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INTERNATIONAL CENTRE FOR THEORETICAL PHYSICS
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FOURTH AUTUMN COURSE ON MATHEMATICAL ECOLOGY

(24 October - 11 November 1994)

"Limitations of Reductionist Approaches in Ecological Modeling: Model Evaluation, Model Complexity, and Environmental Policy"

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These are preliminary lecture notes, intended only for distribution to participants.

Software for Teaching and Research in Ecology

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4th Autumn Course in Mathematical Ecology

ICTP. Trieste - October - November 1994

The below is in no way meant to be a complete survey of resources available to aid student training and research. rather it is designed to be a stepping stone from which you may jump off to many other resources availablefreely on various computer networks, and as a means of summarizing some of the software which I have found to be useful. The below is broken into two sections: the first deals with resources available over the Internet and the second deals specifically with descriptions of particular software.

Internet Guidance:

One of the best guides to getting started on the Internet, designed inparticular for biologists is:

A Biologist's Guide to Internet Resources
Version 1.7, 10 November 1993

ISSN: 1071-9857
by Una Smith (smith-una@yale.edu)
Yale University, Department of Biology, Osborn Memorial Laboratories,
PO Box 6666, New Haven, Connecticut 06511-8155 USA

This contains info on USENET, LISTSERVs, etc. Below is just the section on Biological Information Archives after the info on how to get the full Guide:

1.3. How to Get the Latest Version

This guide is updated more-or-less monthly. The most current version is available via Usenet, gopher, anonymous FTP and e-mail. Please do not ask the author to send you a copy, nor refer others to the author.

- In Usenet, look in sci.bio or sci.answers.

- Gopher to sunsite.unc.edu, and choose this sequence of menu items:

Sunsite Archives
Ecology and Evolution

Or, from any gopher offering other biology gophers by topic, look for the menu item "Ecology and Evolution [at UNC and Yale]". The guide is stored there in two ways: as a file for easy retrieval

and as a menu for browsing.

- FTP to rtfm.mit.edu. Give the username "anonymous" and your e-mail address as the password. Use the "cd" command to go to the directory

| pub/usenet/news.answers/biology/guide/

| and use "prompt" and "mget *" to copy all 6 parts of the guide to your computer. For information about how to get many other useful documents from this archive, send the message "help".

You can also use anonymous FTP to sunsite.unc.edu, where this guide is stored as
pub/academic/biology/ecology+evolution/FAQ

- Send e-mail to mail-server@rtfm.mit.edu with the text

| send usenet/news.answers/biology/guide/*

| You will receive 6 files in response, one for each part: save each part separately, delete the e-mail headers and footers, and merge them.

3. Biological Information Archives

Many archives are mentioned throughout this section and elsewhere in this document. The access methods available for each archive are presented in section 3.5, List of Archives.

A number of people have begun to organize the many free biological information archives, databases and services on the Internet into well-organized menus using gopher servers. These include Don Gilbert's IUBio service on ftp.bio.indiana.edu and Mike Cherry's collection on weeds.mgh.harvard.edu in the United States, Rob Harper's "Finnish EMBnet BioBox" on gopher.csc.fi in Finland, and Reinhard Doelz's "Information servers in biology (gopher based)" on gopher.embnet.unibas.ch in Switzerland.

Yanoff (1993) is an excellent list of unusual and useful Internet services, a few of which are mentioned in this guide. Services listed include: an on-line dictionary, weather maps, a general weather report service, an archive of statistical programs and data sets, and various computers allowing public telnet sessions so that people who have Internet access but not Usenet can read and post Usenet articles.

Stern (1993b) offers an extensive list of anonymous FTP archives offering meteorological data.

|| Reinhard Doelz's Biocomputing Survival Guide (Doelz 1993) covers basic
|| Unix and VMS commands and the GCG software.

-*- 3.1. Bibliographies

Many Internet archives have searchable bibliographic databases, complete with abstracts. Only a few are mentioned here.

A bibliography of 52,000 Drosophila research publications, dating from 1684 through this year, is offered on ftp.bio.indiana.edu.

The US Department of Energy (DOE) Climate Data bibliography and the NASA Global Change Data Directory are archived on ridgisd.er.usgs.gov. The North American Benthological Society (NABS) offers a bibliography of recent literature in benthic biology on gopher.nd.edu. The Long-Term Ecological Research (LTER) program has put a bibliographic database and catalog of data sets on lternet.edu. (The actual data is not available on-line.) Check gopher.genethon.fr for bibliographies of sequence analysis and human genome research papers.

The U.S. Department of Agriculture (USDA) Extension Service offers the Research Results Database (RRDB), containing brief summaries of recent research from the USDA's Agricultural Research Service (ARS) and Economic Research Service (ERS), by e-mail. For details, send the e-mail message "send guide" to almanac@esusda.gov. To receive notices of new RRDB titles, send the message "subscribe usda.rrdb".

The U.S. Environmental Protection Agency (EPA) National Library on-line database can be accessed for bibliographic searches via anonymous telnet to epaibm.rtpnc.epa.gov. A collection of GIS-related bibliographies is available on bastet.sbs.ohio-state.edu.

Various Usenet newsgroups and mailing lists provide the tables of contents (TOCs) for current issues of a few journals of interest to biologists. Tom Schneider distributes Unix AWK scripts for converting many of these TOCs into BibTeX-style bibliography records: these scripts are posted in the Usenet newsgroup bionet.journals.note.

The journal TOCs available in bionet.journals.contents include:

Anatomy and Embryology
Applied Microbiology and Biotechnology
Applied and Environmental Microbiology

Binary
Biotechniques
CABIOS
Cell and Tissue Research
Chromosoma
Current Genetics
EMBO Journal
Environmental Physiology
European Journal of Biochemistry
European Journal of Physiology
Experimental Brain Research
Histochemistry
Human Genetics
IEEE Engineering in Medicine and Biology
Immunogenetics
Journal of Bacteriology
Journal of Biological Chemistry
Journal of Comparative Physiology B: Biochemical, Systemic, and
The Journal of Membrane Biology
Journal of Molecular Evolution
Journal of Virology
MGG - Molecular and General Genetics
Mammalian Genome
Microbial Releases
Molecular Microbiology
Molecular and Cellular Biology
Nucleic Acids Research
Photosynthetica
Plant Cell Reports
Planta
Protein Science
Roux's Archives of Developmental Biology
Theoretical and Applied Genetics

Preston Hardison <pdh@u.washington.edu> archives many documents relating to the CONSBIO mailing list via anonymous FTP on ftp.u.washington.edu, in the directory pub/user-supported/consbio/.

The CONSLINK listserver mailing list keeps a large bibliography of conservation biology research papers on its archive (see section 2.4.2.

Archives, for instructions on accessing listserver archives).

The American Physiological Society offers TOCs for the following journals via gopher on gopher.uth.tmc.edu (port 3300):

Advances in Physiology Education
American Journal of Physiology (6 consolidated journals)
Journal of Applied Physiology
Journal of Neurophysiology
News in Physiological Sciences
Physiological Reviews
The Physiologist

Other publishers supporting Internet access to information about their publications include

Publisher	Address	Access
Addison-Wesley	world.std.com	ftp
O'Reilly & Associates	gopher.ora.com	gopher
Kluwer Academic Publishers	world.std.com	ftp

There is a bibliography on the Internet itself available via anonymous FTP on gandalf.iat.unc.edu, file guides/irg-14.txt, and via gopher on sunsite.unc.edu, path UNC-info; IAT.

-*- 3.2. Directories

Searchable directories of scientists and research projects currently funded by the U.S. National Institutes of Health (NIH), National Science Foundation (NSF), Department of Agriculture (USDA), and genome researchers funded by several other departments, together with several topical directories, are available via gopher on gopher.gdb.org. Searches on researcher name, location, and field of interest are supported.

A directory of 2000+ people who read the bionet.* newsgroups is available via gopher and anonymous FTP from net.bio.net; you can add yourself to the directory via gopher or e-mail (see instructions on the archive).
A directory of researchers using Artificial Intelligence in Molecular

Biology (AIMB) is maintained at the National Library of Medicine. To be included, send e-mail to Larry Hunter, hunter@work.nlm.nih.gov.

Several directories of ecologists and plant biologists are kept on huh.harvard.edu, which is accessible via gopher and anonymous FTP. A directory of tropical biologists is kept in the Ecology and Evolution section of the gopher/anonymous FTP archive on sunsite.unc.edu. Richard Thorington keeps a list of mammalogists who use e-mail. To get yourself on the list (required to receive copies of it), send e-mail to mnhvz049@SIVM (via Bitnet) or mnhvz049@SIVM.si.edu.

-*- 3.3. Software

Several archives specializing in software for biologists are accessible via gopher and anonymous FTP. Some of these are listed in section 3.5, List of Archives. The first such archive in South America is the Brazilian Medical Informatics archive, ccsun.unicamp.br. The IUBio archive on ftp.bio.indiana.edu probably has the best collection in the United States. Botanists will appreciate the TAXACOM archive on huh.harvard.edu.

Also, wuarchive.wustl.edu has an excellent collection of educational software, especially for teaching mathematics at the college and university levels. The National Center for Supercomputing Applications has developed a collection of outstanding software tools for electronic communications and image analysis, and makes it publicly available on zaphod.ncsa.uiuc.edu. Many of the latest add-on tools for the popular LaTeX text formatting system are archived on sun.soe.clarkson.edu, while sumex-aim.stanford.edu has a huge archive of Macintosh software, and nic.ddn.mil keeps the important Internet RFC (Request for Comments) documents.

Jan-Peter Frahm has made available via e-mail "A Guide to Botanical Software for MS-DOS Computers". The software is shareware or in the public domain. For a copy, write him at hh216fr@duc220.uni-duisburg.de. Bionet.software is a good place to look for information about specific software programs with applications to biology. There are many Usenet groups devoted to discussion of software, particularly freeware and shareware. The well-known, huge anonymous FTP repositories of software are all mentioned in various published guides to the Internet (Kehoe 1992,

Krol 1992, Lane and Summerhill 1992, LaQuey and Ryer 1992, Tennant et al. 1993), and are part of the common knowledge of many Usenet newsgroups.

-*- 3.4. Data

The wealth of data available on the Internet is staggering, but it is also widely dispersed and often difficult to track down. Rather than compile a list of data sets and pointers to their locations, this guide gives a list of locations with only a name or phrase to suggest what data may be found there (see section 3.5, List of Archives). Many Usenet FAQs (see section 4, Useful and Important FAQs) and other Internet documents mentioned in this guide attempt to list available databases, but many more are known only by word-of-mouth. The Usenet newsgroup sci.answers (also a mailing list; see section 2.4.3, Gateways to Usenet) carries many lists that are updated frequently.

-*- 3.4.1. Repositories

Various genome and other cooperative projects are now well established on the Internet, with large, highly organized databases that support ever more powerful and complex interactive or batch search queries. Most now support WAIS and gopher search access, and are listed in section 3.5, List of Archives. The future utility of these repositories depends on the donation of data by individual researchers. Questions, as well as data submissions and corrections, can be sent to the relevant administrators via e-mail (after Garavelli 1992):

Database	Address of administrator
AAtDB (Arabidopsis thaliana)	curator@weeds.mgh.harvard.edu
ACEDB (Caenorhabditis elegans)	rd@mrc-lmba.cam.ac.uk and

mieg@kaa.cnrs-mop.fr

Brookhaven	pdb@chm.chm.bnl.gov
DDBJ enquiries	ddbj@ddbj.nig.ac.jp
data submissions	ddbjsub@ddbj.nig.ac.jp
updates, publication notices	ddbjupdt@ddbj.nig.ac.jp
EDEX and JARS (Forest Ecology)	goforest@gopher.yale.edu
EMBL problems, feedback	nethelp@embl-heidelberg.de
software submissions, queries	software@embl-heidelberg.de

Data Library enquiries	datalib@embl-heidelberg.de
Data Library submissions	datasubs@embl-heidelberg.de
FlyBase (Drosophila)	flybase@morgan.harvard.edu
Inst. of Forest Genetics DB (IFGDB)	ifgdb@s27w007.pswfs.gov
GDB	help@gdb.org
GenBank enquiries	info@ncbi.nlm.nih.gov
data submissions	gb-sub@ncbi.nlm.nih.gov
updates, publication notices	update@ncbi.nlm.nih.gov
Entrez questions	entrez@ncbi.nlm.nih.gov
BLAST Email server	blast@ncbi.nlm.nih.gov
RETRIEVE Email server	retrieve@ncbi.nlm.nih.gov
EST reports Email server	est_report@ncbi.nlm.nih.gov
Microbial Strains Data Net. (MSDN)	msdn@bdt.ftpt.br and msdn@phx.cam.ac.uk
NCBI	repository@ncbi.nlm.nih.gov
PIR	fileserv@nbrf.georgetown.edu
SWISS-PROT	bairoch@cmu.unige.ch

LiMB, the Listing of Molecular Biology databases (Keen et al. 1992) describes most of these databases, and many more, including the names, regular mail addresses and telephone numbers of their keepers. To get the current version of LiMB by e-mail, send the text "limb-data" to bioserve@life.lanl.gov. For information only, send "limb-info". LiMB is available in hardcopy or on floppy disk: contact limb@life.lanl.gov.

-*- 3.4.2. Search Engines

Help files can be obtained from any of the GenBank e-mail servers listed in the previous section by sending the word "help" in the Subject line or body of an e-mail message to the server in question.

The European Molecular Biology Laboratory (EMBL) supports various types of searches via e-mail. For more information, send the text "help" in e-mail to any one of these servers:

EMBL File Server	NetServ@EMBL-Heidelberg.DE
FASTA	FASTA@EMBL-Heidelberg.DE
Quicksearch	Quick@EMBL-Heidelberg.DE
Swiss-Prot MPsrch	Blitz@EMBL-Heidelberg.DE

The BLOCKS database can be searched via e-mail. For a help file, send

a blank e-mail message to blocks@howard.fhcrc.org, with the word "help" in the Subject line.

The GenMark e-mail sequence search engine was updated in the summer of 1993. For instructions and new feature descriptions, send e-mail to genmark@ford.gatech.edu with the word "instructions" in the Subject line or body of the letter. Or contact M. Borodovsky <mb56@prism.gatech.edu> or J. McIninch <gt1619a@prism.gatech.edu>.

See also Henikoff (1993).

The Sequence Retrival System (SRS) program for VAX VMS computer systems is available via anonymous FTP on the EMBnet node biomed.uio.no (Norway) or genetics.upenn.edu (USA).

Three U.S. herbaria now provide e-mail search support of:

> Type specimens of the mint family from the Harvard Herbaria, comprising 1100 records.
>
> The complete herbarium catalog of Michigan State University, Kellog Biological Station Herbarium, an NSF LTER site, consisting of 6000 specimen records.
>
> The Flora of Mt. Kinabalu; 16,300 specimen records of all vascular plant collections from the mountain.

E-mail addresses for sending queries are:

> Harvard Mint Types: herbdata@huh.harvard.edu
> Kellogg Herbarium: herbdata%kbs.decnet@clvax1.cl.msu.edu
> Flora of Mt. Kinabalu: herbdata@herbarium.bpp.msu.edu

Send the message "help" to receive a usage guide, and if you think there might be difficulties with your return address, send that as well by adding a line with the text "replyaddress=" followed by your prefered e-mail address.

Anyone who does a lot of field work will appreciate the Geographic Name Server, which can provide the latitude and longitude, and the elevation of most places in the United States: all cities and counties are covered.

as well as some national parks and some geographical features (mountains, rivers, lakes, etc.). Telnet to martini.eecs.umich.edu, port 3000 (no username needed) and type "help" for instructions.

-*- 3.5. List of Archives

Computer sites supporting some sort of public access, and of some interest to biologists are listed here, together with means of access.

e - e-mail file requests (see notes this section for e-mail addresses).
E - e-mail search requests (see notes this section).
f - anonymous FTP (see section 3.6.3, Anonymous FTP by E-mail, if you cannot use FTP).
g - gopher server
G - gopher server plus WAIS index searches
t - public telnet access
T - public telnet access plus e-mail returns of search results
W - WAIS server plus WAIS index searches

Internet node name	Topic/Agency	Access method
ftp.bio.indiana.edu (IN USA)	IUBIO Genbank, FlyBase	fG
ncbi.nlm.nih.gov (MD USA)	NCBI	f
ftp.embl-heidelberg.de (Germany)	EMBL Data Library	Efg
coli.polytechnique.fr (France)	EMBLnet	G
ftp.bchs.uh.edu (TX USA)	Genbank, PIR	fG
helix.nih.gov (MD USA)	Genbank, PDB, PIR etc.	G
ncifcrf.gov (MD USA)	Biol. Information Theory	f
finsun.csc.fi (Finland)	Prosite, Rebase-Enzyme	G
pdb.pdb.bnl.gov (NY USA)	Protein Data Bank	G
ftp.tigr.org	Inst. for Genomic Rsch.	f
golgi.harvard.edu (MA USA)		f
megasun.bch.umontreal.ca	Molecular evolution	G
nic.funet.fi (Finland)		
gopher.csc.fi (Finland)		
nic.switch.ch (Switzerland)	EMBnet	fG W [10]
rdp.life.uiuc.edu	Ribosomal DB Project	f
world.std.com	A major entry-point	fG
sunsite.unc.edu (NC USA)	Many subjects	

EfGt [4]					
gopher.ciesin.org		Earth Sciences	G		
locus.nalusda.go (USA)		Nat. Agri. Library	G		
s27w007.pswfs.gov (USA)		Forest Genetics		G	
biomed.uio.no (Norway)		Genome data	T		
gopher.embnet.unibas.ch (Switzer.)					
biox.embnet.unibas.ch (Switzerland)		Genome data	G		
ll gopher.gdb.org (MD USA)		GDB Genome Data Bank	G		
weeds.mgh.harvard.edu (MA USA)		Arabidopsis, C. elegans	G		
mendel.agron.iastate.edu (IA USA)		Soy genome	G		
greengenes.cit.cornell.edu (NY USA)		Triticeae genome	G		
teosinte.agron.missouri.edu (USA)		Maize genome	G		
gopher.duke.edu (NC USA) [2]		Chlamydomonas		G	
picea.cfnr.colostate.edu (CO USA)				f	
poplar1.cfr.washington.edu (WA USA)		Populus genetics	f		
esusda.gov (USA)		USDA Extension Service	G		
infoserver.ciesin.org		CIESIN Global Change	G		
mobot.org (MO USA)		Missouri Bot. Garden		f	
life.anu.edu.au (Australia)		Bioinformatics		fG	
igc.org (CA USA)		EcoNet		f	
gopher.yale.edu (CT USA)		Ecol. Data EXchange	g		
lternet.edu (WA USA)		LTERnet		G	
spider.ento.csiro.au (Australia)	Entomology		f		
gopher.uth.tmc.edu (port 3300)	Physiology		G		
envirolink.hss.cmu.edu (DE USA)	Environment		GT	[6]	
ecosys.drdr.virginia.edu (VA USA)		Ecosystems		GT	
sparc.ecology.uga.edu (GA USA)	Ecology, Coweeta LTER		G		
ngdc1.ngdc.noaa.gov (USA)		Paleoclimatology	f		[1]
huh.harvard.edu (MA USA)		Harvard Univ. Herbaria	fG		
simsc.si.edu (DC USA)		Smithsonian Inst.	f		[3]
ucmp1.berkeley.edu (CA USA)		Vertebrate museum	G		
bdt.ftpt.br (Brazil)	Biodiversity		fG		
coli.polytechnique.fr (France)	Molecular evolution		G		
fconvx.ncifcrf.gov (MD USA)		Mathematical Biology	f		
cheops.anu.edu.au		Radiocarbon Abstracts	fG W		
bluehen.ags.udel.edu (DE USA)	Entomology		G		
minerva.forestry.umn.edu (MN USA)		Forestry	G		
ucsbuxa.ucsb.edu (CA USA)		Biology		G	
evolution.genetics.washington.edu	Evolution		f		

evolution.bchs.uh.edu (TX USA)	Evolution		f	
martini.eecs.umich.edu (MI USA)	Geographic Name Server		t	[7]
wigeo.wu-wien.ac.at	(Austria)	Geography	G	
geogopher.ucdavis.edu (CA USA)	Geology		G	
isdres.er.usgs.gov (VA USA)		US Geological Survey	f	
pippin.memst.edu		CERI Earthquake Center	G	
cdiac.esd.ornl.gov		CDIAC		f
saturn.soils.umn.edu (MN USA)	Geology		G	
kiawe.soest.hawaii.edu (HA USA)	Generic Mapping Tools		f	
tycho.usno.navy.mil		U.S. Naval Observatory		t [8]
nssdca.gsfc.nasa.gov		NSSDC On-Line Service	t	[9]
granta.uchicago.edu (IL USA)	Physics Resources		G	
xyz.lanl.gov (NM USA)		LANL Nonlinear Science	G	
mentor.lanl.gov (NM USA)		LANL Physics		G
info.mcs.anl.gov (IL USA)		Argonne National Lab.	f	
stis.nsf.gov (DC USA)		Nat. Science Foundation	fG	
rtfm.mit.edu (MA USA)		Usenet FAQ repository	ef	[5]
jse.stat.ncsu.edu (NC USA)		Journal of Stat. Educ.	fG	
ftp.sas.com (NC USA)	SAS-related information		f	
zaphod.ncsa.uiuc.edu (IN USA)	Supercomputing		f	
lupulus.ssc gov		Young Scientists Net.	f	
ksuvxa.kent.edu		Directory of lists	f	
sun.soe.clarkson.edu		LaTeX tools	f	

Notes:

1: info@mail.ngdc.noaa.gov;
2: chlamy@acpub.duke.edu;
3: david@simsc.si.edu;
4: info@sunsite.unc.edu, telnet username "swais" for WAIS seaches, telnet username "gopher" for plain gopher access;
5: see section 3.6.2, Anonymous FTP, and section 3.6.3, Anonymous FTP by E-mail;
6: Telnet username "gopher", password "envirolink";
7: Use port 3000, no username, "help" gets instructions;
8: Telnet username "ads".
9: Telnet username "nodis".
10: Anonymous FTP from within Switzerland only.

Using Mosaic on various machines (you can obtain a free copy of Mosaic for most computer platforms using ftp to ftp.ncsa.uiuc.edu) you have access to a host of different biological sciences resources. Some of the sites I have found to be useful are:

The World-Wide Web Virtual Library: Biosciences
http://golgi.harvard.edu/biopages.html

http://www.gdb.org/Dan/softsearch/biol-links.html

Archives for Biological Software and Databases Around the World
http://www.gdb.org/Dan/softsearch/biol-links.html

WWW in Biology
http://www.ch.embnet.org/bio-www/info.html

Artificial Life ONLINE
http://alife.santafe.edu/

Worldwide WWW Information
http://wings.buffalo.edu/world/

University of North Carolina at Chapel Hill SunSITE home page
http://sunsite.unc.edu/

GOPHER, FTP AND WWW SITE FOR LIFE SCIENCE SOFTWARE

This is to announce the availability of a gopher server of interest to the life science community. As part of an NSF-funded curriculum development project on a quantitative curriculum for life science students (USE-9150354 to the University of Tennessee-Knoxville), I've been collecting and evaluating software products of possible use in the life sciences. These reviews have been distributed by e-mail and hard-copy previously (using the wustl archives). The reviews are of software for aiding the development of quantitative skills of life science undergraduates, and the reviewers are all students. Thus, this does not included software such as those to aid in dissection. The reviews are now easily searched and downloaded from

the new Mathematics Archives, which mostly contains a huge assortment of public domain software which can be used to aid mathematics instruction at the college level. Also included are several databases including reviews of commercial software, abstracts of meetings, and links to a number of other relevant gophers. We support anonymous ftp, WWW and gopher with WAIS searching implemented on abstracts and readme files for files in the Archives. The Mathematics Archives is also an NSF-funded resource (DUE-9351398), with additional support from the State of Tennessee Science Alliance, and the Departments of Mathematics at Calvin College and the University of Tennessee, Knoxville. To access this site, gopher to

archives.math.utk.edu (port 70)

or use anonymous ftp to

archives.math.utk.edu (128.169.202.163)

or use WWW by setting the URL to
http://archives.math.utk.edu/

In addition to the above mentioned reviews of life science software, we include public domain software or links to sites where such software is available. We have included several documents of possible interest:

Workshop Reports on a Quantitative Curriculum for Life Science Students
The complete listing of software reviews for the life science curriculum
The B&B Primer on First Job Haggling

If there are documents, software, or reviews you would like to contribute to the life science component of this site, please contact me. Note that my policy for inclusion of reviews in the life science area is that they either be references to published reviews, or be reviews done by students.

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615-974-4295
615-974-6576 (FAX)
615-974-2461 (Secretary)
gross@math.utk.edu

Two of the most pertinent mailing lists in mathematical ecology are:

ECOLOG-L is a LISTSERV list maintained primarily for the benefit of members

of the Ecological Society of America. This electronic discussion forum allows people who have a common interest in ecology and closely related fields to communicate with each other by electronic mail (E-mail). Subscription to the group is free and is not restricted to members of the ESA.
You can subscribe to ECOLOG-L by sending the command (using my own name as an example):
SUB ECOLOG-L David W. Inouye (Univ. of MD)
to listserv@umdd.umd.edu. Replace the second part of the command with your own name, and possibly City and State, or institution. This information (40 characters maximum) is literally copied into the list of subscribers, and should help identify you to someone who is examining the list. You can always change this information by signing off and then re-subscribing.

The ECOSYS-L mailing list is intended to provide a forum to discuss problems in the fields of ecosystem theory and modelling. In addition there should be discussed the current state of the art and future of standardization and documentation of mathematical descriptions for ecological processes.
To subscribe, send the following command to LISTSERV@DEARN (bitnet) or LISTSERV@vm.gmd.de (in the BODY of e-mail):
SUBSCRIBE ECOSYS-L firstname lastname

BIOSCI ELECTRONIC NEWSGROUP NETWORK
The BIOSCI newsgroup network was developed to allow easy worldwide communications between biological scientists who work on a variety of computer networks. By having distribution sites or "nodes" on each major network, BIOSCI allows its users to contact people around the world without having to learn a variety of computer addressing tricks. Any user can simply post a message to his/her regional BIOSCI node and copies of that message will be distributed automatically to all other subscribers on all of the participating networks, including the Internet, USENET, BITNET, EARN, NETNORTH, HEANET, and JANET. To get the latest info on these newsgroups (which are typically read using a news reader on USENET through the "bionet" hierarchy, you can send e-mail to biosci@net.bio.net

To get the FAQ if you don't have Usenet access, you can ftp to rtfm.mit.edu and look for pub/usenet/news.answers/biology/guide.

Or you can get the FAQ via gopher on a number of places, including

the Ecology and Evolution gopher archive on sunsite.unc.edu.

Particular software:

Populus

The Populus software contains a set of simulation models that we use in teaching population biology and evolutionary ecology at the University of Minnesota. All of the simulations share a common format, as follows: After a model is chosen from the menu, the program displays (optionally) several screens of background material which introduce the mathematics and end with basic references. Next, there is a screen listing all of the input parameters; students can move among the parameter boxes and change initial defaults to values of their own choosing. The program maintains a record including permissible maxima and minima for each parameter and filters input values accordingly. Usually there are several possible outputs (e.g., N vs T graphs and phase planes) which can also be selected from the parameter input screen; alternatively, students view the different outputs in sequence, by pressing the space bar between views. Context-sensitive help screens are available (press <F1>) from the input and output screens of every model, and by pressing <F1> twice one can see a menu of additional help screens that include discussions of function and editing key assignments implemented by the program, printing protocols, video options, etc.

Populus is written in Borland Pascal 7.0 to run under DOS on IBM and compatible computers. The program is offered in a protected-mode version for computers with 286, 386, 486, or pentium microprocessors and 2 MB RAM. There is also a real-mode version for XT class computers with the 8088 chip. Full implementation of Populus in real mode requires about 500KB of RAM, free of memory-resident utilities and drivers. The real-mode program will use LIM expanded memory, reducing the frequency of disk reads and speeding program execution. Although the code will emulate an xx87 coprocessor if one is not present, many of the models are computationally intensive and will run much more rapidly on a machine with the floating-point chip.

Sponsorship and Distribution

This software is underwritten by the Undergraduate Course and Curriculum Development Program of the National Science Foundation (USE-9150887, USE-919155967); it is not a commercial venture and we encourage you to distribute it without charge to any colleague or student who will put it to good use. If you find a bug please tell us. We will fix it and

provide you with an update.

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There are two versions of Populus posted on the Minnesota Ecology Server (ecology.ecology.umn.edu, 134.84.102.1) get them by ftp to this.

BioQUEST - A Curriculum Innovation Project

BioQUEST is a Library of Modules based on a common philosophical approach to teaching and learning biology.

BioQUEST is a committment to learning about modern biological research, not towards undergraduate biology textbook materials.

BioQUEST is committed to cooperative group learning rather than individualistic competition.

BioQUEST can be used with a wide range of students - secondary, introductory undergraduate majors and non-majors, advanced level courses, graduate students.

BioQUEST is a growing Consortium of biology educators.

BioQUEST is dynamic, not static.

BioQUEST is a movement, not an object.

The BioQUEST Consortium was formed as a means of initiating curriculum reform in undergraduate biology courses through the creation and dissemination of innovative and flexible instructional learning tools and the establishment of a communication network for like-minded biology faculty. Educators involved with BioQUEST believe that biology courses, particularly introductory and non-majors courses, must foster an understanding of how biologists perceive the world; pose questions; pursue problems from those questions; and ultimately, persuade others of the value of their conclusions. We believe that if students are to understand how biologists think, they must have opportunities to experience science from the point of view of a practicing biologist.

This 3 P's approach (problem posing, problem solving, peer persuasion) to the teaching of biology is vital to the laboratory research experience of a student, and such experience is central to a deep understanding of how scientific knowledge is created, modified, and used. Our students must not only

understand and appreciate the strengths of science, they must comprehend its limitations as well.

The above commitments have led us to develop computer tools that, when used as an integral part of a curriculum that includes laboratories, lectures, and collaborative group work, will increase students' facility for solving realistic problems. We feel that computers can facilitate student laboratory research. However, for computers to be educationally sound, we believe that they must simulate or support realistic problem-solving environments. Three kinds of computer software can do this: simulated laboratories (such as those developed by BioQUEST), professional software tools (such as software to search data bases of DNA sequences), and general productivity tools (word processors and spreadsheets). BioQUEST advocates use of all three types of software.

BioQuest is available as a cd for Macintosh computers from:

Academic Software Development Group
Computer Science Center
University of Maryland
College Park, MD 20742-2411

Phone: (301) 405-7600
e-mail: asdg@umdd.umd.edu

Introductory Hypercard stacks for BioQuest are on the matharchives site:
archives.math.utk.edu
under LifeSciences

Summary of Recommendations
Workshop on Quantitative Training of Life Science Students
University of Tenneessee, Knoxville May 19-21, 1994

This Workshop was designed to bring together a group of life science, mathematics, and statistical researchers and educators to focus on the inclusion of more quantitative concepts directly in life science undergraduate courses. The Workshop was supported by NSF Grant USE-9150354 to the University of Tennessee. It was a follow-up to a previous workshop which focused mostly on entry-level and advanced quantitative courses for undergraduates in biology, health science (e.g. nursing, pre-medicine, etc.), and agricultural science. The prior workshop developed guidelines for content of an entry-level course sequence but additionally emphasized that **it is not sufficient to isolate quantitative components of the curriculum in a few courses on such topics, rather, quantitative methods should be a component of courses throughout the undergraduate life science curriculum**.

General Recommendations:

1. ***The quantitative component of upper division life science courses can readily be enhanced through the addition of modules***, perhaps in conjunction with field or laboratory execises. These modules would contain brief applications of quantitative methods to a particular biological problem appropriate to the course topic. The modules might utilize a software product, if appropriate. The Workshop therefore urges the construction of sets of course modules, dealing with biological topics appropriate to a variety of upper division life science courses, that illustrate the utility of quantitative approaches in analyzing biological problems.

2. ***Workshops should be organized*** along topical lines for standard upper division life science courses (e.g. cell biology, ecology, physiology, etc.) ***to allow biology faculty who are not quantitatively oriented to see how these modules could be incorporated in their courses***, and how the use of particular software might aid a students appreciation of the material of the course. These workshops should be organized at meetings of the appropriate specialized scientific societies most likely to draw the teachers of these courses, as well as at larger gatherings of biology teachers. Such workshops also allow faculty members to learn of the success stories of their colleagues as well as the details of how quantitative concepts may be incorporated within the courses. The workshops could include role-playing, in which the faculty would take the student role, for example involving certain software-based exercises.

3. Regarding ***General Biology***, ideally what should be available to instructors is an ***accessible set of modules, at a relatively simple mathematical level***, that could be coupled to either lab or field exercises or used as a complement to specific topics within lectures. These modules would contain ***brief examples of how quantitative methods***

can lead to non-intuitive, biologically significant results. The modules would cover the range of topics addressed in most General Biology sequences, and might be assembled in a text or pulled out of the text and coupled to lab or field work in the course or used as a complement to specific topics within the lectures.

4. We recommend the ***formation at each institution of interdisciplinary quantitative biology teaching circles*** consisting of a small group of committed faculty from the life sciences and mathematics. These will aid in the incorporation of quantitative modules within life science courses, but additionally will encourage the use of more biological examples in the quantitative courses taken by life science students. They will provide for more effective coupling between quantitative and life science courses, and may lead to the development of truly interdisciplinary courses at institutions where these are appropriate. These teaching circles are particularly important for institutions with little prior quantitative experiences for life science students, in which life science faculty may not feel comfortable with the inclusion of more quantitative topics.

5. This workshop concurred with the recommendation of the 1992 Workshop that ***math faculty, particularly those teaching entry level courses, should be encouraged to include more biological examples*** in these courses, because the students are perhaps more attuned to them than to examples from the physical sciences. In some, but not all institutions, ***the development of specialized entry-level quantitative courses for life science students***, such as those suggested by the 1992 Workshop, are appropriate, and ***should be encouraged***. At the same time, many institutions may not offer such courses, and in these cases the mathematics courses should at least contain sufficient biological examples so that students realize the linkages between the material and the life sciences.

6. The importance of communication between colleagues in different disciplinary units within an institution to foster quantitative concept development for life science students cannot be underestimated. However, at the same time ***communication should be fostered between like-minded individuals at different institutions***. We therefore urge that an electronic list-serve or other group be set up to allow these faculty to make reference to a common body of knowledge. Similarly, we urge the formation of consortia of institutions to deal with quantitative aspects of life science training, in a similar manner to the calculus reform groups which were established and became successful progenitors of new teaching methods and materials.

For further information about this Workshop or on quantitative curricular development for the life sciences, use gopher, ftp, or WWW to connect to: archives.math.utk.edu or http://archives.math.utk.edu/ or contact:

Dr. Louis J. Gross, Department of Mathematics and Graduate Program in Ecology, University of Tennessee, Knoxville, TN 37996-1300. 615-974-4295 (Voice), 615-974-2461 (Secretary), 615-974-6576 (FAX), gross@math.utk.edu.