Malay Kumar Basu

Curriculum Vitæ

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Research Interests

Comparative and evolutionary genomics; Computational Biology; Bioinformatics; Data-mining and machine-learning; developing software tools for bioinformatics; genome informatics; high-performance, cloud and grid computing.

Academic Appointments

2022–Present **Associate Professor**, *Department of Pathology*, Kansas University Medical Center, Kansas City, KS, USA
Academic research, hiring, mentoring, teaching.

2022–Present **Adjuct faculty**, *Computational Biology Program*, Kansas University, Lawrence, KS, USA
Academic research, hiring, mentoring, teaching.

2012–2022 **Assistant Professor**, *Department of Pathology*, University of Alabama, Birmingham, Birmingham, AL, USA
Academic research, hiring, mentoring, teaching. An award-winning teacher and the chief architect of clinical genomics pipeline and led a team of software engineers and bioinformaticians.

2013–2022 **Director**, *Genifx Genome Informatics Facility*, University of Alabama, Birmingham, Birmingham, AL, USA
Genifx genome analysis facility at UAB (http://genifx.uab.edu) is a UAB Health Science Foundation funded project to create a next-generation sequence (NGS) data storage and analysis facility at UAB. I designed, created, and now maintain CHOIR/Genifx compute cluster at Department of Pathology, UAB.

2012–2022 **Associate Scientist**, *Comprehensive Cancer Center*, University of Alabama, Birmingham, Birmingham, AL, USA
Active researcher in cancer center.

2015–2022 **Senior Scientist**, *Informatics Institute*, University of Alabama, Birmingham, Birmingham, AL, USA
Member, educational committee designing graduate and undergraduate curricula.

2014–2022 **Assistant Professor**, *Department of Clinical and Diagnostic Sciences, School of Health Professions*, University of Alabama, Birmingham, Birmingham, AL, USA
Advisor to the master of bioinformatics program.

2020–2022 **Scientist**, *Center for Clinical and Translational Science (CCTS)*, University of Alabama, Birmingham, Birmingham, AL, USA
Develop university-wide bioinformatics collaboration.

2010–2012 **Assistant Professor**, *J. Craig Venter Institute*, Rockville, USA
Academic research, hiring, mentoring and leading a team of about 5 software engineers for developing annotation pipeline.

2009–2010 **Staff Scientist**, *J. Craig Venter Institute*, Rockville, USA
Academic research, hiring and leading a team of 5 software engineers for developing genome annotation pipelines.

Dec 2008–Feb 2009 **Senior Bioinformatics Engineer**, *J. Craig Venter Institute*, Rockville, USA
Wrote several high-performance software for genome annotation.

2003–2008 **Postdoctoral Fellow**, *National Center for Biotechnology Information (NCBI)*, National Institutes of Health (NIH), Bethesda, USA
Research in the field of computational biology and bioinformatics under the supervision of Dr. Eugene V. Koonin.

2002–2003 **Research Associate**, *Center for Cellular and Molecular Biology (CCMB)*, Hyderabad, India
Performed independent research in Bioinformatics. Single-handedly designed and built an eight node Linux cluster; installed hardware, performed software installation; helped in training and recruiting personnel for maintenance of the cluster.

Education

Degrees

2020–2021 **MBA**, *Collat Business School*, University of Alabama, Birmingham, USA
Anticipated 2021.

1995–2002 **PhD (Life Science)**, *Center for Cellular and Molecular Biology*, Hyderabad, India
Degree awarded in 2003.

1993–1995 **MTech (Biotechnology)**, *Jadavpur University*, Kolkata, India

1990–1992 **MSc (Zoology with specialization in Cytology and Genetics)**, *University of Calcutta*, Kolkata, India

1987–1990 **BSc (Honours in Zoology)**, *University of Calcutta*, Kolkata, India

Diplomas

2011 **Certificate in Machine Learning**, *Online course, Stanford University*, Taught by Andrew Ng

2011 **Certificate in Artificial Intelligence**, *Online course, Stanford University*, Taught by Sebastian Thrun and Peter Norvig

1994 **Certificate in Unix and C**, *Computer Science and Engineering Department*, Jadavpur University, Kolkata, India
C programming in Unix environment both PC and mainframe.

1993 **Programming Techniques and System Design Methodologies**, *Regional Computer Centre*, Kolkata, India
Details of software design and database programming is several languages on PC and mainframe— CYBER 180/84A.

1992 **Postgraduate Diploma in Ecology and Environment**, *Indian Institute of Ecology and Environment*, New Delhi, India
Environmental engineering and laws.

1992 **Contact Programme in Molecular Biology**, *Department of Zoology*, Banaras Hindu University, Varanasi, India
Basic molecular biology laboratory techniques.

Publications (* corresponding author)

Invited book chapters and reviews

[1] *__Basu M. K.__ Bioinformatics over the Web: SeWeR, as you may think. In R P Grant, editor, *Computational Genomics: Theory and Application*. Horizon Press, UK, 2004.

[2] **Basu M. K.** and Mishra R. K. Bioinformatics and the art of sequence analysis. In N C Gautam and M P Singh, editors, *Recent Advances in Biotechnology*. Shree Publishers, New Delhi, 2004.

Other publications

[3] Koo H., **Basu, M. K.**, Crowley M., Aislabie J, and Bej A. K. Draft Genome Sequence of Pseudomonas sp. Strain Ant30-3, a Psychrotolerant Bacterium with Biodegradative Attribute Isolated from Antarctica. *Genome Announc.*, 2(3):e00522–14, June 2014. PMID: 24903870.

[4] Haft D. H., **Basu. M. K.**, and Richter R. A. Braingrab: Capturing curator expertise as reusable annotation rules. *Nature Precedings*, 2009. doi:10.1038/npre.2009.3313.1.

[5] Spurlock B., Parker D., **Basu M. K.**, Hjelmeland A., and Mitra K. Modulation of mitochondrial fission activity maintains ovarian tumor initiating cells dependent on mitochondrial energetics. *Free Radical Biology and Medicine*, 128:S74, November 2018.

[6] Massicano F., Staley E. M., Halkidis K., Kocher N. K., Williams L. A., Marques M. B., Guillory B. K., Cao W, **Basu M. K.**, and Zheng X. L. Exome Sequencing Identifies Glycosylation Defects As a Probable Cause of Immune Thrombotic Thrombocytopenic Purpura. *Blood*, 134(Supplement_1):217–217, November 2019.

Software Publications

SaucePan Protein clustering software meta-package. Implements a novel language-modeling algorithm to identify orthologs. Internally used in JCVI.

ProPhylo — A high-performance parallel Perl framework for genome-scale phylogenetic profile comparison and the associated databases. Available at https://github.com/malaybasu/ProPhylo.

NCBIWeb — Perl modules to automate NCBI web server.

AnnotationRules — Functional annotation of protein using rules. Used in annotation pipeline at JCVI.

SeWeR — A very popular and widely used interface for bioinformatics services. SeWeR has been translated into several languages, and written using JavaScript and DHTML. Available at http://www.bioinformatics.org/sewer.

Pastel — A Perl framework for generating Scalable Vector Graphics (SVG) and animation. The API closely resembles Java Graphics2D API with state-of-the–art computational geometry support. Available at http://www.bioinformatics.org/pastel.

BioSVG — The first application of SVG in bioinformatics. A Perl framework for generating high-resolution vector graphics for biological data. Available at http://www.bioinformatics.org/biosvg.

Savvy — A CGI-based plasmid drawing software that generates print-quality, editable plasmid maps in SVG format. Available at http://www.bioinformatics.org/savvy.

ABI.pm — A module for parsing ABI chromatogram files. Available from CPAN (http://search.cpan.org/~malay/ABI-0.01).

SeqToolBox — My personal sequence analysis toolbox. Used in many projects that I wrote. Available at https://github.com/malaybasu/SeqToolBox

Font::TTFMetrics — A Perl module for parsing True Type Font file. Available from CPAN (http://search.cpan.org/~malay/Font-TTFMetrics-0.1/).

pastel-ttf2svg.pl — Converts TTF file to SVG font file. Available from CPAN. (http://www.cpan.org/pub/CPAN/authors/id/M/MA/MALAY/pastel-ttf2svg-0.04.zip).

Clinical genomics pipeline — I was the chief architect of the clinical genomics pipeline of at UAB, Dept. of Pathology.

Awards and honors

2020 — Excellence in Teaching Award by Graduate school, University of Alabama, Birmingham.

2017–2019 — Elected member of UAB faculty senate.

2017 — Nominated for Dean's excellence award in teaching, School of Medicine, University of Alabama, Birmingham.

2016 — Nominated for Dean's excellence in teaching award, School of Medicine, University of Alabama, Birmingham.

2012–Present — Adjunct faculty F1000 prime.

2003–2008 — NIH intramural fellowship.

2002 — Travel award from O'Reilly publishing.

2002 Travel award from Council for Scientific and Industrial Research, India.

1997–2001 Senior research fellowship from Council for Scientific Industrial Research, India.

1995–1997 Junior research fellowship from Council for Scientific Industrial Research, India.

1993–1995 Fellowship from Department of Biotechnology, Govt. of India.

Awards and honors from lab

2019 Felipe Massicano won departmental travel award to attend American Society of Hematology annual meeting held in Orlando, FL.

2019 Felipe Massicano won Abstract Achievement Award at the American Society of Hematology annual meeting held in Orlando, FL.

2018 Amrita Lakhanpal, high school student. Her project was awarded Intel Excellence in Computer Science award, 2018.

Editorial boards

2021–Present Editor, BMC Genomics Data (Springer).

2020–Present Reviewing board Member, Cancers (MDPI, IF: 6.126).

2015–2020 Editorial board Member, Heliyon (Elsevier).

2014–Present Appointed editorial board member; Bioinformatics section, BioMed Research International (Impact: 2.88).

2013–Present Appointed editorial Board member; Evolutionary Biology Section, BioMed Research International

2011–Present Reviewing board member, Frontiers in Bioinformatics and Computational Biology.

Grant review

2023 National Science Foundation (NSF), USA.

2021 Israel Science Foundation (ISF), Israel.

2017 National Science Foundation (NSF), USA.

2017 Selected for NIH Early Career Reviewer (ECR) program.

2015 National Science Foundation (NSF) career award.

Grants

Ongoing

2023-2028 *"The Role of ANKRD Proteins in Modulating Thrombotic Thrombocytopenic Purpura"*; NIH; Zheng (PI); role: co-investigator.

Completed

2013-2022 *Genifx service center*; Health Science Foundation; role: PI.

2015–2022 *RT-SQuARED-M method to study the precise role of mitochondria in the oxidative damage caused by environmental toxins*; NIH; Mitra(PI); role: co-investigator.

2019–2021 *Research subcontract from Yale University*; Yale University; role: co-investigator.

2018-2019 *Pathogenesis of Thrombotic Microangiopathy.*; NIH; Zheng (PI); role: co-investigator.

2017-2018 *Studying the translational impact of the mitochondrial fission protein, Drp1, in epithelial ovarian cancer*; UAB CCTS; role: co-PI.

2015-2016 *The role of the mitochondrial protein, Drp1, in ovarian cancer chemoresistance*; UAB CCC; Mitra (PI); role: co-investigator.

2015-2016 *Genetic basis of glioblastoma*; UAB research acceleration fund; Nabors (PI); role: co-investigator.

2012-2015 Acted as co-investigator and collaborator in many NIH funded projects at JCVI.

Councils and committees

2023 Poster judge, Greenwald Symposium. Kansas University Medical Center.

2022 Poster judge, Greenwald Symposium. Kansas University Medical Center.

2021 Moderator, Annual Translational and Transformative Informatics Symposium (ATTIS).

2020 Judge, COVID-19 hackathon, University of Alabama, Birmingham.

2019 Member, organizing committee, Midsouth Bioinformatics Conference (MCBIOS), 2019.

2019 Poster judge, Midsouth Bioinformatics and Computational Biology society conference, 2019

2019 Faculty Advisory Committee of Bryan Guillory.

2018 Member, faculty search committee, Genomic Diagnostic and Bioinformatics division, Department of Pahtology.

2018 Judge, Pathology research day symposium.

2017–Present Member, Bioinformatics Educational Committee, Informatics Institute, UAB.

2017–Present Member, Informatics Gateway Committee, a research evaluation committee created by CCTS and Informatics institute for facilitating bioinformatics collaborations.

2017–Present Member, departmental IRB review committee.

2017–2019 Elected member of UAB faculty senate.

2017–2019 Member, graduate curriculum committee, UAB faculty senate.

2017–2018 Chair, Bioinformatics Power Talks steering committee, a joint initiative between Informatics Insitute and CB2 computational biology and bioinformatics group at UAB.

2015–Present Thesis advisory committees of, Joseph Palmer, John Schoelz, Sean Wilkinson

2014–Present Advisor to the Molecular Tumor Board, UAB.

2012–2014 Faculty Advisory Council member for representing the following divisions of Department of Pathology: Informatics, Neuropathology, Forensic Pathology.

2012–Present Founder, Computational Biology and Bioinformatics activity (CB2; http://uab.edu/cb2) at UAB.

2006–2007 Institute selected member of Fellows Committee (FELCOM) at NIH.

2007 Chief judge of Bioinformatics and Computational Biology section of Fellows Award of Research Excellence (FARE) at NIH.

2006 Judge, RECOMB satellite workshop on comparative genomics, Montréal, Canada.

Invited talks and workshops

2023-09-25 Invited speaker, Kidney Institute, Kansas Univeristy Medical Center, Kansas, USA.

2023-09-08 Invited speaker, Department of Biochemistry, Kansas Univeristy Medical Center, Kansas, USA.

2023-01-10 Invited speaker, symposium on "Biology for better health". Department of Zoology, University of Calcultta, India.

2022-10-18 Invited speaker, Center for Computational Biology, University of Kansas, Lawrence, KS, USA.

2020-04-(06–09) Bioinformatics workshop at Yale School of Medicine.

2020-04-06 Department of Immunology, Yale University, Connecticut, USA. (Postponed for lockdown).

2020-03-13 Annual Translational and Transformative Informatics Symposium (ATTIS), 2020. "Reading the book of life: the grammar of genes".

2019-10-07 Department of Microbiology and Immunology, University of Mississippi Medical Center, University of Mississippi, Oxford, Mississippi, USA. Visited various department and delivered a talk entitled: "Reading the book of life: The language of the genes".

2019-03-30 Midsouth Bioinformatics and Computational Biology Society Conference, 2019. "Reading the book of life: Language of Genomes".

2018-04-25 Translational Bioinformatics Symposium, UAB. "DBGES: A Novel Gene Expression signature for developing a mitochondria based targeted therapy".

2018-01-29 UAB department of medicine, Hematology and Oncology conference: "Cancer genome data-mining to identify a novel gene-expression signature for ovarian cancer prognosis".

2017-05-03 UAB 1st Annual Translational Bioinformatics Mini-Symposium. "A novel gene-expression signature for ovarian cancer prognosis".

2018-01-29 UAB department of medicince, Hematology and Oncology conference: "Cancer genome data-mining to identify a novel gene-expression signature for ovarian cancer prognosis".

2017-05-03 UAB 1st Annual Translational Bioinformatics Mini-Symposium. "A novel gene-expression signature for ovarian cancer prognosis".

2016-09-21 UAB Department of Biology. "Language of the genes".

2016-02-09 UAB Department of Pathology. Molecular and Cellular Pathology Seminar "Unraveling Novel Biological Paradigms from Large-scale Analysis of Cancer Genomes".

2014-03-06 Invited speaker, Hudson Alpha Institute of Bioinformatics, AL.

2013 Genetics and Genomics Seminar Series (Jan 2013): "Investigating Biological Systems Using Phylogenetic Profiling".

2011 Invited faculty to teach in the training course "Molecular Methods for Characterization, conservation and utilization of biodiversity", held in Feb-March, 2011 in Hyderabad, India.

2012 University of Alabama, Birmingham.

2011 Center for DNA fingerprinting and Diagnostics, Hyderabad, India.

2008 Memorial Sloan-Kettering Cancer Center, NY.

2008 Institute of Genome Sciences, Baltimore, MD.

2008 University of Maryland, College Park, MD.

2002 Speaker in *O'Reilly Bioinformatics Technology conference*, 2002, held in Tucson, Arizona. I delivered a talk entitled, *"DHTML and Scalable Vector Graphics in Bioinformatics"*.

Teaching Experience

2023–Present Course master of "CB2-101: Bioinformatics Shop Class". A highly rated (rating score 9.5/10) hands-on 48 hours training course, open to everyone, at KUMC. Also a graduate course of 3 credit hours. http://cb2edu.org

2021–2022 Co-director and designer of a new undergraduate bioinformatics course, "Introductory bioinformatics".

2018–2022 Co-director and designer of a new bioinformatics course, "INFO 510: Programming with biological data".

2014–2022 Course master of "CB2-101: Introduction to Scientific Computing". A highly rated (rating score 9.5/10) hands-on 48 hours training course, open to everyone, at UAB. Also a graduate course of 3 credit hours. http://cmb.path.uab.edu/training/cb2-101.html.

2015–2022 Course master of "CB2-201: Bioinformatics and Computational Biology". A highly rated (9.5/10) 40hr hands-on training course. Also a 3 credit graduate course. http://cmb.path.uab.edu/traning/cb2-201.html.

2018 Taught in GBS779: Translational Research. Course master: Eddy Yang.

2017–2018 Organizer and course master of "Bioinformatics Power Talks". This is a new university-wide bioinformatics research and journal discussion club, jointly sponsored by Computational Biology and Bioinformatics (CB2) and Informatics Institute, UAB. This is also a registered GBS course with 1 credit.

2014 Course master of "Computational Genomics". Advanced bioinformatics course. GBS 787. No longer offerred.

2014-02-05 Taught and evaluated evolutionary genomics GBS 722.

2013–2017 Course master of a highly rated Computational Biology and Bioinformatics (CB2) journal club. Also a graduate school course of 1 credit hour.

2013 Taught and evaluated “Molecular Evolution” GBS 722.

2013 Highly rated laboratory medicine course on “Genomics” (Rating 4.65/5.00).

2012 School of Health Professionals “Introduction to Bioinformatics.”

Mentoring

2023–Present Dincer Killic, Research Assistant.

2018–2020 Filepe Massicano, Postdoctoral fellow.

2019–2020 Christopher Coffee, Undergraduate student intern.

2016–2018 Lijia Yu, Visiting Fellow. Joining Cambridge University, UK to pursue Ph.D.

2017–2018 Amrita Lakhanpal, high school students. Her project was awarded Intel Excellence in Computer Science Award.

2017 Margaret Bell. GBS Rotation student

2014–2016 Deepak Tanwar, Visiting Fellow then Research Assistant. Currently pursuing Ph.D. in ETH Zurich.

2014–2016 Emannuel Penha, Visiting Fellow. Now faculty in Brazil.

2014–2015 Aseygul Bulut, Part-time student assistant.

2013 Paul Boothe, Medical student intern in Cancer Research Experience for Students (CaRES) program.

2013 Darshan Patel, Biotechnology Intern, School of Health Professions.

2011 Meghna Yadigiri, Summer Intern at J. Craig Venter Institute.

Conferences

Oral presentation

2023-01-10 Invited speaker, symposium on ”Biology for better health”. Department of Zoology, University of Calcultta, India.

2021-07-27 Basu MK (2021) Linguistic modeling of proteome complexity in cancer: evolutionary implications. Intelligent Systems in Molecular Biology (ISMB).

2020-10-29 Basu MK (2020) Reading the book of life: the language of proteins. ISCB-Latin America, SolBio BioNetMX.

2020-07-14 Basu MK (2020) Reading the book of life: the language of proteins. Intelligent Systems in Molecular Biology (ISMB).

2020-07-13 Basu MK (2020) Exome sequencing identifies abnormalities in glycosylation and ANKRD36C defects as probable causes of immune-mediated thrombotic thrombocytopenic purpura (TTP). Intelligent Systems in Molecular Biology (ISMB).

2019-12-7 Massicano F, Staley E, Halkidis K, Kocher N, Williams LA, Marques MB, Guillory B, Cao W, Basu MK, Zheng XL (2019) Exome sequencing identifies glycosylation defects as a probable cause of immune thrombotic thrombocytopenic purpura, American Society of Hematology annual conference, Dec 7-10, 2019, Orlando, FL.

Posters and abstracts

2023 Moreno A, Basu MK, Soares M (2023) Single cell analysis of placental cells, Greenwald Symposium, Kansas University Medical Center.

2020-11-16 Harada S, Iriabho E, Flannery A, Worthey E, Basu MK, Yemelyanova A, Morlote D, Mackinnon AC (2020) Pindel as a Back-Up INDEL Caller to a GATK4 Mutect2 Based In-House Developed Somatic Secondary Analysis Bioinformatics Pipeline for a Custom Clinical Cancer NGS Panel. *Association for Molecular Pathology (AMP) 2020 Annual Meeting & Expo. Vancouver, BC, Canada*.

2020-07-13 Basu MK (2020) Exome sequencing identifies abnormalities in glycosylation and ANKRD36C defects as probable causes of immune-mediated thrombotic thrombocytopenic purpura (TTP). Intelligent Systems in Molecular Biology (ISMB).

2019-12-7 Massicano F, Staley E, Halkidis K, Kocher N, Williams LA, Marques MB, Guillory B, Cao W, Basu MK, Zheng XL (2019) Exome sequencing identifies glycosylation defects as a probable cause of immune thrombotic thrombocytopenic purpura, American Society of Hematology annual conference, Dec 7-10, 2019, Orlando, FL.

2018-11-14 Spurlock B, Parker D, Basu MK, Hjelmeland A, Mitra K (2018) Modulation of mitochondrial fission activity maintains ovarian tumor initiating cells dependent on mitochondrial energetics. Presented at The Society for Redox Biology and Medicine's 25th Annual Conference (SfRBM 2018), November 14-17, 2018, Chicago, IL, USA.

2018-04-25 Yu L, Mitra K, Arend R, Basu MK (2018) DBGES-a predictive and prognostic gene-expression signature for ovarian and other cancers, UAB translational bioinformatics conference.

2017-07-09 Parker D, Spurlock B, Tanwar D, Basu MK, Mitra K (2017) Mitochondrial energetics regulated by mitochondrial fission modulates cell cycle towards maintaining stemness. GRC Cell Growth and Proliferation, July 9-14 , 2017

2017-06-17 Yu L, Basu MK (2017) The language of protein domains, Pathology research retreat.

2016-11-05 UAB Comprehensive Cancer Center Symposium Mutation distribution and codon usage bias in oncogene and tumor-suppressor genes.

2016-09-09 UAB Core day: Genifx: Genome Informatics Facility at UAB.

2016-07-11 Intelligent Systems in Molecular Biology (ISMB), Orlando, FL "Position-dependent mutation distribution and codon usage bias in oncogene and tumor-suppressor genes".

2016-02-03 Parker D, Archana I, Basu MK, Mitra K (2016) Mitochondrial regulation of Cyclin E, AACR Precision Medicine Series: Cancer Cell Cycle.

2015-07-19 Parker D, Archana I, Basu MK, Mitra K. (2015) Mitochondrial fission protein Drp1 controls cell proliferation in a cell density dependent manner by regulating Cyclin E. Cell Symposia, Multifaceted Mitochondria, Chicago, IL, USA , July 19-21, 2015.

2014-11-18 UAB Core Day. "Genifx: Genome Informatics Facility @ UAB".

2014-10-06 UAB Comprehensive Cancer Center Symposium "ContrastRank: A New Method for Ranking Cancer Driver Genes and Tumor Samples Classification".

2013-11-05 UAB Comprehensive Cancer Center Symposium. Cancer Center Symposium. "The Role of Mitochondrial Fission and Fusion in Evolution of Cancer Genes", with Paul Boothe.

Skills

Bioinformatics

All aspects of classical bioinformatics, comparative genomics, evolutionary genomics, Next-generation sequence anlysis (NGS), RNASeq, whole-genome and exome analysis, single-cell data analysis, cancer genomics.

Data mining and AI

Traditional machine learning, regressions, SVM, Radom Forrest, clustering, PCA, PSLDA, SPLSDA, NMF, Deep learning using Keras, TensorFlow.

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Computers

Software development: Algorithm design, object-oriented system design, design patterns, cross-platform and platform-dependent software development on GNU/Linux platform using different languages, network programming, database development, system programming, code maintenance and debugging.

Languages: C, C++, Java, Perl, Python, JavaScript, SQL, R, Octave, Matlab, LaTeX.

Databases: MySQL, SyBase, SQLite, Barkley DB.

Cloud computing and containers: AWS, Google cloud, Docker

High Performance Computing

Extensive knowledge in hardware, purchasing, and setting up and running Linux cluster, parallel programming using MPI and PVM, and programming job schedulers like SGE and SLURM.