This brochure contains brief descriptions of The BioQUEST Library Volume VI modules. For more information please visit our web site at http://bioquest.org.
The BioQUEST Library

Volume VI

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The BioQUEST Library is a peer-reviewed publication of computer-based curricular materials for biology education. The current volume, Volume VI, includes more than 75 software simulations, tools, datasets, and other supporting materials from many areas of biology, including ecology, evolution, genetics, molecular biology, physiology, developmental biology, botany, and neurobiology.

The modules in the Library are intended to provide a flexible problem-solving space for investigations that can range from simple to sophisticated and challenging. As they use each of the modules, students are expected to craft a research question, pursue solutions to their problem, and define the criteria for closure and publication, just as scientists do. The educational philosophy that underlies this approach has become known as BioQUEST’s 3Ps: Problem-posing, Problem-solving, and Persuasion of peers.

The materials in the Library are designed to provide robust problem spaces in which students may pursue multiple hypotheses and generate and analyze large datasets. The modules are open-ended: they require students to take responsibility for evaluating the completeness of their problem-solving endeavors and the validity and utility of their solutions. For the most part, the simulations and tools found in The BioQUEST Library are not tutorials, although there are some tutorials included. Most modules will require nearly the same preparation and background knowledge as actual laboratory investigations.

The modules in The BioQUEST Library are divided into six sections—the BioQUEST Collection, the Collection Candidates, the First Review folder, the Learning Resources folder, the Software Archives folder, and the Support folder. Each of these sections corresponds to one of the levels of software review that all of the modules in the Library must go through.
The BioQUEST Collection

The BioQUEST Collection is the heart of The BioQUEST Library. The modules in the BioQUEST Collection folder have been selected through an intensive peer-review process which involves extensive review, testing and validation in actual classroom use.

Introduction to BioQUEST: Problem-Posing, Problem-Solving, and Persuasion in Biological Investigations

John R. Jungck (Beloit College),
Jim Stewart (University of Wisconsin - Madison),
Nils S. Peterson (Washington State University)

A text chapter that introduces and explores some of the key issues in the 3Ps (Problem-posing, Problem-solving, and peer Persuasion) philosophy behind the activities of the BioQUEST Curriculum Consortium and the material included in The BioQUEST Library.

This document is available in Adobe Acrobat PDF format or Microsoft Word 98 format.

New Version – Biostatistics Tutorial Now Available for Macintosh and Windows

Biometrics and Biostatistics

Daniel Hornbach (Macalester College)

The Biometrics text module and the Biostatistics tutorial encourage students to explore some of the factors that influence the choice of an appropriate statistical test and to understand why they might decide to use a particular test, not just how they would use it. The Biometrics chapter presents an explanation of statistical analysis and its underlying philosophy. Students learn how to design the systematic collection and organization of their data so their hypotheses can be appropriately tested. Biostatistics is an interactive, hyperlinked tutorial that is designed to support the Biometrics text manual. Students decide, based on their own data, which statistical tests are the most appropriate for their situation.

The Biometrics text is available in Adobe Acrobat PDF format or Microsoft Word 98. A web browser such as Internet Explorer or Netscape is needed to use the Biostatistics tutorial.

Biota


Biota is a rich system for modeling and simulating population dynamics. It supports the study of multiple species in diverse environments with migration between regions and multiple species interactions. An integrated set of "field tools" is also provided so that pre-authored models can be used as "black box" problems for simulated field studies.

Macintosh or Power Macintosh.
Data Collection and Organization (DC&O)

Frank Price (Hamilton College)

The Data Collection and Organization text module is designed to give the student background and experience with some useful, commercially available, general-purpose software tools. This text – used in conjunction with a database, spreadsheet, and other generic productivity tools of the instructor's choice – provides a tool-oriented introduction to scientific data collection and organization.

This document is available in Adobe Acrobat PDF format or Microsoft Word 98 format.

Includes New Java Version for Macintosh and Windows

Demography

Daniel Udovic, Jasper Barber, Will Goodwin, and Gordon Hennesy (University of Oregon)

Demography is an application that simulates exponential growth in age-structured populations. By manipulating values for age-specific mortality rates, fertility rates, and initial population characteristics, and using the simulation to see how population characteristics change through time, users of Demography can investigate important questions in population biology, develop a deeper understanding of fundamental population concepts, and explore issues related to population policy.

Standard Version: Macintosh or Power Macintosh
Java Version: Macintosh Power PC and Windows

Environmental Decision Making (EDM)

Elisabeth C. Odum (Santa Fe Community College), H.T. Odum (University of Florida–Gainesville), and Nils S. Peterson (Washington State University)

With Environmental Decision Making, students use “connect-the-components” visual programming tools to create and study model ecosystems. Students build models of increasing complexity, which can include social and economic forces, and study parameter variations to develop an understanding of ecosystem function and productivity.

Macintosh, Power Macintosh, and Windows

Evolve

Frank Price (Hamilton College), and Virginia Vaughan (BioQUEST Curriculum Consortium)

Evolve allows students to model evolution and get quick results from population genetics experiments that would be impossible to perform in the usual classroom laboratory. Students can pose a variety of questions involving Hardy-Weinberg equilibrium, selection, genetic drift, and gene flow, singly and in combination, to gain an understanding of evolutionary processes and interactions. Users may control the starting population size, overall population size, intensity of natural selection, pattern of inheritance and proportion of migration in a hypothetical population.

Macintosh or Power Macintosh.
Genetics Construction Kit (GCK)  
John N. Calley (University of Arizona), and  
John R. Jungck (Beloi College)

*Genetics Construction Kit* is a simulation of a classic Mendelian genetics laboratory. It provides students with a set of organisms with unknown patterns of inheritance, and gives them the tools to design and perform experiments to discover these inheritance patterns. The students are able to cross the unknown organisms and analyze the crosses in ways much like those used by practicing scientists.  
*Macintosh or Power Macintosh.*

Isolated Heart Laboratory (IHL)  
Nils S. Peterson (Washington State University), and  
Virginia G. Vaughan (BioQUEST Curriculum Consortium)

The *Isolated Heart Laboratory* is a software simulation that explores the pressure-volume relationships found in hearts in a variety of physiological states. The *IHL* simulation allows the student to explore how the ventricle of the heart performs as a blood pump and how changes in the physiological environment can alter its performance. By manipulating the variables that affect the performance of the heart, students can design experiments to investigate a variety of questions.  
*Macintosh or Power Macintosh.*

Modeling  
William Wimsatt (University of Chicago) and  
Jeff Schank (Indiana University)

In this text-based module students explore how to use, analyze, and criticize some important and historically influential models in biology. Using a variety of modes of visualization provided by the *Logistic Growth* and *Blending Inheritance* programs (also available on the CD) students explore mathematically simple models in ecology and population genetics, two disciplines that have a long-standing tradition of model-building.  
*This document is available in Adobe Acrobat PDF format or Microsoft Word 98 format.*

SequenceIt!  
Allen Place and Tom Schmidt (Center of Marine Biotechnology, University of Maryland Biotechnology Institute)

*SequenceIt!* is a simulation program that allows students to experience the art and logic of protein sequencing through experimentation. Students have access to most common lab techniques as they design and carry out analyses of polypeptides of unknown lengths and sequences. Unknown sequences can be computer-generated or user-generated for various levels of difficulty.  
*Macintosh or Power Macintosh.*
Collection Candidates

Modules in the Collection Candidates folder are in the third stage of review. All have successfully completed a cycle of classroom testing and review and have been approved for further review and evaluation.

To be included in the Collection Candidates section of The BioQUEST Library, all materials and/or software must be fully usable in a classroom setting. All materials must have received an initial round of classroom testing. Additionally, they must have passed through, at minimum, one iteration of review, revision, testing, evaluation, and post-evaluation revision.

Axon

Robert Macey (University of California - Berkeley) and John N. Calley (University of Arizona)

Axon is a simulation of the classic Hodgkin-Huxley (1952) model for axon excitation formulated from their voltage clamp measurements upon the squid axon. It provides a simulated excised peripheral nerve from a squid and allows the student to perform experiments by setting the environment of the axon, applying stimuli or clamps, and generating one or more action potentials. Students can create experiments which explore a variety of nerve properties, such as threshold, refractory period, accommodation, and summation.

Macintosh or Power Macintosh.

Virtual Laboratory, a completely rewritten and updated version of the Axon software, is also available in the Collection Candidates section of the Library.

Includes EcoBeaker BQ, a Limited Version of EcoBeaker 2.0

EcoBeaker

Eli Meir (University of Washington)

EcoBeaker is an ecological simulation program designed primarily for use in the classroom although it can also be useful for researchers interested in quickly constructing ecological models. EcoBeaker creates a two-dimensional world on the computer, upon which you can place creatures whose behaviors you design. You can then watch as the creatures eat, reproduce, move around, die, and do all the other things that creatures normally do, observing patterns that you can compare against patterns seen in the real world and patterns predicted from various ecological theories.

Original EcoBeaker: Macintosh
EcoBeaker BQ: Macintosh and Windows
Includes New Java Version for Macintosh and Windows

**Epidemiology**

Daniel Udovic and Will Goodwin (University of Oregon)

*Epidemiology* simulates the spread of an infectious disease through a population. This program allows users to graphically enter population and disease characteristics (e.g., the virulence of the pathogen, the likelihood of transmission), to set up an initial population, and then to observe the changes in population characteristics and the prevalence of the disease through time. Using modified SIR-type models (Susceptible-Infected-Recovered), *Epidemiology* allows students to ask a variety of “what if” questions, to design and perform their own investigations, and to explore the implications of various public health policies.

*Standard Version: Macintosh or Power Macintosh*

*Java Version: Macintosh Power PC and Windows*

**Fractal Dimension**

Center for Polymer Studies (Boston University)

*Fractal Dimension* is a tool for measuring and analyzing the fractal dimensions of objects, including scanned in images of a variety of biological specimens that are usually considered fractured, fissured, or fingered. Images can be measured by the box or circle method any number of times, using different measurement sizes. It is also possible to measure the perimeter of an object or the fractal dimension of the perimeter. The results of accumulated measurements can be displayed in tabular form in the data window or graphed in the graph window.

*Macintosh or Power Macintosh.*

**MacRetina**

Richard F. Olivo (Smith College)

*MacRetina* simulates an experiment in which students record data from retinal ganglion cells. By sampling neural activity while stimulating with small spots of light, students can see the dynamic excitatory and inhibitory responses of these neurons, and map the organization of the retinal region that drives each cell. *MacRetina* is modeled accurately on published data and is a realistic simulation of a lab experiment that would otherwise be beyond the reach of the typical undergraduate laboratory.

*Macintosh or Power Macintosh.*
Microbial Genetics Construction Kit (µGCK)  
John N. Calley (University of Arizona), and  
John R. Jungck (Beloit College)

*Microbial Genetics Construction Kit* is a simulation of a microbial genetics laboratory that allows students to explore auxonography, complementation, and conjugation of unknown bacteria. The simulation provides a set of unknown bacteria on a petri plate or in a test tube. Using tools similar to those used in a real laboratory - serial dilution, phenotype identification by replica plating, complementation testing, and conjugation mapping - students can investigate many of the characteristics of these bacteria. *µGCK* enables students to work with problems that have the complexity of realistic scientific research.

Macintosh or Power Macintosh.

Modeling Tools

*Logistic Growth*  
*Blending Inheritance*  
Jeff Schank (Indiana University),  
and William Wimsatt (University of Chicago)

The *Logistic Growth* and *Blending Inheritance* programs are designed to accompany the text module *Modeling*. These programs allow users to explore mathematically simple models that are important in ecology and population genetics using various visualization modes. The *Logistic Growth* program provides a number of ways to graphically analyze, interpret, and understand the behavior of the logistic growth equation and the minimum density limited logistic growth equation. The *Blending Inheritance* application is used to explore the uses and effects of "false models". This kind of simulation (i.e., a simulation based on what we now accept as a false model of inheritance) can be crucial for understanding why we accept certain theories as opposed to their competitors and may help us understand the similarities and differences between these theories.

Macintosh or Power Macintosh.

New in Volume VI

Virtual Laboratory

Robert Macey and Tim Zahnley (University of California - Berkeley)

*Virtual Laboratory* is a simulation program based on the Nobel Prize winning Hodgkin-Huxley model for excitation of the squid axon. The program simulates an excised squid axon by applying stimuli or clamps after setting the environment of the axon, changing its properties, and/or adding drugs or toxins. By using the program tools, experiments can be developed that explore a variety of nerve properties, ranging from classical phenomena such as threshold, summation, refractory period, and impulse propagation to more modern concepts of channels, gates, and eventually even molecular events. *Virtual Laboratory* is a completely rewritten and updated version of the Axon software.

Macintosh or Power Macintosh.
The modules in the First Review Folder are in the second stage of the review process. These modules have passed a preliminary review by the BioQUEST Curriculum Consortium staff and are presented here for classroom testing and evaluation.

**BeeVisit**

*Barbara Thomson and James Thomson (State University of New York-Stony Brook)*

*BeeVisit* is an interactive model of pollen transfer that enables students to evaluate the relative contributions of different pollinator species to a plant’s reproductive success. The model tracks a plant’s presentation of pollen through time. Pollen may be presented gradually or all at once, and the program lets you choose from a family of power curves to model the shape of the cumulative pollen presentation curve over a set number of time intervals.

**Windows**

**BENZER: An Interval Graph Tool for Deletion Mapping, Restriction Mapping, Complementation Mapping, Sequencing, & Food Web Analysis**

*John R. Jungck (Beloit College), Vince Streif (University of Wisconsin-Madison), Ivica Ceraj (University of Zagreb), and Stephen J. Everse (University of Vermont)*

*BENZER* is a software program that uses the matrix manipulation approach developed by Shkurba in 1965 to investigate a variety of biological problems related to the “Benzer problem.” Most students find Shkurba’s approach easier to use than the graph theoretical approach. *BENZER* can be used to generate problem sets, to interactively solve problems from actual biological experiments by heuristic matrix manipulation, and to automatically solve problems with a built-in algorithm that recognizes incompatibilities in datasets.

**Windows**

New in Volume VI

**BGuILE: Biology Guided Inquiry Learning Environments**

**The Galapagos Finches – The Struggle for Survival**

*Iris Tabak, Brian J. Reiser, William Sandoval, T.J. Leone, and Francis Steinmuller (BGuILE Project, Northwestern University)*

*The Galapagos Finches* is a software application that depicts an episode on the Galapagos island, Daphne Major, where a prolonged drought caused a severe decline in the population of ground finches. Using the data and tools in the software, students are asked to explain why so many finches in the population are dying, and more importantly, what enables the surviving finches to survive. The goal of *The Galapagos Finches* software is to help students understand how variation, structure-function relationships, and environmental changes interact in the process of natural selection.

**Macintosh**
New in Volume VI

**BGuILE: Biology Guided Inquiry Learning Environments**

**TB Lab—Antibiotic Resistant Bacteria**

William Sandoval, Brian J. Reiser, Renee Judd, and Richard Leider
(BGuILE Project, Northwestern University)

*TB Lab* is a simulated microbiology laboratory for the Macintosh that allows users to explore how the bacteria responsible for the disease tuberculosis develop resistance to antibiotics. Students perform simulated experiments on strains of *Mycobacterium tuberculosis* to investigate how antibiotics affect bacteria and how bacteria can become resistant to antibiotics. The simulation is designed to help students understand the direct connection between genetic differences and structural differences, particularly as they potentially lead to a survival advantage in the face of a selective pressure.

Macintosh

New in Volume VI

**Biology Student WorkBench—Problem Solving with Molecular Data**

Sam Donovan and Ethel Stanley (Beloit College), and
Chip Bruce, Kris Engelsen, Eric Jakobsson, and Umesh Thakkar
(University of Illinois at Urbana-Champaign)

The *Biology Student WorkBench* is a web based collection of teaching and learning resources including problem sets, investigative laboratories, and tutorials that support the use of molecular data to address biological questions. By linking rich data sources and powerful analysis tools to concrete biological problems, this module helps students build biological meaning from sequence and structure data. The curricular resources in the *Biology Student WorkBench* take advantage of the Biology WorkBench, a publicly available web-based tool for finding, analyzing, and visualizing molecular data. (http://glycine.ncsa.uiuc.edu/educwb)

The text portions of this module are available in Adobe Acrobat PDF format and Microsoft Word 98 format. An internet connection is needed to make full use of the resources.

Macintosh

New Version

**BIRDD: Beagle Investigations Return with Darwinian Data**

Frank Price (BioQUEST, Hamilton College), Sam Donovan (Beloit College, University of Wisconsin -Madison), Jim Stewart (University of Wisconsin - Madison), and John R. Jungck (Beloit College)

*BIRDD* is a rich collection of primary scientific data and supporting materials about the Galápagos Islands and Darwin’s finches. *BIRDD* provides information ranging from island names, maps, and weather, to summaries of taxonomy song recordings, DNA and protein sequences, and measurements of specimens. These resources are organized in a database that is easy to navigate, view, and print. Users can export data to spreadsheets, statistics packages, image analysis, DNA analysis, systematics, and other software. The new version includes expanded datasets and numerous examples and suggestions for classroom use and for teaching evolution.

Macintosh and Windows
Convince Me

Patricia Schank, Michael Ranney and Christopher Hoadley
(University of California–Berkeley)

Convince Me is a computer program designed to help students learn to think about their own reasoning strategies. The program provides a structure within which students can explicitly define and quantify their reasoning on a problem or argument and then attempt to “convince” the computer program of the validity of their reasoning. By repeatedly testing and refining the coherency of their arguments, students are encouraged to critically examine their reasoning.

Macintosh or Power Macintosh

Curaçao

Phil Arneson and Barr E. Ticknor (Cornell University)

Curaçao is a computer program that simulates the use of the sterile insect release (SIRM) method to control an insect population on a small island. The user can investigate the effects of several variables on the effectiveness of the method and determine what happens when some of the basic assumptions of the model are relaxed or violated in some way.

Windows

New in Volume VI

Developmental Selection: Seed Abortion and Pollen Tube Competition

Donald Buckley (Quinnipiac University), and Martin Cohen (University of Hartford)

The Developmental Selection module is a research simulation that allows students to investigate the possible causes of incomplete embryo development in perennial legume fruits. Two competing hypotheses are proposed to explain patterns of seed abortion —the pollen tube competition hypothesis and the maternal resource limitation hypotheses. Students can explore these competing hypotheses by setting up experimental problems and then collecting and analyzing their data.

Macintosh

Diffusion Laboratories

Ben Jones (Beloit College), and Douglas Green (St. Michael's College)

The Diffusion Laboratories are two simulations that explore mathematical models of embryological pattern formation. Particle Diffusion introduces students to the behavior of particles moving at random in a liquid, such as water. The software provides tools for manipulating particles which diffuse across a cell matrix, interacting with it using the Gierer-Meinhardt reaction-diffusion equations. Pattern Formation simulates some of the theories that attempt to explain how regular patterns form in development of embryos. Pattern Formation provides several tools for experimenting with the Gierer-Meinhardt reaction-diffusion equations from both experimental and theoretical points of view.

Macintosh or Power Macintosh
**DNA Electrophoresis/Southern Blotting—Case It! v3.0**  
*Mark Bergland and Karen Klyczek (University of Wisconsin-River Falls)*

DNA Electrophoresis is an open-ended simulation which cuts any DNA sequence with any combination of restriction enzymes, runs realistic gels and Southern blots of the resulting DNA fragments, and converts DNA fragments to mapping fragments for restriction mapping. A Resource Manual describes several case studies that were developed using DNA sequences obtained from GenBank via the Internet. The new version includes Case It Investigator, an organizing tool with links to internal html pages and external web sites and a revised and expanded Resource Manual.

*Macintosh and Windows*

**New in Volume VI**

**Endangered Species Laboratory with RAMAS® EcoLab**  
*Sheryl L. Soucy, Steven D. Carroll, and Lev R. Ginzberg (Applied Biomathematics)*

In the Endangered Species Laboratory, students use population models to explore the effects of changes in survivability, fecundity, and variability upon the probability that a species will become extinct. Students create and run models of a Brook Trout population and a Northern Spotted Owl population. The task at hand is to devise several conservation strategies (each of which would affect a change in one or more of the parameter values) and to compare them using the RAMAS® EcoLab software.

*Windows*

**HH: A Hodgkins-Huxley Neuron Simulation**  
*Mark Dimaline, Randell Beer and Hillel Chiel (Case Western Reserve)*

HH is a program that graphically models the physical and electrical characteristics of a multiple compartment neuron with Hodgkin and Huxley’s voltage-gated potassium and sodium ion channels. Each compartment can be stimulated by injecting an electrical current and the voltage of each compartment can be clamped at one to six constant levels. The resulting system of equations is numerically integrated with the exponential technique and the time course of various compartment components is plotted in graph windows.

*Macintosh or Power Macintosh.*

**Image Analysis**  
*Robert Blystone and Richard Cooper (Trinity University)*

The Image Analysis module is a set of data resources and text guides that introduces students to digital imaging analysis. Using NIH-Image (Macintosh) or Scion Image (Windows) and the included images of starfish embryos in cleavage, students learn some techniques for estimating the size of an image, get a brief introduction to sampling theory, create a model of the "ideal" image, and learn to analyze their own images to find the ones that best fit their model.

*The text portions are available in Adobe Acrobat PDF format and Microsoft Word 98 format. NIH-Image (Macintosh) or Scion Image (Windows) is needed to make full use of the materials.*
Inherit

Ben Jones, Patti Soderberg, and John R. Jungck (Beloit College)

Inherit is a pedigree drawing and analysis tool that can be used in educational, clinical, and research settings. Using Inherit you can explore questions regarding the role of inheritance in human traits and syndromes. It allows you to enter a variety of data for members of a pedigree, and to change the display to reflect the presence or absence of combinations of medical symptoms, background information, your own diagnoses, or any type of data you care to enter.

Macintosh or Power Macintosh.

Interactive Calculus Problems in Biology

Joseph M. Mahaffy (San Diego State University)

The Interactive Calculus Problems in Biology module provides a set of calculus problems that address some of the mathematical issues underlying the models and theories that students commonly encounter in their biology courses. The module consists of a series of labs developed for a two-semester “Calculus for Life Sciences” course in which students interested in biology, chemistry, medicine, and other fields use Maple ™, a commercially available symbolic algebra system, to solve bioscience-oriented calculus problems.

Macintosh and Windows

New Version

Investigative Case-Based Learning (ICBL)

Margaret A. Waterman (Southeast Missouri State University) and Ethel Stanley (Beloit College)

This text and web based module focuses on the use of narrative cases as a way to initiate student-centered investigation. Cases are descriptions of richly complex, realistic situations and the people, organisms, and systems involved in those situations. Three cases in multiple parts are presented in “Kingdoms Entangled: Molecules, Maize, and Malaria.” The cases all share a central event that organizes the action, namely a blight of corn caused by a fungus. In addition to the cases, there are multiple resources for both students and instructors. In the new version the case and selected resources are now accessible using a standard web browser, new cases have been linked to the module and examples of classroom assignments have been added, and the resources have been updated and extended

This document is available in Adobe Acrobat PDF format and Microsoft Word 98 format.
LateBlight

Phil Arneson and Barr E. Ticknor (Cornell University)

The LateBlight application is a simulation that allows students to manipulate the variables that affect the development of late blight, a disease of potatoes and tomatoes caused by the fungus Phytophthora infestans, and to adjust the economic parameters that determine the cost-effectiveness of the disease management procedures. Students can vary the weather conditions, the characteristics of the potato cultivar they are simulating, the amount of initial inoculum, the production costs and market price for the harvested potatoes, and what sort of fungicide to apply and when to apply it.

Windows

Metabolic Pathways

Brian White (Massachusetts Institute of Technology), John W. Moon, Jr. (Harding University), Jülyet Benbasat (University of British Columbia), Presley Martin (Drexel University), and Allen Place (University of Maryland Biotechnology Institute)

The Metabolic Pathways module is designed to allow the user to model multistep pathways of enzymatic and non-enzymatic chemical reactions. The model allows the user to change kinetic and thermodynamic properties and observe their effects on the concentrations of the compounds in a pathway over time.

Macintosh, Power Macintosh, and Windows

Morphogenetic Construction Kit

Douglas Green (St. Michael's College)

The Morphogenetic Construction Kit provides students with a virtual lab where they can examine mathematical models of developmental pattern formation. The main object in the laboratory is a one-dimensional tissue of cells that represents a developing embryo. The cells contain different concentrations of an activator compound. Students can use various tools to determine which of several mathematical models might cause the observed patterns, or they can systematically assess the behavior of the models by varying parameter values and correlating them with the patterns that result.

Windows

PEACH

Yaffa L. Grossman (Beloit College), Theodore M. DeJong (University of California, Davis), and Scott FVosburg (Independent Software Developer)

PEACH simulates the annual carbon supply and demand in peach trees. Calculations represent the amount of carbon produced in photosynthesis and the amount of carbon used for growth and respiration. The program simulates tree growth on a daily basis for one growing season and can show the effects of different
environments on tree growth and crop yield. Students may use *PEACH* to test their understanding of integrated plant growth. Peach also models typical horticultural operations such as thinning and pruning.

**Windows**

**Phylogenetic Investigator**

![Phylogenetic Investigator logo](image)

*Steven Brewer and Robert Hafner (Western Michigan University)*

**Phylogenetic Investigator** is designed to facilitate creative problem-solving in phylogenetic analysis for the purpose of teaching and learning phylogenetic inference. Students can identify characters and states, polarize characters, and engage in directed-search phylogenetic tree construction. It allows students to make inferences and represent them one step at a time, vary representational features of their trees, create reticulate tree patterns, and view all of the character transformations at one time. In addition, *PI* can generate plausible data stochastically for modeling and practicing tree construction.

*Macintosh or Power Macintosh.*

**PurifyIt!**

![PurifyIt! logo](image)

*Allen Place and Tom Schmidt (Center of Marine Biotechnology, University of Maryland Biotechnology Institute)*

**PurifyIt!** is a simulation laboratory for protein purification and characterization. The program generates a mixture of proteins whose composition and quantity can be defined or unknown. Using the tools available to a biochemist, the student designs a purification strategy which will provide a pure preparation of the protein with the highest yield.

*Macintosh or Power Macintosh*

**RateIt!**

![RateIt! logo](image)

*Allen Place and Tom Schmidt (Center of Marine Biotechnology, University of Maryland Biotechnology Institute)*

**RateIt!** allows users to experience the art of enzyme kinetics through experimentation. The program can select a set of solutions containing enzymes, substrates, inhibitors, etc. The objective is to deduce and characterize the kinetic properties of an enzyme-catalyzed reaction using all the tools available to a enzymologist. You can also define the kinetic properties of an enzyme and then

*Macintosh or Power Macintosh*
**Resistan**

Phil Arneson and Barr E. Ticknor (Cornell University)

*Resistan* is a mechanistic simulation model of the process of selection of fungicide-resistant biotypes of a hypothetical fungal pathogen of a hypothetical crop. *Resistan* can be made to simulate different fungi and different fungicides by changing the parameters that control the model. All of the parameters, including several of the options and the initial values of many of the variables, can be changed during execution of the program.

*Windows*

**Sampling**

Daniel Udovic, Gordon Hennesy, and Will Goodwin (University of Oregon)

*Sampling* is a computer tool designed to help biology students obtain a qualitative understanding of basic concepts related to estimation and statistics. The program presents the user with a group of hypothetical populations distributed throughout an area, and with tools for sampling these populations to estimate characteristics such as population size and density, the nature of each population’s spatial patterning, and spatial correlations in abundance between populations.

*Macintosh and Power Macintosh.*

**SimBio2—Simulating Biosphere 2**

Elisabeth C. Odum (Santa Fe Community College) and H.T. Odum (University of Florida - Gainesville)

*SimBio2* is a simulation of Biosphere 2, the giant glass chamber constructed in Arizona to enable scientists to study the ecology of the earth (Biosphere 1). *SimBio2* offers several scenarios using actual data from the Biosphere 2 experiment that students can use to generate simulation graphs and to explore some of the problems that could, or did, affect Biosphere 2. The module includes *EarthSys—A Minimodel of Earth Metabolic Processes*. *EarthSys* is a whole-earth (Biosphere 1) simulation similar to *SimBio2*. This mini-model of earth’s metabolism in the thin outer geobiosphere includes photosynthetic production, input of fossil fuels, and consumption by nature and the human urban civilization.

*Macintosh and Windows*

**Wading Bird**

Wilfried Wolff (KFA - Jülich, Germany)

*Wading Bird* simulates behaviors (such as feeding nestlings, searching for fish, flying to nest, foraging, and idle time) of a nesting colony of birds. The model is an individual-oriented model in which a population of interest is modeled as an
Learning Resources

The Learning Resources folder contains high-quality tools, demonstrations, and other material whose primary focus is to provide collateral support for research-based learning or to offer background information on a particular topic.

New in Volume VI

4D Data Visualization with 4D Viewer

Kevin Eliceiri and Charles Thomas (University of Wisconsin – Madison)

4D microscopy is the study of three-dimensional specimens as they grow or change over time. The 4D Viewer is part of a suite of software applications developed by the Laboratory for Optical and Computational Instrumentation which allow researchers to perform 4D studies on Macintosh computers. The program allows the viewing, analysis, and annotation of a 4D dataset. The user can roam through a 4D dataset backward and forward in time while simultaneously moving up or down in focus through the sample.

Macintosh and Power Macintosh

Action Potential Experiments

Mark Bergland (University of Wisconsin-River Falls)

Action Potential Experiments is a demonstration/simulation laboratory for neurophysiology based on the "sodium theory" as originally formulated and tested by A. L. Hodgkin and his colleagues. The application includes simulations of the original experiments of Hodgkins and his colleagues, and of the classic voltage clamp and patch clamp experiments.

Macintosh, Power Macintosh, and Windows

Cardiac Dynamics Introduction

Nils S. Peterson (Washington State University)

The Cardiac Dynamics Introduction is a tutorial composed of four HyperCard stacks. The Cardiac Dynamics Intro stack, The Heart Plumber’s Kit, the Pressure-Time animation, and the Pressure Volume Loop animation - that can be used to explore some of the basic dynamics of the heart.

Macintosh or Power Macintosh.
**New in Volume VI**

**Cell Differentials: A White Blood Cell Identification Exercise**  
*Donald Buckley and Deborah Clark (Quinnipiac University) and Karen Barrett Lynn Gugliotti and JoAnne Morrica (University of Hartford)*

*Cell Differentials* offers a visual dataset of white blood cells that gives students practice in developing strategies and techniques for the recognition of these blood cell types. Over 100 different cell images are randomly presented with feedback on successful identification. *Cell Differentials* was developed as a wet lab preface to provide students with abundant real-time feedback and tools to evaluate their own learning progress.

*Macintosh*

**New in Volume VI**

**Geographical Information Systems & Student Research: An Introduction**  
*Marc Albrecht (University of Nebraska – Kearney)*

A geographical information system (GIS) is a computer-based tool for holding, displaying, manipulating, and analyzing large amounts of spatial data. This module presents a brief introduction to GIS through two PowerPoint presentations. The first presentation, “What Is GIS?”, presents some of the basics of GIS, including a discussion of mapping systems and vector and raster data representations. It then gives some examples of some GIS operations such as proximity analysis, overlay analysis, and spatial analysis. The second presentation, “GIS Resources and Projects,” continues this discussion by showing numerous project ideas and examples of investigations that would be feasible in the classroom. Possible sources of data are discussed as well as the basics of what you need to get started.

*The PowerPoint Viewer is required to view the presentations. Versions of the Viewer for both the Macintosh PPC and Windows 95/98 are included on the CD.*

**New in Volume VI**

**Search for the Hereditary Molecule: Avery Transforms the Search**  
*Donald Buckley (Quinnipiac University) and William Coleman (University of Hartford)*

*Avery* is a research simulation that gives students control of a famous investigation—the historic first demonstration that the hereditary molecule is DNA. The simulation provides students with the tools used by Oswald Avery and his colleagues to test whether the hereditary molecule is protein, RNA, or DNA.

*Macintosh*

**Taxonomic Features Data Manager**  
*Nils S. Peterson (Washington State University)*

The *Taxonomic Features Data Manager* is designed to store and edit a database of characters and states for a group of operational taxonomic units (OTUs) and to export data about selected operational taxonomic units to *MacClade 2.1* (found in the Support Materials folder) for cladistic analysis.

*Macintosh or Power Macintosh.*
A Trip to a Forest

Ray Russo (Indiana University-Purdue University at Indianapolis)

A Trip to a Forest is a simulation laboratory with accompanying tool set for quantitative exploration of an Eastern deciduous forest. Macintosh or Power Macintosh.

New in Volume VI

Using the Berkeley Madonna Modeling System

Robert Macey, George Oster, and Tim Zahnley
(University of California-Berkeley)

Berkeley Madonna is a fast, easy-to-use program for the modeling and analysis of dynamic systems. Models can be constructed using the equation editor, or you can use the flowchart editor to build models graphically. In the flowchart editor models are constructed by dragging icons from a toolbar onto a diagram. These icons are connected with arcs and flows to represent dependencies and flows between reservoirs. As you construct your model graphically, Madonna generates textual equations representing your model’s structure. Macintosh and Windows

Visual Data Sets

Ethel Stanley (Beloit College)

The Visual Datasets text module discusses the concept of visual learning and presents some suggestions for ways to design learning environments that support students in developing visual literacy skills. Three visual datasets that can be used for problem-solving activities in evolution, classification, development, and botany are included: "Caminacules", a dataset of imaginary animals, "Dendrogrammaceae", a dataset of imaginary animals, and "Oh Phlox!", a dataset of close-up images of late season garden phlox plants and selected leaves with leaf miner damage. The text documents are available in Adobe Acrobat PDF format and Microsoft Word 98 format. The datasets are available in PICT, GIF, and BMP format and can be viewed with any application capable of opening these file formats.

Winter Twig Key

Ethel Stanley (Beloit College), Joseph Armstrong (Illinois State University), and Dent Rhodes (Illinois State University)

Winter Twig Key is an interactive visual key designed to help users become familiar with features found in winter twigs or to identify deciduous trees native to Illinois. Modified from a dichotomous key to deciduous trees written by E. Lucy Braun, Winter Twig Key combines updated twig illustrations with hypertext. A brief tutorial on twig features is also available. Windows
The Software Archive folder contains “legacy” software that is still valuable, but which will no longer run reliably on the newest computers or operating systems. This software is still useful to users who have older Macintoshes or DOS machines, but it cannot be relied upon to work with Macintosh System 7 or later, or on computers running newer versions of Windows.

**Cardio-Vascular Construction Kit (CVCK)**

*Sarah Douglas and Daniel Udovic (University of Oregon)*
*Nils S. Peterson (Washington State University)*

CVCK allows students to design and construct a wide range of cardiovascular systems, testing each one to see how it behaves and whether it could actually exist and survive in a real organism.

*Macintosh (System 6.05 to System 6.07 recommended; will not run on the Power Macintosh or under System 8 or later)*

**Grafit**

*George Lisensky (Beloit College)*

A graphing tool for routine analysis and plotting of small sets of laboratory data.

*Macintosh (Will not run on Power Macintosh computers.)*

**Real Time Data Acquisition**

*Marc Roy (Beloit College)*

*Real Time Data Acquisition* is a text embedded with QuickTime movies which describes and illustrates the use and advantages of using computerized real time data acquisition systems in biology labs.

*This document is available in Adobe Acrobat PDF format and Microsoft Word 98 format.*
Support Materials

The Support Materials folder contains a collection of freeware, shareware and demonstration tools, data, and text. These materials are included here because of their usefulness in the classroom, but they are not part of the Library review process. Included in this edition are resources for image analysis, phylogenetics, systematics, neurophysiology, embryological gene expressions, modeling, and molecular biology.

Freeware/Shareware and Demonstration Software

**GENE DOC**  (Windows)
A multiple sequence alignment editor and shading utility with numerous analytical features.

*Karl Nicholas (Pittsburgh Supercomputing Center)*

**MacClade version 2.1**  (Macintosh)
A graphic program for analyzing phylogenies and studying character evolution.

*Wayne Maddison and David Maddison (University of Arizona)*

Molecular Biology Tools

*Don Gilbert (Indiana University)*

**Dotty Plotter**  (Macintosh)
A tool for drawing dot matrix comparisons of sequences in molecular biology.

**Enzyme Kinetics**  (Macintosh)
A tool to calculate and plot biochemical values for the kinetics of enzyme-catalyzed reactions.

**GelFrag Sizer**  (Macintosh)
A tool that calculates restriction fragment sizes from their mobilities.

**LoopDLoop/LoopViewer**  (Macintosh)
An RNA secondary structure drawing program in which users define the base pairings and can then manipulate the resulting secondary structure.

Molecular Visualization Tools

**Chime**  (Macintosh and Windows)
A Netscape plug-in that displays 2D and 3D molecules on a web page.

*MDL Information Systems, Inc.*

**MacMolecule2 and PCMolecule2 — Evaluation version**
A visualization program for the exploration of very large molecules.

*Molecular Ventures, Inc.*

**MAGE and PREKIN**  (Macintosh and Windows)
Two utilities that view and explore "kinemages" – scientific illustrations presented as three-dimensional, interactive computer displays.

*David C. Richardson and Jane S. Richardson (Duke University)*
Molecular Visualization Tools - continued

**RasMol** (Macintosh and Windows)
A graphics program for the visualization of proteins, nucleic acids and small molecules.

*Herbert J. Bernstein (St. Joseph's College-Long Island, New York)*

**NIH Image** (Macintosh)
A public domain image processing and analysis program.

*Wayne Rasband (National Institutes of Health)*

**Programming the Fly** (Windows)
A pilot project to investigate the integration of current theory and experimental data into a mechanism for programming *Drosophila* embryogenesis.

*John W Bodnar (United States Naval Academy)*

**SeqApp/SeqPup** (Macintosh and Windows)
Two versions of a biological sequence editor and analysis program.

*Don Gilbert (Indiana University)*

**Spike Studio** (Macintosh)
A program to digitize and analyze physiological signals for neurobiology laboratories.

*Eli Meir (University of Washington)*

**STELLA** (Macintosh and Windows)
A run-time version of an icon-based system for modeling and simulation of dynamic interrelationships within biological systems.

*High Performance Systems, Inc.*

**WinPP** (Windows)
A program for computational modeling and analysis of nonlinear dynamical systems (systems that change over time.)

*Bard Ermentrout (University of Pittsburgh)*

**Tools**

- **Adobe Acrobat Reader** (Macintosh and Windows versions)
- **HyperCard Player** (Macintosh)
- **Internet Explorer** (Macintosh and Windows versions)
- **Microsoft PowerPoint Viewer** (Macintosh and Windows versions)
- **Netscape** (Macintosh and Windows versions)
- **Simple Text** (Macintosh)

**BioQUEST Notes**

Back issues of *BioQUEST Notes*, the newsletter of the BioQUEST Curriculum Consortium, are available in PDF and HTML format. They can also be found on the BioQUEST Curriculum Consortium web site at http://bioquest.org.
General System Requirements

Requirements for individual modules vary greatly. Please see the individual module descriptions on the BioQUEST web site at http://bioquest.org.

For modules that run on the Apple Macintosh platform:

Minimum (unless otherwise indicated):

• Apple Macintosh with access to CD-ROM drive. Math coprocessor recommended for older machines.

• 8 MB of application RAM. (Application RAM is the amount of memory remaining after the memory used by the operating system.)

• System 7.61 or higher.

Recommended (unless otherwise indicated):

• At least a Macintosh PowerPC.

• At least 16 MB of application RAM. (Application RAM is the amount of memory remaining after the memory used by the operating system.)

For modules that run on the PC (IBM compatible) platform: (unless otherwise indicated)

• Windows 95 or later (and Win32s 1.2 or later for some modules).

• 80386 processor or greater (80486 or Pentium recommended).

• At least 4 MB of RAM.

Accessing the online documentation:

The online documents are available in both Adobe Acrobat format (not editable) and Microsoft Word 98 format (editable). The Acrobat Reader, provided on the CD in the Support Materials folder, is required to access the documents in the Adobe Acrobat format. The Macintosh version requires System 7.0 or greater; the Windows version requires Windows 3.1, Windows 95, Windows NT 3.5, or later. Software that recognizes Microsoft Word 98 format is needed to access the documents in MSWord format.

Using Cross-platform Emulators

Many of the Macintosh compatible modules in the Library can be run in Windows by using software that emulates the Macintosh operating system on a PC. Similarly, many of the PC compatible modules can be run on a Macintosh by using a Windows emulator. For more information see the BioQUEST web site (http://bioquest.org).
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The BioQUEST Library is a project of the BioQUEST Curriculum Consortium and is published by Harcourt/Academic Press. The Library package contains two CDs, one for Macintosh and one for Windows. Each CD contains all of the Library modules that will run on that platform. All of the documentation and other related information is available in electronic form on both CDs.

Volume VI of the Library can be purchased from Harcourt/Academic Press in single user packages or multiple user Lab Packs.

Three different types of packages or Lab Packs are available:

- An Individual Package for one user: $149.95 + tax
- A Lab Pack of 3 boxes: $295.00 + tax
  Valid for up to 3 individual users at the same time;
- A Lab Pack of 10 boxes: $695.00 + tax
  Valid for up to 20 individual users at the same time.

Networked or distributed learning users should make a good faith estimate of the maximum number of simultaneous users and buy the appropriate number of packages. Special licensing terms can be arranged for institutions with more than 60 simultaneous users (more than three ten-package lab packs.)

To order in the US and Canada:
  - For individual users, call 1-800-321-5068 Ext 2566
  - For Lab Packs (multiple users), send email to: textbook@acad.com
For international orders: cservice@harcourt.com

For additional information, visit the BioQUEST Curriculum Consortium website: http://bioquest.org.
The BioQUEST Curriculum Consortium

The BioQUEST Curriculum Consortium is a community of bioscience educators and researchers who are involved in undergraduate science curricular reform. The Consortium is a community of individuals who are interested in issues related to teaching and learning biology, the use of technological innovation, and the potential impact of these technologies on learning theory and the structure of schools. Members of the consortium represent a diverse range of subject areas as well as educational levels. Most of the members are from colleges and universities, but the number of middle school and high school educators is rapidly growing.

The Consortium believes that students learn science most effectively when they are provided with opportunities to solve complex problems using the same methodologies and reasoning skills that research scientists use. In other words, students should have the opportunity to develop the long-term strategies of inquiry that sustain and guide practicing scientists. This philosophical framework has become known as BioQUEST’s 3Ps of science education: that is, that science, and therefore science learning, involves Problem-posing, Problem-solving, and the Persuasion of peers.

For more information on the activities of the BioQUEST Curriculum Consortium, please visit our website at:
http://bioquest.org

Funding

Major funding for the BioQUEST Curriculum Consortium has been provided by:

The Annenberg/CPB Project

Major additional support has been provided by:

The National Science Foundation’s Division of Undergraduate Education,

The Howard Hughes Medical Institute

The Education, Outreach and Training Partnership for Advanced Computational Infrastructure (EOT-PACI) program, part of the NSF Partnerships for Advanced Computational Infrastructure (NSF PACI) project,

The Foundation for Microbiology, and

Apple Computer.