Amy Michelle (Kryder) Hauth

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Education

2002 **Doctor of Philosophy**

Computational Molecular Biology
Thesis: Identification of tandem repeats: Simple and complex pattern structures in DNA sequences
Thesis Advisor: Deborah A. Joseph, Computer Sciences
University of Wisconsin, Madison, Wisconsin, USA

1992 **Master of Science**

Computer Sciences, University of Wisconsin, Madison, Wisconsin, USA

1990 **Bachelor of Science**

Botany (major) and Computer and Information Science (minor)
with Honors in the Liberal Arts
with Distinction in Botany
Thesis: Computerized analysis of root growth patterns: Characterization of circumnutation and its relationship to gravity sensing
Thesis Advisor: Michael L. Evans, Plant Biology (formerly Botany)
The Ohio State University, Columbus, Ohio, USA

1986 **Valedictorian**

Patrick Henry High School, Hamler, Ohio, USA

Research Experience

2003 - present **Post-Doctoral Fellow**

Complex repetition and recurring patterns in genomics
B. Franz Lang and *Gertraud Burge*r, Université de Montréal, Québec, Canada.

1991 - 2002 **Graduate Research Assistant**

Identification of tandem repeats having simple and complex pattern structures
Deborah A. Joseph, University of Wisconsin, Madison, Wisconsin, USA.

Summer 1994 **Graduate Research Intern**

Identification of signals in 3' UTRs: Development of statistics-based signal model
Masato Ishikawa, Institute for New Generation Computer Technology, Tokyo, Japan

Summer 1992 **Graduate Research Assistant**

Time efficient version of tRNA identification: tRNAscan 2.0
Christian Burks, Los Alamos National Laboratory, Los Alamos, New Mexico, USA

Summer 1991 **Graduate Research Assistant**

Fragment assembly for shotgun sequencing in large-scale genome sequencing projects
Fred R. Blattner, *Deborah A. Joseph*, University of Wisconsin, Madison, Wisconsin, USA

1987 - 1990 **Undergraduate Research Assistant**

Root tip growth and gravity sensing: Software enhancement and mutant characterization
Michael L. Evans, The Ohio State University, Columbus, Ohio, USA

Honors and Awards

Bioinformatics Training Fellowship (2003 – present)

Competitive training program for the promotion of excellence in Bioinformatics. Primarily focused on research and publications but also mentoring and teaching skills.

Université de Montréal, Montréal, Québec, Canada.

Biotechnology Training Program (1991 – 1995)

Competitive training program providing cross-disciplinary training between the biological and physical sciences. Primary activities involve cross-disciplinary coursework, research project spanning biological and physical sciences, a seminar series featuring research and annual poster sessions.

University of Wisconsin, Madison, Wisconsin, USA.

Summer Institute in Japan (1994)

Competitive summer program for graduate students in science and engineering to explore Japan's work environment, language and culture with the goal of encouraging collaborations between scientists in Japan and the United States. Primary activities involve an internship and language instruction.

Tsukuba and Tokyo, Japan.

Best Paper in Software Support for Genome Mapping and Sequencing (1993)

W. Istvanick, **A. Kryder**, G. Lewandowski, J. Meidanis, A. Rang, S. Wyman and D. Joseph. Dynamic methods for fragment assembly in large-scale genome sequencing projects. Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences (HICSS), Volume 1: Architecture and Biotechnology Computing, edited by T. N. Mudge, V. Milutinovic and L. Hunter, IEEE Computer Society Press, pp. 534-543.

University of Wisconsin, Madison, Wisconsin, USA.

Honors in the Liberal Arts and Distinction in Botany (1990)

Bachelor of Science.

The Ohio State University, Columbus, Ohio, USA

Research Experience for Undergraduates, National Science Foundation (1989 – 1990)

Funding for research to characterize a *Zea mays* mutant unable to sense gravity.

The Ohio State University, Columbus, Ohio, USA

Biological Sciences Honorary (Helix) (1988 – 1990)

The Ohio State University, Columbus, Ohio, USA

Junior Class Honorary (Chimes) (1988 – 1989)

The Ohio State University, Columbus, Ohio, USA

Senate Page (1988)

Senator M. Ben Gaeth

State of Ohio, Columbus, Ohio, USA

Valedictorian (1986)

Patrick Henry High School, Hamler, Ohio, USA

Membership in Professional Societies

International Society of Computational Biology (2002 – present)

Ohio Academy of Science (1986 – 1990)

Refereed Publications

All publications are available at http://www.cs.wisc.edu/~kryder/documents/papers

A. M. Hauth, U. G. Maier, B. F. Lang and G. Burger (2005). The *Rhodomonas salina* mitochondrial genome: Bacteria-like operons, compact gene arrangement and complex repeat region. **Nucleic Acids Res.** 2005 Aug 5;33(14):4433-42.

A. M. Hauth and D. A. Joseph (2002). Beyond tandem repeats: Complex pattern structures and distant regions of similarity. Proceedings of the 10th International Conference on Intelligent Systems for Molecular Biology (ISMB), Edmonton, Alberta, Canada. **Bioinformatics** 2002 Jul;18 Suppl 1:S31-7.

W. Istvanick, **A. Kryder**, G. Lewandowski, J. Meidanis, A. Rang, S. Wyman and D. Joseph (1993). Dynamic methods for fragment assembly in large-scale genome sequencing projects. Proceedings of the Twenty-Sixth Annual Hawaii International Conference on System Sciences (**HICSS**), Volume 1: Architecture and Biotechnology Computing, edited by T. N. Mudge, V. Milutinovic and L. Hunter, IEEE Computer Society Press, pp. 534-543. (Best Paper in Software Support for Genome Mapping and Sequencing Minitrack).

Technical Reports

A. M. Hauth and M. K. Clayton (2000). Statistical analysis of DNA sequences using overlapping windows. Computer Sciences Department Technical Report 1474, University of Wisconsin, Madison, Wisconsin, USA.

A. Kryder, G. Fichant and C. Burks (1995). Identifying potential tRNA genes in genomic sequences: Version 2.0 of tRNAscan. Theoretical Biology and Biophysics Group (T-10), Los Alamos National Laboratory, Los Alamos, New Mexico, USA.

Manuscripts in Preparation

A. M. Hauth and G. Burger. Methodology for defining bioinformatics problems. Submitted to *Bioinformatics*.

S. Kannan, **A. M. Hauth** and G. Burger. Mitochondrial ORF Prediction System (MOPS). To be submitted to *BMC Bioinformatics*.

B. Schäfer, **A. M. Hauth**, C. Bullerwell, K. Wolf and B. F. Lang. Divergent trends in mitochondrial genome evolution in the genus *Schizosaccharomyces*. To be submitted to *Nucleic Acids Research.*

A. M. Hauth. Finding a needle in a haystack: Highly recurrent sequences in highly repetitive genomes. To be submitted to *Bioinformatics*.

Software Distribution and Web Service

Complex Repetition Analysis Tools (http://www.megasun.bch.umontreal.ca/People/ahauth/tools)

A. M. Hauth (2004 – present). Distribution of bioinformatics software: TRIplot and ComplexTR. TRIplot identifies direct and inverted repeats and provides expert-interactive analysis for comprehension of complex repetition. ComplexTR identifies and characterizes tandem repeats in nucleotide sequences.

Université de Montréal, Montréal, Québec, Canada.

ComplexTR Web Service via AnaBench (http://malawimonas.bcm.umontreal.ca:8091/anabench)

A. M. Hauth (2004 – present). Web-based sequence analysis using ComplexTR. AnaBench is a bioinformatics analysis workbench offering customization of *in silico* analysis pipelines for genomics.

Université de Montréal, Montréal, Québec, Canada.

Tandem Repeat Identification (http://www.cs.wisc.edu/gensoft)

A. M. Hauth and Deborah A. Joseph (1994 – 2003). ComplexTR web server for identification of tandem repeats. Website deactivated in 2003 and converted to static webpages depicting analysis.

University of Wisconsin, Madison, Wisconsin, USA.

Invited Conference Presentation

2002 **10th International Conference on Intelligent Systems for Molecular Biology**

Edmonton, Alberta, Canada. August 3 – 7, 2002. **A. M. Hauth** and D. Joseph. Beyond tandem repeats: Complex pattern structures and distant regions of similarity.

Contributed Conference Presentations

2005 **Fourth European Conference on Computational Biology**

Madrid, Spain. September 28 – October 1, 2005. **A. M. Hauth**. Automating contiguous and non-contiguous repetition in genomic sequences.

Annual Meeting of the CIAR Evolutionary Biology Program

Parksville, British Columbia, Canada. September 15 – 19, 2005. **A. M. Hauth**. Complex repetition in mitochondrial genomes.

2004 **Annual Meeting of the CIAR Evolutionary Biology Program**

Pine Hill, Québec, Canada. October 13-17, 2004. **A. M. Hauth**, G. Burger and B. F. Lang. *Rhodomonas salina*: Analysis of structure and history of complex repetitive genome regions.

Robert-Cedergren Colloquium

Montreal, Québec, Canada. September 23-24, 2004. **A. M. Hauth**, G. Burger and B. F. Lang. TRIplot: Towards an automated analysis of complex repetition in genomes.

12th International Conference on Intelligent Systems for Molecular Biology

Glasgow, Scotland, United Kingdom. July 31 – August 4, 2004. **A. M. Hauth**, G. Burger and B. F. Lang. Analysis of structure and history of complex repetitive genome regions.

1992 **First International *E. coli* Genome Meeting**

Madison, Wisconsin, USA. September 10 – 14, 1992. **A. Kryder**, G. Lewandowski, J. Meidanis, A. Rang, S. Wyman and D. Joseph. Dynamic methods for fragment assembly in large-scale genome sequencing projects.

Invited Talks

2005 **University of Victoria, Department of Biochemistry and Microbiology**

Victoria, British Columbia, Canada. September 13, 2005. Analysis of complex repetition in genomes.

2003 **Université de Montréal, Department of Biochemistry**

Montréal, Québec, Canada. May 6, 2003. Tandem repeat identification: Simple and complex pattern structures in DNA sequences.

Université de Montréal, Department of Computer Science

Montréal, Québec, Canada. May 7, 2003. ComplexTR: An algorithm for identification and characterization of tandem repeats.

2001 **DNAStar, Inc.**

Madison, Wisconsin, USA. December 2001. Practical identification of tandem repeats in DNA sequences.

Invited Course Lectures

2005 **Advanced Bioinformatics (BIF 7002)**

Université du Québec à Montréal, Montréal, Québec, Canada. February 10, 2005. Simple and complex repetitive patterns in nucleotide sequences.

2003 **Integration of Life and Computational Sciences (BIN 3001)**

Université de Montréal, Montréal, Québec, Canada. September 19, 2003. ComplexTR: Identification of tandem repetition in genomic sequences.

Research Projects

***In silico* Genomic Feature Discovery: Recurring Patterns of Known Features (2003 – present)**

This project employs a systematic comparative approach towards discovery of recurring patterns. It is based on the premise that constraints at the sequence, structure and interaction levels enforce conservation in DNA, RNA and proteins. Numerous groundbreaking discoveries in biology started with the recurring observation of similar regulatory sequences upstream of genes, of differences between genes and transcripts and of similar secondary and tertiary structures in nucleotide and amino acid sequences. Thus, recurring observation of a particular feature or combination of features may indicate a new biologically interesting feature. This project, which is currently in design phase, includes four components: (1) feature identification using third-party tools and resources, (2) a database to store feature annotations, (3) a discovery system to combine features and discover recurring combinations and (4) an evaluation procedure for predicting biological interest in a recurring pattern.

Complex Repetition: Analysis of Contiguous and Non-contiguous Repetition (2003 – present)

This project develops computational techniques to determine relationships between pairs of direct and inverted repeats, to define sequence-similar patterns present in three or more locations and to untangle pattern super-structures. Tools that exclusively pair similar regions become cumbersome when many repeat pairs are present. Further, local (contiguous) or dispersed (non-contiguous) patterns of repetition are difficult to decipher. My initial work focused on two case studies. The *Rhodomonas salina* mitochondrial genome has a complex, highly repetitive region representative of contiguous repetition (see project below). Non-contiguous repetition is evident in the *Saccharomyces japonicus* mitochondrial genome where repeats accounted for 80% of the genome (see project below). In both genomes, expert annotation of repetition was extremely difficult due to a massive number of repeat pairs and complex super-structure. To enable annotation, I developed the TRIplot tool suite that assists experts in analysis of complex repetition. Research is on-going towards complete automation.

***Schizzosaccharomyces japonicus* Mitochondrial Genome (2004 – present)**

The *Schizosaccharomyces japonicus* mitochondrial genome has massive repetition scattered throughout the genome (>80% of 110 kbp genome). My comparison of two isolates indicated massive gene rearrangement. Further, several sequence motifs recurred between syntenic gene blocks, suggesting either a signature marking locations of recombination or locations that directly enabled recombination leading to gene rearrangement.

Collaborators: B. Franz Lang, Université de Montréal (Canada); Charles Bullerwell, Dalhousie University (Canada); Bernd Schäfer and Klaus Wolf, Aachen Technical University (Germany)

***Rhodomonas salina* Mitochondrial Genome (2003 – 2005)**

The *Rhodomonas salina* mitochondrial genome has a highly compact gene organization that contrasts with the presence of a 4.7 kbp long, highly repetitive intergenic region (~10% of genome). My analysis revealed a complex repeat structure and prediction of both replication and transcription initiation sites.

Collaborators: B. Franz Lang and Gertraud Burger, Université de Montréal (Canada); Uwe Maier, Phillips-University Marburg (Germany)

Bioinformatics Standards: Methodologies for Defining Bioinformatics Problems (2003 – present)

This project proposes a methodology for defining bioinformatics problems that includes three components: a biological model, a bioinformatics transformation from biological to computational requirements and a computational model. My methodology describes how to specify each component. Establishment of standards will require community-wide involvement and cooperation.

Tandem Repeat Identification (1993 – 2003)

This project explored methods for identifying tandem repeats in DNA sequences having simple and complex pattern structures. Analysis of sequences containing repeat related annotations revealed numerous complexities, in particular nested tandem repeats and patterns across more than one tandem sequence copy. My identification software addressed both simple and complex pattern structures as well as poor region edge definition and noisy pattern signals. The goal was to identify and characterize tandem repeats comparable to expert annotation and to discover higher-order patterns often difficult to identify visually.

Thesis Advisor: Deborah A. Joseph, Computer Sciences Department, University of Wisconsin, Madison, Wisconsin, USA.

Research Projects (continued)

3' UTR Signal Identification (Summer 1994)

A research group at the Institute for New Generation Computer Technology developed software to identify a signal present within the 3' UTR region. Their model assumed complete conservation for positions at the left and right ends and no conservation for positions in the middle. I analyzed the training datasets to determine position-by-position conservation and discovered variable conservation dependent on position. My model based on a four-nucleotide profile included all positions in the region but assumed a variable contribution by each position to the signal. Incorporation of this alternative model improved signal identification in the 3' UTR regions.

Supervisor: Masato Ishikawa, Institute for New Generation Computer Technology (ICOT), Tokyo, Japan.

Transfer RNA Identification: tRNAscan version 2 (1992 – 1994)

tRNAscan identifies transfer RNAs in DNA sequences. The project's goal was to improve time efficiency while ensuring comparable identification results. I designed and implemented a time-efficient algorithm that minimized redundant identification of individual stems. For large sequences, version 2 of tRNAscan exhibits a 24-fold reduction in running time.

Supervisor: Christian Burks, Theoretical Biology and Biophysics Group (T-10), Los Alamos National Laboratory, Los Alamos, New Mexico, USA.

Fragment Assembly (1991 – 1993)

This project sought to develop software for assembling fragments produced during shotgun sequencing. To understand the process of fragment generation during shotgun sequencing and to form good biological and chemical assumptions, I met with members of the *E. coli* Genome Project and attended their lab meetings. My work involved exploring statistical analyses associated with predicting whether two fragments had sufficient similarity to justify origination from the same sequence.

Supervisor: Deborah A. Joseph, Computer Sciences Department, University of Wisconsin, Madison, Wisconsin, USA.

E. coli Genome Project: Case Study for Laboratory Management Systems (Fall 1991)

The "Zoo" Project aimed to develop a generic laboratory management system for scientists to manage experimental studies using object-oriented databases. The *E. coli* Genome Project served as a case study. The primary goal was to develop an entity-relationship model that captures all management aspects including tracking of DNA samples, supplies, reagents, selection and amplification of sequence, shotgun fragmentation, PCR amplification, gel electrophoresis, gel "reads" and conversion into sequence fragment data files, fragment assembly and reconstruction of the original DNA sequence. I developed the first piece of this model through interviews of project members regarding management of DNA samples prior to shotgun fragmentation and sequencing.

Zoo Database Project: Yannis E. Ioannidis, Computer Sciences Department, University of Wisconsin, Madison, Wisconsin, USA.

***E. coli* Genome Project**: Frederick R. Blattner, Genetics Department, University of Wisconsin, Madison, Wisconsin, USA.

3-D Tracking of Plant Root Growth (1987 – 1990)

Dr. Evans' research group studies the effect of gravity on plant root growth. Existing in-house software tracked root tip growth in two dimensions. I designed and implemented new software for three-dimensional tracking of root tip growth, the display of "live" tracking data and numerous analyses. Further, I utilized this software for characterizing a *Zea mays* mutant that had lost its gravity sensing capabilities.

Thesis Advisor: Michael L. Evans Plant Biology (formerly Botany), The Ohio State University, Columbus, Ohio, USA.

Supervisor: Hideo Ishikawa, Plant Biology (formerly Botany), The Ohio State University, Columbus, Ohio, USA.

Research Interests

In general terms, my current research focuses on acquisition of biological knowledge through genomics, knowledge storage in biological databases and knowledge integration into bioinformatics tools. The research programs I seek to establish in bioinformatics encompass (1) *in silico* genomic analysis, (2) biological resource development and management, (3) algorithmics and (4) software development. In addition, I will actively pursue collaborative research with both life and computational scientists.

A primary focus is the integration of biological complexity into bioinformatics tools. Many existing analyses resolve the "easy" portion of bioinformatics problems. Yet, it is well known in computer science that about 80% of a problem is solved relatively easily while the last 20% requires the most effort. I want to address the remaining 20%. In bioinformatics, resolution of the "hard" portion requires a profound understanding of the biology involved in a particular problem.

Recurring patterns: Identification and characterization of known genomic features

Many bioinformatics tools are available for identifying hidden instances of known genomic features. Yet, further development is necessary not only to identify missed occurrences but also to characterize more fully all instances. First, many tools utilize simplified biological models that do not address the biological complexities associated with a specific feature. Second, the perpetual discovery of novel genomic features requires on-going development of tools tailored to these new features. Therefore, I envision research to improve automated feature identification and characterization through integration of biological complexities and to develop new tools for initial *in silico* analysis of genomic features. Here are three sample projects.

The first project aims to improve tRNA identification. Current tools identify canonical tRNA molecules composed of four stems. Yet, non-canonical tRNAs exist that lack one stem but have compensatory stabilization interactions. Current tools cannot identify these alternative but equally functional structures. The solution requires expansion of the biological model to allow alternative structures of the tRNA molecule.

Second, organelle introns have underlying RNA primary sequence and secondary structure requirements. Though algorithms exist that identify certain intron classes, sensitivity is low. Generic secondary structure prediction tools do not perform well as they do not account for important primary sequence constraints. Basic sequence constraints and structural domains for introns are known. The difficulty is translating this biological model into a computationally tractable problem. My current research group is addressing two-dimensional structure classification and benchmarking of existing tools. My future research on this topic will involve collaboration with this group.

Third, RNA editing changes position-specific nucleotides in transcripts. Edits are precise, occur consistently and involve insertions, deletions or substitutions of one or several nucleotides. Both guide RNAs and proteins are known to mediate change by binding to a target sequence located near the transcript edit position. In some taxa, experimental evidence documents the mediating elements, in others, the target region. Dr. Gertraud Burger's group is exploring statistical and learning methods for automatic detection of target sites given well-characterized transcript edit positions in plant mitochondria. My future research on this topic will address more general detection of editing sites, in collaboration with this group (see also "*in silico* discovery" below).

Research Interests (continued)

Recurring patterns: Discovery of features under sequence, structure and/or interaction constraints

Development of many *in silico* tools required identification and characterization of biological features by life scientists. Comparative identification is possible due to structural or functional constraints within DNA, RNA and proteins that enforce sequence, structure or interaction conservation. *In silico* comparative genomics has proven to be a powerful method for discovering conserved, recurring features within a genome and across genomes. Yet, current approaches are mostly sequence-centric.

My research seeks to expand *in silico* exploration to discover not only conserved sequences but also recurring structures and new interactions. I will explore several comparative approaches including discovery of recurring combinations of known, identifiable features, discovery of interactions through identification of complementary patterns and discovery of interactions within the context of a constraining biological question. One of my current projects is addressing discovery of recurring feature combinations (see research projects). A future project aims to detect RNA edit sites, edit mediators and mediator binding sites in systems having limited experimental evidence.

Bioinformatics standards

Development of standards is crucial for scientific advancement. The life sciences have experimental, measurement and reporting standards. The computational sciences have standards for problem definition, complexity and efficiency measurement as well as benchmark establishment and comparison. Bioinformatics standards are still in their infancy. Standards are necessary to integrate life and computational science considerations: for example, (1) establishing methodologies for defining bioinformatics problems, (2) setting criteria for defining complete life science datasets and (3) defining measures of software effectiveness. One of my current projects tackles the issue of defining bioinformatics problems.

Teaching Experience

Integration of Life and Computational Sciences (BIN 3001)

Together with Dr. Gertraud Burger, I developed, presented and graded the database module of BIN 3001 for ~20 students. This is a required course in the bioinformatics undergraduate program. Université de Montréal, Montréal, Québec, Canada. Fall 2004, Fall 2005.

Introduction to Programming (CS 302)

I prepared, taught and graded an introductory programming course for ~25 students. At the time, this was a required course in numerous undergraduate science and engineering programs including computer sciences. University of Wisconsin, Madison, Wisconsin, USA. Fall 1990, Spring 1991, Fall 1995.

Student Co-Supervision

I supervised together with Dr. Gertraud Burger a broad range of bioinformatics graduate student projects across many biological research areas and utilizing numerous computational approaches. Students had varied scientific backgrounds, from strong biological with little computational knowledge to strong computational with little biological knowledge. Below is a brief project synopsis for each student.

Doctoral Candidates

Sivakumar Kannan – Protein function prediction for open reading frames (ORFs) without detectable sequence similarity using decision tree techniques

Yaoqing Shen – Prediction of nuclear-encoded mitochondrial proteins from expressed sequence tag (EST) sequences using support vector machine techniques

Master of Science Candidates

Premkumar Natarajan – Intron identification and folding approaches based on both primary sequence and secondary structure information

Hamsa Tadepally – Duplication history of zinc finger proteins in the human genome using phylogenetic and comparative approaches

Claudia Kleinman – Identification of target binding sites for RNA substitution editing exploring statistical approaches

Eric Chan – Hairpin structure identification in intergenic regions using a custom approach

Graduate Interns

Aurelie Lacoste – Genome map design tool for web and stand-alone applications

Dariouch Babaï – Identification of target binding site for RNA editing using neural networks

Teaching Experience, Interests and Philosophy

Experience

I have taught for several semesters an introductory programming course offered by the Department of Computer Sciences at the University of Wisconsin-Madison and an advanced bioinformatics course in the bioinformatics undergraduate program at the Université de Montréal. For the programming course (CS 302), I adapted teaching materials provided to me. For the bioinformatics course (BIN 3001), I developed together with Dr. Gertraud Burger a new module focusing on biological database design. I created and presented most lectures of the database module. This experience provides a solid basis for both new course development and teaching of future bioinformatics and computer science courses.

I am able to teach introductory and advanced bioinformatics courses. In computer science, I can teach introductory and mid-level courses as well as most database courses. Further, my 'translation skills' enable me to teach cross-disciplinary courses such as introductory life science courses for computer scientists and vice versa.

Interests

My primary teaching interest is training future scientists in both the utilization and development of bioinformatics tools. Tool users need to know which tool is appropriate for a specific biological problem. In addition, they need to learn how to write scripts to streamline their analysis. Developers, while designing new tools, need to know existing ones as well as which approaches are most feasible and timely for the problem. Bioinformatics specialists should have skills spanning both utilization and development of tools.

In addition, I am interested in developing a new bioinformatics program or expanding an existing one. My previous experience demonstrates my ability to develop bioinformatics courses for majors and non-majors.

Philosophy

Teaching is an art that draws students to learn and challenges them to step beyond their own expectations. Not all students are brilliant and naturally motivated. Some students find learning difficult; others need encouragement. Further, individuals learn orally, visually or experientially.

Learning becomes easier when materials are clear and concise, when the course encompasses both conceptual knowledge and hand-on experience, when the instructor is accessible and most when students enjoy and engage in the subject. In my lectures, I try to employ oral and visual learning and encourage in-class participation. Out-of-class work, early in a course, helps students interact with the material. Posing challenges and difficult problems entices bright students. Course projects enable students to apply their new knowledge. Team projects require communication and interaction, two skills that are especially important in bioinformatics.

Teaching and Research Reference

Dr. Gertraud Burger

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Director, Bioinformatics Undergraduate and Graduate Programs
Robert Cedergren Center for Bioinformatics and Genomics Research

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Research References

Dr. B. Franz Lang

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Director, Robert Cedergren Center for Bioinformatics and Genomics Research

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Dr. Deborah A. Joseph

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University of Wisconsin-Madison
1210 West Dayton Avenue
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Dr. Gary Lewandowski

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Department of Mathematics and Computer Science
Xavier University
3800 Victory Parkway
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