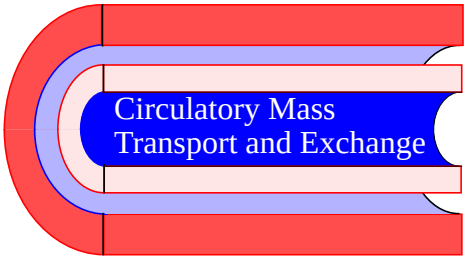
National Simulation Resource

NSR

University of Washington



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Fractal time series analysis

Traditional time series analysis is based on simple questions that can reveal information about underlying processes: Is the signal fundamentally periodic but partially obscured by noise? What is the mean and the variance? Do these change with time? Is the signal filtered random noise? Is it noise smoothed by a windowed averaging system? What is the character of the filter? What is the correlation structure in the signal?

Time series analysis tools are well known, and well taught in various texts, e.g., Diggle (1990) and Chatfield (1989), from a statistical point of view. These tools include defining the probability density function (*pdf*) and its shaping factors (mean, variance, skewness, kurtosis), Fourier analysis (obtaining the amplitude and phase of sinusoidal components), and autocorrelation analysis.

Finding the *pdf* and its features can be thought of as "moment analysis": the mean is the first moment around the origin, the variance is the second moment around the mean, the skewness is derived from the third moment around the mean, and the kurtosis is derived from the fourth central moment.

Fourier analysis (Blackman and Tukey, 1959) is an approach to determining the power spectrum of a time series. The spectrum identifies frequency components that dominate the time series. The shape of the power spectrum contains useful information about the character of the time series.

Autocorrelation analysis examines the self-similarity in signal structure. It reveals the rate of falloff in correlation, the decay in correlation with distance (time) between points, and assumes that the correlation falloff is the same throughout the period of recording the signal. These two features of autocorrelation analysis presage some more difficult questions that require more complex techniques to evaluate. Is the signal stationary? (Does it have the same statistical properties over all time? Is our sampling of the signal giving the same information as might a sampling yesterday or tomorrow?) What process gives rise to the correlation?

The accuracy of all these techniques is widely recognized to be compromised if the series is short. A huge body of literature has evolved to provide means of estimating the accuracy of the estimates of means, variances, correlation coefficients and such. These means of estimating accuracy are the heart of "elementary" modern statistics.

A set of strategies has also evolved based on the idea that a signal with correlation structure occurs by filtering random white noise. One approach is autoregression, AR, which postulates that the signal is formed from white noise but retains a "memory" or weighting of preceding points in each point. A related approach is noise filtered with a weighted moving average, MA. These approaches are similar, one being prospective and the other retrospective; they can be combined: ARMA analysis covers this. These ARMA signals are generally not fractals. However, fractal signals may well be considered susceptible to standard ARMA analysis and presumably are identifiable by the characteristic coefficients revealed by ARMA analysis.

A reason for thinking in these terms is that fractal analysis should not be regarded as anything other than a special set of statistical analyses (Bassingthwaighte et al., 1994). Finding that a signal is fractal does imply more than is ordinarily inferred from noise with short term correlation; the long term correlation always begs the question of why the persistence is so long. This is a prime reason for testing to see whether or not a signal is fractal.

The next steps for fractal analysis are nailing down the methodology (e.g., Bassingthwaighte and Raymond, 1994). Then it will be easier to make the case to biostatisticians and statisticians that this set of tools merits their attention and should be added to their ARMAmentarium.

References

Blackman, R. B., and J. W. Tukey. *The Measurement of Power Spectra, from the Point of View of Communications Engineering*. New York: Dover, 1959.

Chatfield, C. *Analysis of Time Series: An Introduction*. London: Chapman and Hall, 1989.

Diggle, P. J. *Time Series: A Biostatistical Introduction*. Oxford: Oxford Science, 1990.

James B. Bassingthwaighte

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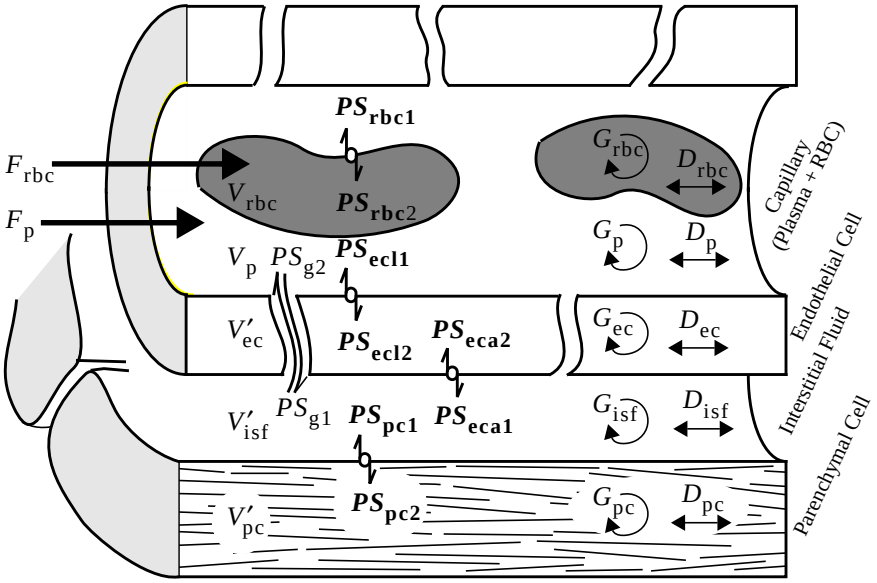
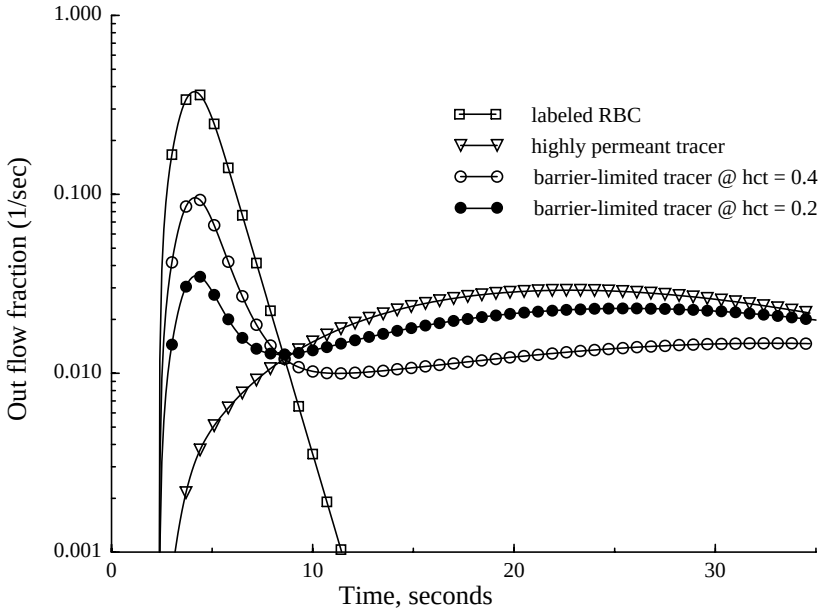
Nonlinear red blood cell model for blood–tissue exchange

A nonlinear red blood cell (RBC) model for multiple region blood–tissue exchange (BTEX) has been implemented for SIMCON. This model differs from previously developed axially distributed BTEX models (Bassingthwaighte, Wang and Chan, 1989) in that RBCs are modeled as a separate region from plasma within the vascular space. One reason for modeling RBCs as a separate region is that many substrates are carried in both RBCs and plasma, and RBC kinetics may play an important role in capillary–tissue exchange.

The model accounts for nontracer and tracer material, and up to five species. Each species is modeled using a Krogh tissue cylinder (Fig. 1) consisting of five concentric regions of equal length (RBCs, plasma, endothelial cells, interstitial fluid space and parenchymal cells) separated by four transport barriers (the red cell membrane, the luminal and abluminal membranes of endothelial cell, and the membrane of parenchymal cell). The nonlinear facilitated transporters are used to model substrate transport across the barriers. In addition, there is a passive diffusional path from plasma to ISF bypassing endothelial cells via intercellular clefts. Other features of the model include a choice of first order consumption, Michaelis-Menten kinetics and *enzyme* binding and reaction, and equilibrium binding and axial diffusion in each region. For consumption, any species can undergo transformation into any other species.

Fig. 1. Blood–tissue exchange (BTEX)





Different RBC and plasma convective velocities are described in order to model "red cell carriage" and "red cell precession," by means of which substrate in RBCs reaches the venous outflow ahead of substrate in the plasma. A dual-flow sliding algorithm has been devised to deal with the two flowing fronts. The algorithm uses the Lagrangian stepped flow, in which the contents of the plasma region are shifted "downstream" by exactly one space step during each internal time step. For the RBC, the model uses the random choice method for convection (Chorin, 1977), in which the space step is determined by the velocity ratio of RBC to plasma, and instantaneous mixing is assumed in all segments. After the spatial shift, a time splitting method is used. Analytical solutions for equilibrium binding, radial exchange, consumption, and axial diffusion are obtained separately within that time step to achieve computational efficiency and solution stability. This "internal" time step is equal to $V_p/(F_p \times n_{seg})$ where V_p is plasma volume, F_p is the plasma flow and n_{seg} is the number of segments into which all of the five regions are divided. In presence of nonlinear membrane transport and consumption the nonlinear terms (dependent on nontracer concentration) are updated at the start of each internal time step and remain constant during the time step.

Two examples will serve to illustrate the model. The first, an example of modeling the red cell carriage effect, used three tracers: RBC reference tracer, a second reference tracer with high permeability, and the tracer of interest with relatively low permeability. Fig. 2 shows the outflow curves following an injection of a bolus consisting of pre-equilibrated red cells and plasma. For the tracer with low permeability (barrier-limited), the outflow curve is bimodal. The first peak occurred simultaneously with the RBC reference tracer, while a second peak is later than that of the highly permeant tracer. It is

evident that a portion of the tracer was carried through the capillary in red cells. The red cell carriage effect is more marked when the hematocrit is higher. This result reproduces the experimental findings of Goresky and his colleagues (1975) on red cell carriage.

The second example of the application of the RBC model for analyzing physiological data is represented by Fig. 3, which shows coronary venous outflow curves of tracer adenosine following bolus injection into arterial plasma. The model describes high uptake and retention of adenosine in capillary endothelial cells, and describes an RBC *PS* for adenosine that is equivalent to the observed half-time of three minutes for RBC uptake of tracer adenosine from plasma in dog blood *in vitro*. The model results are in good agreement with measurements obtained in indicator dilution experiments in the anesthetized dog heart.

The model is widely applicable to simulations of the transport and exchange of oxygen, substrates, receptor agonists, hormones, and pharmaceuticals.

References

Bassingthwaighte, J.B., C.Y. Wang, and I.S. Chan. Blood-tissue exchange via transport and transformation by endothelial cells, *Circ. Res.* 65:997-1020, 1989.

Chorin, A.J. Random choice methods with application to reacting gas flows. *J. Comp. Phys.* 25:253-272, 1977.

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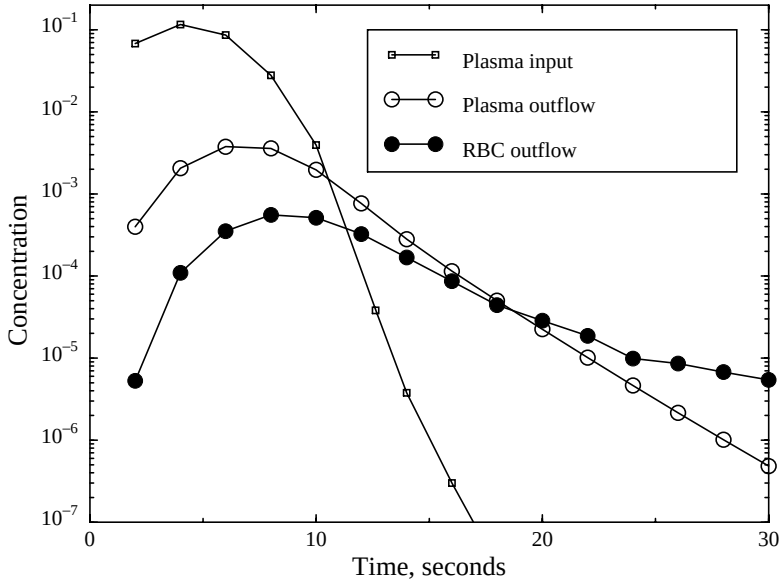
Zheng Li and Keith Kroll

Fig. 3. Simulated plasma and RBC adenosine outflow after plasma injection

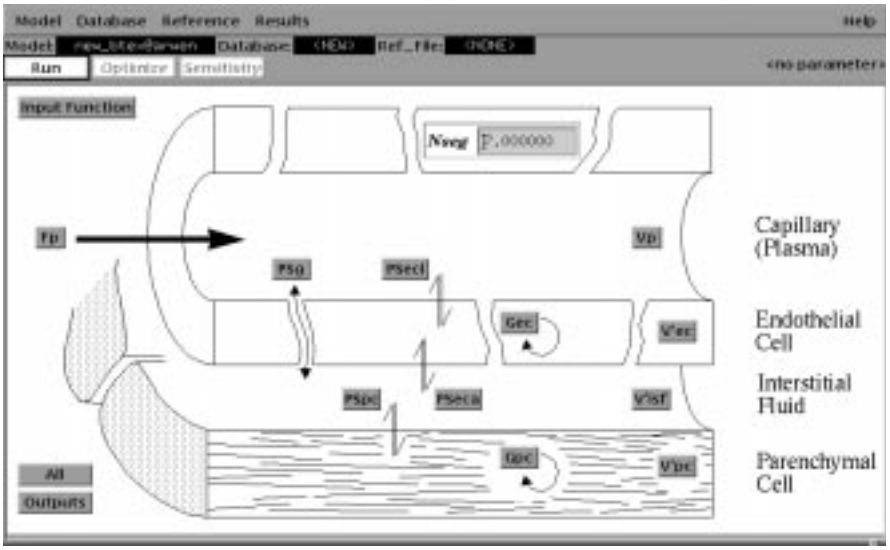


XSIM Project Update

XSIM will be a friendly, elegant graphical user interface (GUI) to SIMCON models. It will use the multi-window displays and point-and-click functionality contemporary computer users expect. Converting a traditional text-based application like SIMCON to a GUI involves much more than simply arranging buttons on the screen. Usually the application has to be completely revamped, and XSIM was no exception. The result, however, is that controls and popups are carefully designed to afford experienced SIMCON modelers greater power, while at the same time making it easier for novice modelers to develop expertise.

An important feature of XSIM is network access that lets the modeler use powerful computers on the local area network or global Internet. These powerful computers may perform better than the modeler's desktop computer. For example, if model MMID4 runs too slow, the modeler can try MMID4@CRAY.

A prototype version of the XSIM was demonstrated at Experimental Biology '94. Based on the feedback we received there, several features were redesigned and some new capabilities were added. From the user's point of view, a major addition is that windows may include a bit-mapped diagram that depicts a model or model component in a graphical manner. For instance, when connected to a four region BTEX model, the model window shows the standard BTEX diagram with parameter values placed in appropriate positions on the diagram as shown in the figure below.



XSIM continued on page 4

XSIM from page 3

Many features planned for XSIM extend rather than replicate SIMCON features. Some of these features are: 1) contour plots, 2) dynamic array plots, 3) three-dimensional plots, 4) a labeled database structure, 5) use of color, 6) a script control language for running in batch mode, 7) dynamic communication with external image analysis programs, 8) graphic support for two- and three-dimensional cellular models, and 9) a point-and-click on-line help system.

The first release of XSIM (Version 1.0) is planned for 15 April 1995. This release will offer all the functionality of SIMCON and will include some of the extensions mentioned above. Prior to this official release of XSIM, a preliminary version, XSIM 0.9, will be delivered to selected users for evaluation. The target date for XSIM 0.9 is 1 January 1995, and we are on schedule to meet that target.

XSIM 0.9 will provide the essential capabilities of SIMCON but will not include all SIMCON features. Model run, loop and optimization functions will be available, but model sensitivity and residual analyses will not be. Two major enhancements in loops will be implemented: 1) several model parameters can be modified in parallel for each loop, and 2) the values for the parameter can be specified as an algebraic expression (e.g., period $*$ 2 + 1) or as a list (e.g., 2, 3, 5, 7, 11, 13).

Plotting of model outputs and reference data will also be improved in several ways. All plots will have autoscale options, so manual setting of axis scales will often be unnecessary. More of a model's output will be captured at run time. This will allow the modeler to plot different model outputs, or render them in a different way, without having to rerun the model. Additionally, the modeler will be able to specify an algebraic expression of parameters to be plotted (e.g., (sinout – cosout) ^2). This will allow users to display, and optimize, quantities that are not explicitly programmed into the model.

Erik Butterworth and Richard King

The future of SIMCON

In past issues of the NSR Newsletter, we discussed the upcoming release of SIMCON 3.0, which would separate a modeling session into interface and model tasks, running as separate processes that do not have to be on the same computer. This approach would have several advantages, including the ability to shift among models without leaving the interface, and the ablity to run complex models on remote, high performance computers. Model programs would be smaller, because they would not include the code for the interface, and models would not have to be remade whenever the interface was modified to include a new feature or fix a bug.

As work on SIMCON 3.0 progressed, two things became clear. First, the full implementation of this approach is not compatible with the structure of the existing SIMCON. Second, XSIM, which includes all the features planned for SIMCON 3.0 and many more, will be released at about the same time as would SIMCON 3.0. (See *XSIM project update*, page 3 of this issue.) For these reasons, the plan to release a version of SIMCON that uses interprocess communication (IPC) has been superseded.

An example of the problems that surfaced in implementing IPC code for SIMCON is the difficulty encountered in killing a model program that has stalled on a remote computer. Because SIMCON only looks for keyboard input at the end of each evaluation of the solution section of the model, a model that has gone into an "infinite loop" will never detect the "k" typed by the user to kill a simulation run. In general, the signal handling that terminates the remote model task in XSIM is not compatible with SIMCON, a FORTRAN program.

The effort that has gone into the design, implementation, and testing of the IPC code for SIMCON will not be wasted, as the same code is being used in XSIM. For most users, XSIM will replace SIMCON. It will be implemented on UNIX platforms beginning with Sun workstations. Implementation on other UNIX workstations will be straightforward. Current SIMCON users should note that the code for their SIMCON model programs will not need to be changed to work with XSIM. To build an XSIM model program, the model code is simply linked with the XSIM communication code rather than the SIMCON program code.

SIMCON will continue to be available for modelers who cannot use XSIM. For example, since XSIM requires X-windows, modelers who run terminal emulators on their PC or Macintosh to access the NSR computers will not be able to use XSIM to run simulations. We will continue to fix bugs and implement new features in SIMCON. However, due to the small size of our software engineering group and the on-going emphasis on XSIM development, requests for modifications to SIMCON will have to be screened carefully to determine whether or not they merit implementation. We are still working on a release of SIMCON for PCs running LINUX. This effort is secondary to the XSIM project but will continue.

Richard King

SIMCON status report

Version 2.8.3 of SIMCON is installed. This version contains two changes and fixes seven bugs. A summary of the release notice is given below. The major change, in the formula used for calculating the coefficient of variation for optimization and simulation runs, is shown at right. In this formula the data is y_i, $\hat{y}_i$ is the simulation output, w_i is the weight, N_p is the number of parameters being optimized, and N_d is the number of data points. When the *CV* is calculated during a simulation run, N_p is assumed to be 1.

$$CV = 100 \cdot \frac{\sqrt{\dfrac{\Sigma w_i^2 (\hat{y}_i - y_i)^2}{(1 - N_p/N_d)\Sigma w_i^2}}}{\Sigma w_i^2 y_i / \Sigma w_i^2}$$

Release notice summary

Changes

C1. When the SIMPLEX optimizer is used, the user can control when the covariance matrix is calculated. (E43)

C2. Some internal changes have been made to facilitate usage of SIMCON code modules in other applications. (B82)

C3. A new formula for the coefficient of variation has been implemented. (B87)

Bug fixes

B1. Periodic crashes after interrupting a simulation run have been eliminated. (B56)

B2. SIMCON behaves properly when the reference data file is not found. (B77, B78)

B3. All information on all curves in a reference data file can now be viewed from the reference data index menu. (B79)

B4. SIMCON no longer crashes if reference data curve having no data points is specified when calculating residuals. (B80)

B5. Protection against division by zero has been added to the calculation of curve weights and using a curve weight of zero. (B67, B70)

Compatibility with previous release

This release is completely compatible with SIMCON version 2.8.2.

Richard King

Recent NSR Publications

Deussen, A., T. R. Bukowski, J. D. Ploger, K. Kroll, J. M. Link, K. A. Krohn, and J. B. Bassingthwaighte. Modeling of oxygen-15 transport and metabolism in the heart. *FASEB J.* 7:A238, 1993.

Slaaf, D. W., S. M. Yamashiro, G. J. Tangelder, R. S. Reneman, and J. B. Bassingthwaighte. Nonlinear dynamics of vasomotion. In: *Vasomotion and Flowmotion. Prog. Appl. Microcirc.Vol. 20:*, edited by C. Allegra, M. Intaglietta and K. Messmer, 1993, pp. 67-80.

King, R. B., A. Deussen, G. R. Raymond, and J. B. Bassingthwaighte. A vascular transport operator. *Am. J. Physiol.* 265 (Heart Circ. Physiol.34):H2196-H2208, 1993.

Chan, I. S., A. A. Goldstein, and J. B. Bassingthwaighte. SENSOP: A derivative-free solver for non-linear least squares with sensitivity scaling. *Ann. Biomed. Eng.* 21:621-631, 1993.

Bassingthwaighte, J. B., J. R. Revenaugh, A. Deussen, M. M. Graham, T. K. Lewellen, J. M. Link, and K. A. Krohn. Evaluation of coronary perfusion by positron emission tomography. In: *Recent Advances in Coronary Circulation*, edited by Y. Maruyama, F. Kajiya, J. I. E. Hoffman and J. A. E. Spaan. Tokyo: Springer-Verlag, 1993, pp. 2-16.

Bassingthwaighte, J. B. Chaos in cardiac signals. In: *Interactive Phenomena in the Cardiac System*, edited by S. Sideman and R. Beyar. New York: Plenum, 1993, pp. 207-218.

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Kroll, K., I. S. Chan, and J. B. Bassingthwaighte. Enzyme holdup in capillary endothelial cells. *Proc. Int. Fed. Automat. Control "Modeling and Control in Biomedical Systems"*:220-221, 1994.

Wilke, N., K. Kroll, H. Merkle, Y. Wang, Y. Ischibaschi, Y. Xu, J. Zhang, M. Jerosch-Herold, A. Mühler, A. E. Stillman, J. B. Bassingthwaighte, R. Bache, and K. Ugurbil. Regional myocardial blood volume and flow via MR first pass imaging in concert with polylysine-gadolinium-DTPA. *Magnetic Resonance in Medicine*, 1994.

Bassingthwaighte, J. B., and G. M. Raymond. Evaluating rescaled range analysis for time series. *Ann. Biomed. Eng.* 22:432-444, 1994.

Caldwell, J. H., G. V. Martin, G. M. Raymond, and J. B. Bassingthwaighte. Regional myocardial flow and capillary permeability-surface area products are nearly proportional. *Am. J. Physiol.* 267:H654-H666, 1994.

Bassingthwaighte, J. B., L. S. Liebovitch, and B. J. West. *Fractal Physiology.* New York, London: Oxford University Press, 1994, 364 pp.

Software in NSR's ftp site

Along with the NSR newsletters, User Guides, and Quick References, software from NSR and elsewhere is archived in the public (pub) ftp directory at NSR (see the sidebar, "Anonymous ftp at NSR," for details on how to use our ftp service). Two subdirectories of pub, SENSOP and FRACTAL, contain files related to the SENSOP problem solver, and fractal routines. Of the other files in pub the two largest, libmath.tar.Z and cmlib.tar.Z, are collections of subroutines used for circulatory model development and numerical analysis. Many of the smaller files in the pub directory also contain subroutines useful in developing circulatory models and solving numerical problems.

The SENSOP subdirectory contains the Fortran language source files and subroutines for a nonlinear least-squares problem solver. Other files in this subdirectory are documentation of SENSOP in Postscript™, nroff and ASCII formats. For more complete information on SENSOP, see Chan et al., 1993.

One-dimensional fractal series may be generated and analyzed with the tools collected in the FRACTAL subdirectory. SSM (spectral synthesis method) generates a fractal series (see Peitgen and Saupe, 1988, pages 86 and 94, respectively). HURST (the Hurst rescaled analysis) may be used to analyze fractal series. For more complete information on the fractal analysis routines see Bassingthwaighte and Raymond, 1994.

Subroutines used to develop many of the circulatory models of NSR are collected in one of the larger files in pub, libmath.tar.Z. Among these are subroutines used for the blood tissue exchange models (BTEX), the compartmental tissue exchange models (CTEX) for multiple regions and multiple metabolites, and the Sangren-Shepard (1953) and the Rose-Goresky-Bach (1977) models. Additional subroutines of interest in libmath.tar.Z are deconvolution routines, function generators, and operators to simulate dispersive vascular flow. A complete list can be found in the adjunct file libmath.man.

Easily ported, public domain subroutines for solving computational problems in mathematics and statistics are collected in the other large file in pub, cmlib.tar.Z. Some major applications of these subroutines are statistical analysis, spline fitting, differential equation solving, Fourier transforms, and linear algebra. A complete list of the major areas of application is in the adjunct file cmlib.man.

Other files in the pub directory comprise a diverse collection of useful software. Among them are files of NSR routines: NSR_vasop.tar contains all of the routines necessary to implement the vascular dispersive operator known as vasop (King et al., 1993), and NSR_btex30.tar contains all of the routines necessary to implement the blood tissue exchange model for three regions, BTEX30 (Bassingthwaighte et al., 1992), including its test program. In addition to the files of routines specific to NSR, some files contain routines of more general application: a deconvolution routine and directions for its use are in deconv.tar, and routines (written in the C language) for transferring binary data across computer architectures in conformance with IEEE standards are in db.tar.Z.

Our ftp archive will grow as software now in development becomes available. If you have any questions about retrieving or using the software, please e-mail your inquiries to garyr@nsr.bioeng.washington.edu. We hope the archive will continue to be a valuable source not only of information about NSR, but also of software solutions to problems that come up in your day-to-day modeling tasks.

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Bassingthwaighte, J. B., I. S. Chan, and C. Y. Wang. Computationally efficient algorithms for capillary convection-permeation-diffusion models for blood-tissue exchange. *Ann. Biomed. Eng.* 20:687-725, 1992.

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King, R. B., A. Deussen, G. R. Raymond, and J. B. Bassingthwaighte. A vascular transport operator. *Am. J. Physiol.* 265 (Heart Circ. Physiol.34):H2196-H2208, 1993.

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Rose, C. P., C. A. Goresky, and G. G. Bach. The capillary and sarcolemmal barriers in the heart: An exploration of labeled water permeability. *Circ. Res.* 41:515-533, 1977.

Sangren, W. C., and C. W. Sheppard. A mathematical derivation of the exchange of a labeled substance between a liquid flowing in a vessel and an external compartment. *Bull. Math. Biophys.* 15:387-394, 1953.

Gary M. Raymond

Anonymous ftp at NSR

You may get files from NSR by using anonymous ftp. If you are using a UNIX system, use the following steps to get the "Readme" file first, then read it carefully for detailed instructions. Macintosh and PC users may use similar procedures specific to their system and communication software.

1. Enter `ftp nsr.bioeng.washington.edu` at the system prompt.
2. Enter `anonymous` at the resulting prompt, `Name:`
3. Enter a complete electronic mail address at the prompt, `Password:`
4. Enter `get Readme` at the prompt, `ftp>`.
5. Enter `quit` to return to your system.

The "Readme" file is a text file that can be read with your usual text editor (e.g., vi) or word processing application.

Reprise: summer workshop

The Seventh Annual Computer Simulation Summer Workshop offered by the National Simulation Resource was held September 11-16, 1994. This one week course in applying modeling to the analysis of flow, transport, and reaction in metabolizing cells and organs was kicked off with a four hour seminar on the basics of the UNIX operating system.

Because the workshop was designed to provide hands-on experience, enrollment was limited to eighteen participants. This year the participants were from Medical College of Wisconsin, University of California at Davis, Auburn University, University of Minnesota, W. K. Warren Medical Research Institute (Tulsa, OK), Case Western University, Yale University, Marquette University, V. A. Medical Center (Kansas City, MO), U. S. Army Research Center (Bel Air, MD), Aarhus Hospital PET Center (Aarhus, Denmark), and the University of Washington.

The agenda for the 1994 course is shown at right. The 1995 workshop will be held September 17-22, 1995. If you or a colleague would like a registration form, please send an e-mail request to Rita Jensen or a postal request to the National Simulation Resource (see bottom of first page for e-mail and postal addresses).

Rita Jensen

Tracer Exchange Kinetics in Organs

UNIX workshop	R. King
Introduction to modeling of biological systems	J. Bassingthwaighte
The National Simulation Resource computer system	L. Weissman
An overview of simulation software	M. Epstein
Stella and P-Opt	M. Graham
SAAM II	P. Barrett
XSIM and SIMCON	R. King
Basic blood–tissue exchange (BTEX) modeling	J. Bassingthwaighte
Distributed BTEX modeling	J. Bassingthwaighte and R. King
The multiple indicator dilution experiment	J. Ploger
Estimation of membrane PS products	K.Kroll
Parameter adjustment to fit models to data	R. King
Influences of data acquisition on parameter estimates	M. Graham
Statistical assessment of data	M. Epstein
Flow estimation using extracted markers	J. Bassingthwaighte
Heterogeneity in flow and PS	J. Caldwell
Accounting for heterogeneity	R. King
Barrier-limited, carrier-mediated transport	K. Kroll
Countertransport via complex carriers	J. Bassingthwaighte
Nonlinear models and red cell carriage effects	J. Bassingthwaighte and Z. Li
Experimental methods for estimating Km and Vmax	K. Kroll
Oxygen transport and metabolism	J. Bassingthwaighte and Z. Li
Models of reaction sequences of adenosine	K. Kroll
Methods for assessing spatial fractals	J. Bassingthwaighte
Regional myocardial flow by external detection	J. Bassingthwaighte and K. Kroll
Spatial variation and fractal characterization	R. Glenny
Strategies for modeling large scale systems	J. Bassingthwaighte
Course review and discussion	J. Bassingthwaighte
NSR remote usage: Staying in touch	R. King

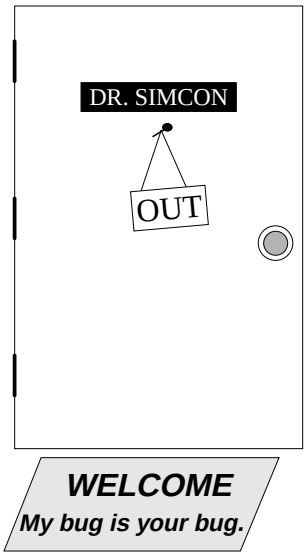
Visitors at NSR

Anne Clough is visiting NSR from the Mathematics, Statistics and Computer Science and the Biomedical Engineering Departments at Marquette University in Milwaukee, Wisconsin, where she is an Assistant Professor. Anne's research, based on dynamic images obtained from PET, MRI and X-ray angiography, is supported by an NSF grant to investigate regional flow and volume measurement techniques. Her analyses will contribute to developing methods for estimating regional perfusion heterogeneity and responses to pathophysiologic interventions.

Peter Tonellato, also an Assistant Professor visiting from the Mathematics, Statistics and Computer Science Department at Marquette University, will be collaborating with the NSR group to explore and develop novel fractal and chaos analyses which can be applied to physiological time series derived from hypertensive populations.

Tada Yipintsoi, formerly Dean of the Faculty of Medicine at Songkla University in Thailand, is now a Visiting Professor here at the Center for Bioengineering. Tada previously worked with Jim Bassingthwaighte at the Mayo School of Medicine in Rochester, Minnesota from 1966-1972 and will be here at the University of Washington until next October. After taking some time away from research and tending to administrative duties, Tada is now re-learning how to use models in looking at small regions of blood flow in the heart.

Angie Kaake



World Wide Web and NSR

NSR has a World Wide Web (W3) home page at the Uniform Resource Locator (URL) address: http://nsr.bioeng.washington.edu. For the nonce, you can use Mosaic© or your favored W3 browser to access the NSR User Guide at our site: development of the site continues, however, so tune in from time to time for more goodies. While you're there, check out the link to the home page of the *Annals of Biomedical Engineering*, where you will find the tables of contents for previous and forthcoming issues of the journal, as well as information for authors. To go directly to the *Annals* home page, use the URL http://biorobotics.ee.washington.edu/ABME/annals.html.

COMPUTER SIMULATION SUMMER WORKSHOP SEPTEMBER 17–22, 1995

SEE PAGE 7 FOR REGISTRATION INFORMATION AND DETAILS OF LAST YEAR'S WORKSHOP

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