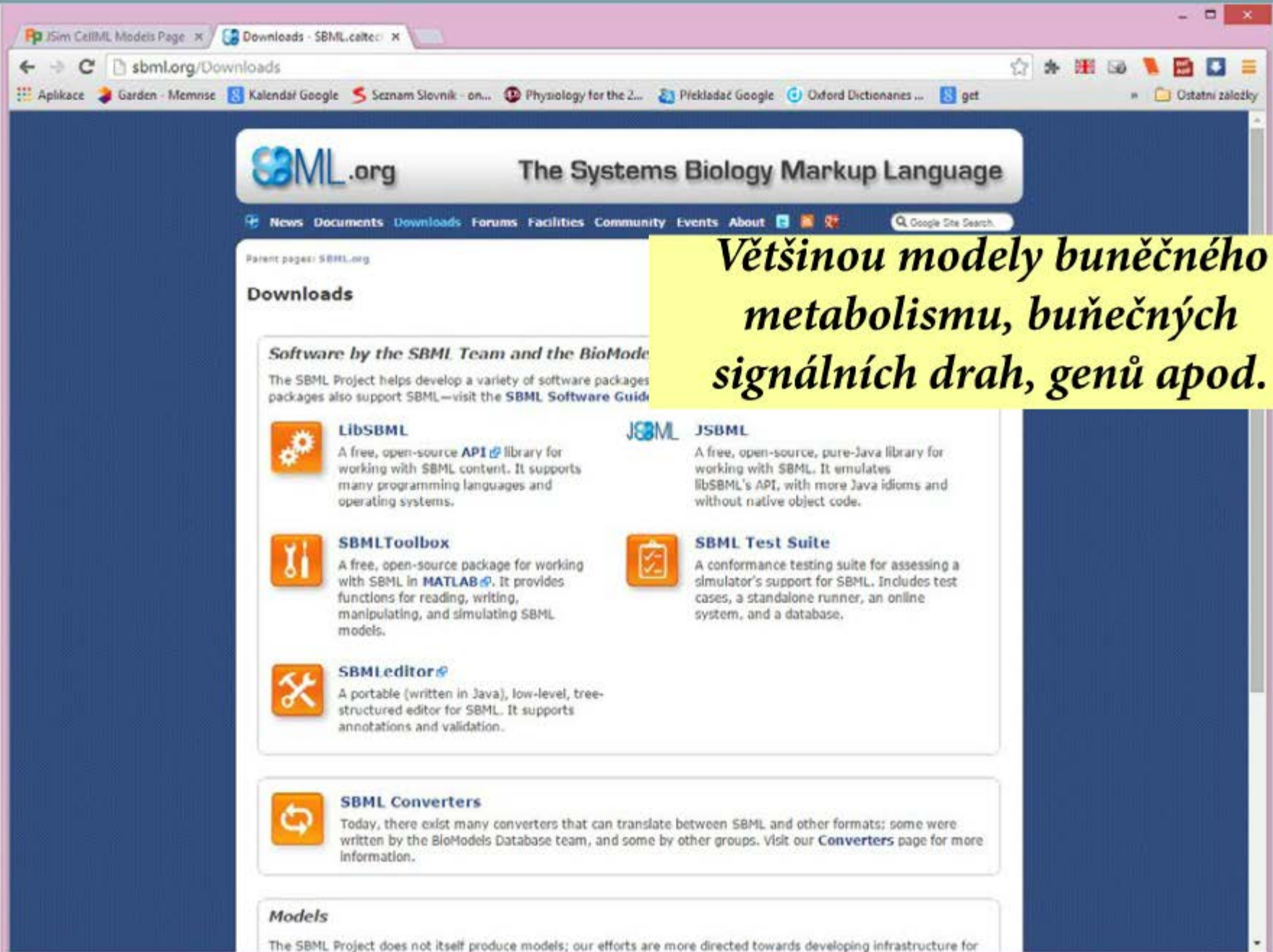
On the right side of the page, there are two news sections:

- SBML News:**
  - JSBML 1.0** (11 Dec '14) The final 1.0 release of JSBML is now available.
  - SBML L2v5 RC1** (28 Nov '14) Release candidate 1 of the Level 2 Version 5 specification is now available.
  - SBML FBC v.2 RC1** (28 Nov '14) Release candidate 1 of Version 2 of the SBML Flux Balance Constraints specification is now available.
- Community News:**
  - HARMONY 2015 registration** (27 Nov '14) Registration for HARMONY 2015 is now open.
  - Whole-cell modeling summer school** (22 Sep '14) A hackathon-like event to convert a published whole-cell model to use COMBINE standards.
  - BioUML 0.9.R** (19 Sep '14) The new release fixes bugs and adds features such as Galaxy ToolShed integration.

At the bottom of the right sidebar, there is a link: 'You can tell us what to announce'.

The footer of the page contains the text: 'Please use our [issue tracking system](#) for any questions or suggestions about this website. This page was last modified 16:22, 27 November 2014.'

# Nástroje a repozitáře modelů - SBML



The screenshot shows the SBML.org website with the following content:

- Page title: **SBML.org** The Systems Biology Markup Language
- Navigation: News, Documents, Downloads, Forums, Facilities, Community, Events, About
- Search: Google Site Search
- Parent page: SBML.org
- Section: **Downloads**
- Text: *Software by the SBML Team and the BioModels Database*
- Text: The SBML Project helps develop a variety of software packages that also support SBML—visit the [SBML Software Guide](#)
- Software items:
  - libSBML**: A free, open-source API library for working with SBML content. It supports many programming languages and operating systems.
  - JSBML**: A free, open-source, pure-Java library for working with SBML. It emulates libSBML's API, with more Java idioms and without native object code.
  - SBMLToolbox**: A free, open-source package for working with SBML in MATLAB. It provides functions for reading, writing, manipulating, and simulating SBML models.
  - SBML Test Suite**: A conformance testing suite for assessing a simulator's support for SBML. Includes test cases, a standalone runner, an online system, and a database.
  - SBML editor**: A portable (written in Java), low-level, tree-structured editor for SBML. It supports annotations and validation.
  - SBML Converters**: Today, there exist many converters that can translate between SBML and other formats; some were written by the BioModels Database team, and some by other groups. Visit our [Converters](#) page for more information.
- Section: **Models**
- Text: The SBML Project does not itself produce models; our efforts are more directed towards developing infrastructure for

**Většinou modely buněčného metabolismu, buňkových signálních drah, genů apod.**



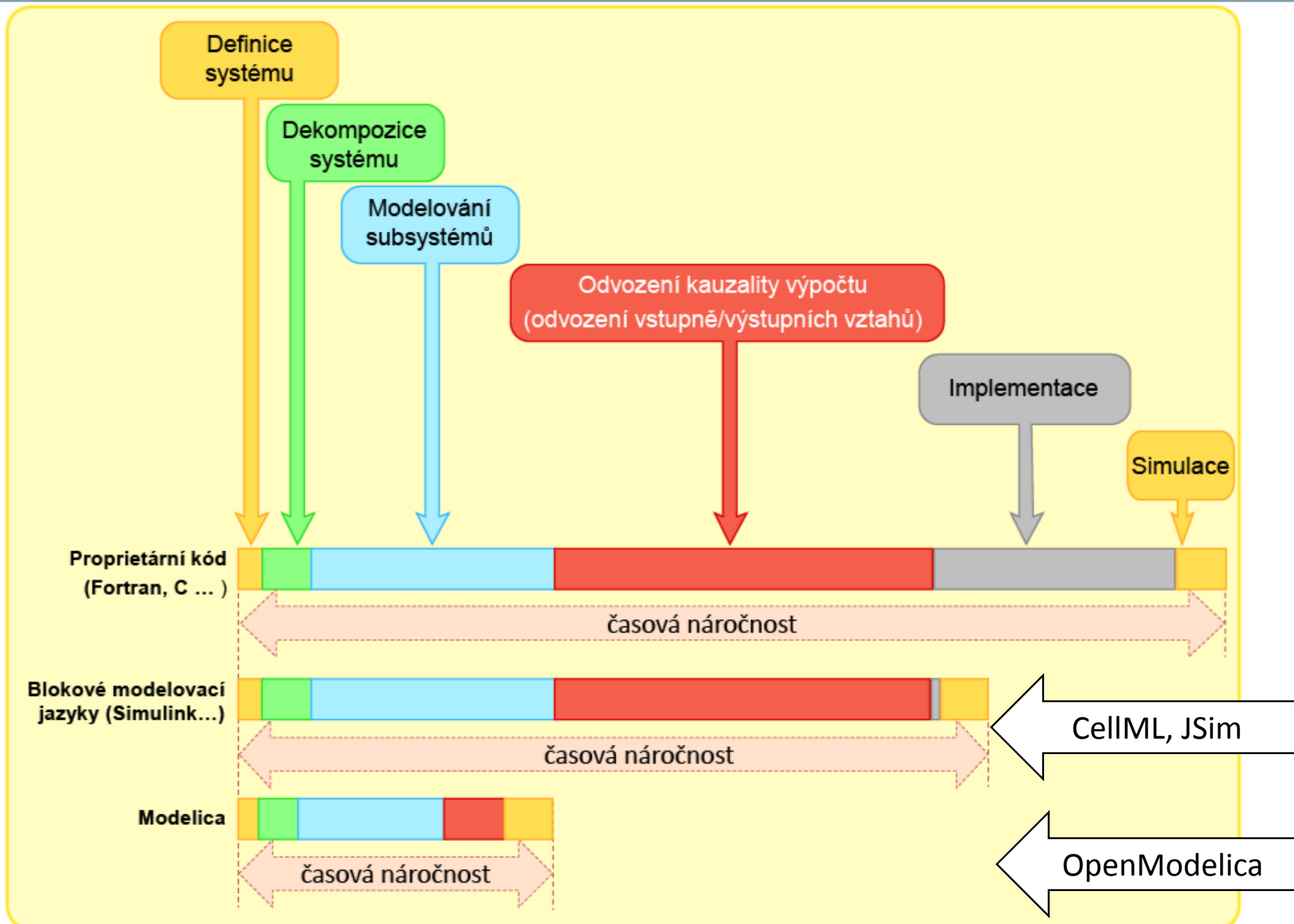
# Nástroje a repozitáře modelů - SBML

The screenshot shows the BioModels Database website interface. At the top, there is a navigation bar with 'BioModels Database' and a search box. Below the navigation bar, a large green banner contains the BioModels Database logo and a search box. The main content area is divided into several sections:

- BioModels Database is a repository of computational models of biological processes.** Models described from literature are manually curated and enriched with cross-references. All models are provided in the Public Domain. More information about BioModels Database can be found in the FAQ.
- Models published in the literature**
  - Browse
    - Manually curated (561 models)
    - Non curated (664 models)
  - Alternative access
    - Gene Ontology classification (new)
    - Gene Ontology tree
    - Advanced search
- Models automatically generated from pathway resources (Path2Models)**
  - Browse
    - Metabolic (112,898 models)
    - Non-metabolic (27,531 models)
    - Whole genome metabolism (2,641 models)
  - Alternative access
    - Taxonomy
    - Dedicated search

On the right side, there is a 'Model of the month' section for November 2014, featuring a diagram of a signaling cascade and a 'News' section with recent updates.

At the bottom, there is a footer with contact information and logos for EMBL and BBSRC.



# Modelica jako standardizovaný jazyk pro popis fyziologických modelů

## Aplikační knihovna PHYSIOLOBRARY

*www.physiolibrary.org*

# Physiolibrary

Modelica library for Physiology



Download

## Physiolibrary

Physiolibrary is a free open-source [Modelica library](#) designed for modeling human physiology. This library contains basic physical laws governing human physiology, usable for cardiovascular circulation, metabolic processes, nutrient distribution, thermoregulation, gases transport, electrolyte regulation, water distribution, hormonal regulation and pharmacological regulation.

### Library description

Our laboratory have a long tradition building physiological libraries, starting with [Physiolibrary in Matlab/Simulink](#) environment. The origin of this Modelica Physiolibrary was in the first version of our [HumMod Golem Edition](#) model implementation, where it was called HumMod Library. As the successors of Guyton's Medical Physiology School write, the original [HumMod](#) model is "The best, most complete, mathematical model of human physiology ever created". In cooperation with this group we are now developing together the new complex integrative model of physiology called [Physiomodel](#) based on Physiolibrary and HumMod.

We are also developing many types of smaller physiological models for use in [medical education](#), so it was essential to separate this library from our Modelica model implementations. Our Physiolibrary contains only carefully-chosen elementary physiological laws, which are the basis of more complex physiological processes. For example from only three type of blocks (ChemicalReaction, Substance and MolarConservationMass) it is possible to compose the allosteric transitions or the Michaelis-Menten equation.

Library contains also the icons for higher level (HumMod) subsystem implementations:



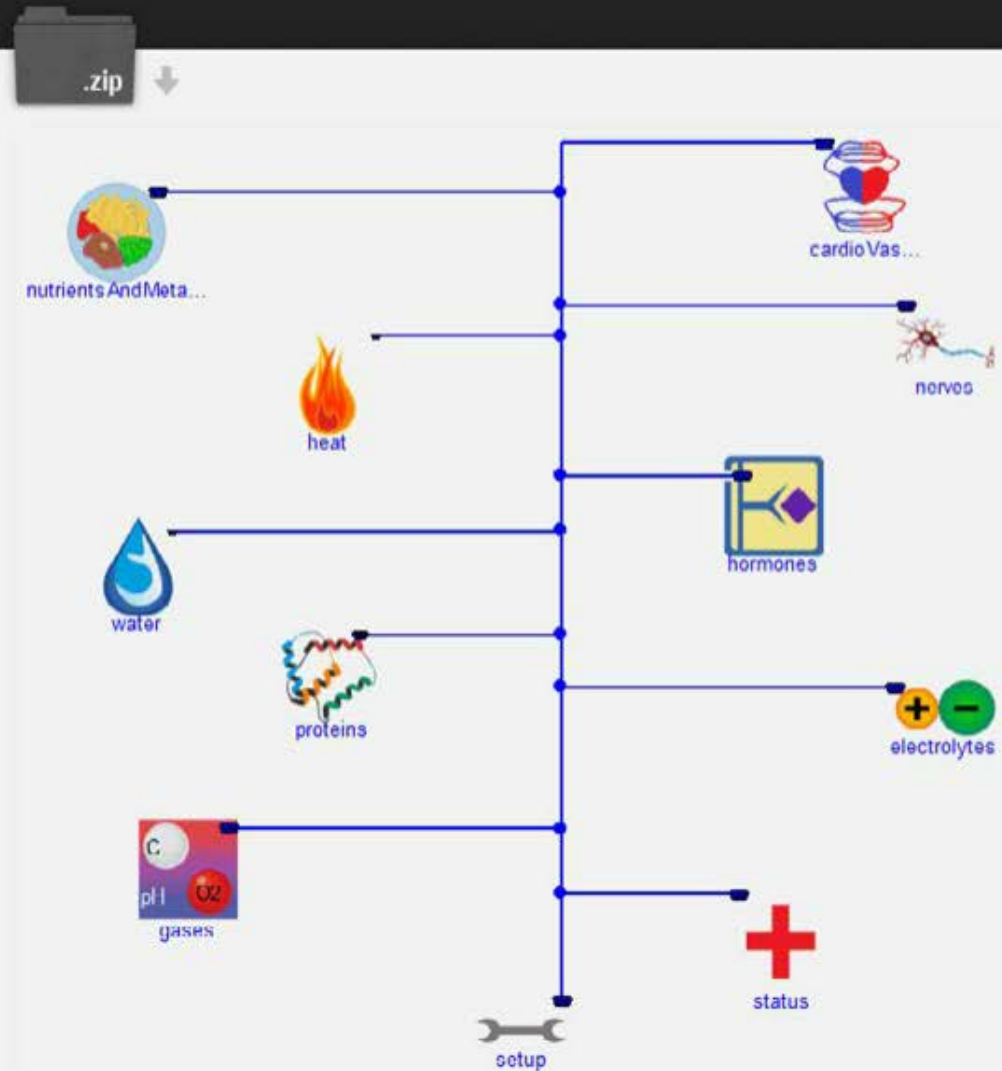
# PHYSIOMODEL

*rozsáhlý model  
integrativní fyziologie  
člověka*

*[www.physiomodel.org](http://www.physiomodel.org)*

## Physiomodel

Model of physiology in [Modelica](#) based on [HumMod](#) and [Physiolibrary](#)



## Physiolibrary

Modelica library for Physiology



Download

### Physiolibrary

Physiolibrary is a free open-source Modelica library designed for modeling human physiology. This library contains basic physical laws governing human physiology, usable for cardiovascular circulation, metabolic processes, nutrient distribution, thermoregulation, gases transport, electrolyte regulation, water distribution, hormonal regulation and pharmacological regulation.

### Library description

Our laboratory have a long tradition building physiological libraries, starting with Physiolibrary in Matlab/Simulink environment. The origin of this Modelica Physiolibrary was in the first version of our HumMod Golem Edition model implementation, where it was called HumMod Library. As the successors of Guyton's Medical Physiology School write, the original HumMod model is "The best, most complete, mathematical model of human physiology ever created". In cooperation with this group we are now developing together the new complex integrative model of physiology called Physiomodel based on Physiolibrary and HumMod.

We are also developing many types of smaller physiological models for use in medical education, so it was essential to separate this library from our Modelica model implementations. Our Physiolibrary contains only carefully-chosen elementary physiological laws, which are the basis of more complex physiological processes. For example from only three type of blocks (ChemicalReaction, Substance and MolarConservation/Mass) it is possible to compose the allosteric transitions or the Michaelis-Menten equation.

Library contains also the icons for higher level (HumMod) subsystem implementations:



## Physiomodel

Model of physiology in Modelica based on HumMod and Physiolibrary

