

MCB4324 Computational Genomics and Epigenomics

Spring 2026 – 3 credits

Class Location: This course and all class materials (e.g. lecture podcasts, discussion papers, quizzes, assignments, exams, and final project) are available online through the Canvas course website (see below).

Instructor Information

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Office Hours: Mondays & Wednesdays 2:00 pm - 3:00 pm or by appointment through Zoom Conferences under Canvas.

Course Description

Genomics and epigenomics utilize high-throughput sequencing technologies in understanding biology questions. The primary goal of this course is to introduce history, theory, latest advances, and computational approaches in (epi)genomics for conducting large-scale genomic analyses. Course topics include sequence alignment, genome assembly and annotation, variant identification, transcriptomics, small RNAs, DNA methylation, histone modification, open chromatin region, and 3D chromatin interaction.

Course Objectives

After successful completion of this course, students should be able to:

- use basic command skills in UNIX.
- show mastery of the fundamental concepts and methodology of genomics and epigenomics.
- recognize and differentiate the advantages and disadvantages of different computational approaches and methods.
- employ and compare the computational approaches and methods in analyzing different types of high-throughput genomic data.
- interpret data generated by different computational approaches and methods.

Course Website

Login available through Canvas <https://elearning.ufl.edu/>

Course Prerequisite

None. Many of the computational tools we will use are installed on the HiPerGator supercomputers. Every student will be provided with user accounts on the HiPerGator UNIX server. Access to the course UNIX server is required to complete the laboratory exercises and assignments.

Important Dates

- Midterm Exam: Feb 21-Mar 2, 2026.
- Final Exam: Apr 25-May 1, 2026.

Textbook Information

Textbook is not required. Prior to each class, PDF and other relevant documents will be curated and accessible online. In addition, supplementary handouts will be provided for your review.

Students are also required to read research articles pertinent to the subjects, which will be posted on the course website.

Here are some recommended textbooks that could prove beneficial or engaging:

- Concepts in Bioinformatics and Genomics. 2017. Jamil Momand, Alison McCurdy, Notes by Silvia Heubach, and Nancy Warter-Perez. ISBN: 9780190610548.
- Computational Epigenetics and Diseases. 2019. ISBN: 978-0-12-814513-5.

The following research articles are **OPTIONAL** for you to read:

Weeks 1 & 2:

- Nayfach S. et al. 2021. A genomic catalog of Earth's microbiomes. *Nat Biotechnol* 39, 499-509. <https://doi.org/10.1038/s41587-020-0718-6>.
- Gauthier J., Vincent A.T., Charette S.J., Derome N. 2019. A brief history of bioinformatics. *Brief Bioinform.* 20, 1981-1996. <https://doi.org/10.1093/bib/bby063>.

Week 3:

- Nurk S. et al. 2022. The complete sequence of a human genome. *Science* 376, 44-53. <https://doi.org/10.1126/science.abj6987>.
- Zhou X., Ren L., Meng Q., Li Y., Yu Y., Yu. J. 2010. The next-generation sequencing technology and application. *Protein Cell* 1, 520-536. <https://doi.org/10.1007/s13238-010-0065-3>.

Week 5:

- Deciphering developmental disorders study. 2017. Prevalence and architecture of de novo mutations in developmental disorders. *Nature* 542, 433-438. <https://doi.org/10.1038/nature21062>.
- Uffelmann, E. et al. 2021. Genome-wide association studies. *Nat Rev Methods Primers* 1, 59. <https://doi.org/10.1038/s43586-021-00056-9>.

Week 6:

- Logsdon G.A., Vollger M.R., Eichler E.E. 2020. Long-read human genome sequencing and its applications. *Nat Rev Genet* 21, 597-614. <https://doi.org/10.1038/s41576-020-0236-x>.
- Nicholas J.D., Wayne A., Kim K., Amanda C., Christopher J.C. 2022. No one tool to rule them all: prokaryotic gene prediction tool annotations are highly dependent on the organism of study, *Bioinformatics*, 38, 1198–1207, <https://doi.org/10.1093/bioinformatics/btab827>.

Week 7-9:

- Love M.I., Huber W., Anders S. 2014. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. *Genome Biol* 15, 550. <https://doi.org/10.1186/s13059-014-0550-8>.
- Kim D., Paggi J.M., Park C. et al. 2019. Graph-based genome alignment and genotyping with HISAT2 and HISAT-genotype. *Nat Biotechnol* 37, 907-915. <https://doi.org/10.1038/s41587-019-0201-4>.
- Liu Y., Zhou J., White K.P. 2014. RNA-seq differential expression studies: more sequence or more replication? *Bioinformatics* 30, 301–304. doi:10.1093/bioinformatics/btt688.

Week 10:

- Lafzi A., Moutinho C., Picelli S., Heyn H. 2018. Tutorial: guidelines for the experimental design of single-cell RNA sequencing studies. *Nat Protoc* **13**, 2742–2757. <https://doi.org/10.1038/s41596-018-0073-y>.
- Vallejos C., Risso D., Scialdone A., Marioni J.C. 2017. Normalizing single-cell RNA sequencing data: challenges and opportunities. *Nat Methods* **14**, 565–571. <https://doi.org/10.1038/nmeth.4292>.

Week 11:

- Chen X., Rechavi O. 2022. Plant and animal small RNA communications between cells and organisms. *Nat Rev Mol Cell Biol.* **23**, 185–203. <https://doi.org/10.1038/s41580-021-00425-y>.
- Iwasaki Y.W., Siomi M.C., Siomi H. 2015. PIWI-Interacting RNA: Its Biogenesis and Functions. *Annu Rev Biochem* **84**: 405-433. <https://doi.org/10.1146/annurev-biochem-060614-034258>.

Week 12:

- Field A.E., Robertson N.A., Wang T., Havas A., Ideker T., Adams P.D. 2018. DNA methylation clocks in aging: categories, causes, and consequences. *Mol cell*, **71**, 882-895. <https://doi.org/10.1016/j.molcel.2018.08.008>.
- Tse O.Y.O. et al. 2021. Genome-wide detection of cytosine methylation by single molecule real-time sequencing. *Proc Natl Acad Sci U S A* **118**, e2019768118. <https://doi.org/10.1073/pnas.2019768118>.
- Yang J.H. et al. 2023. Loss of epigenetic information as a cause of mammalian aging. *Cell* **186**: 305-326.e27. <https://doi.org/10.1016/j.cell.2022.12.027>.

Week 13:

- Whyte W.A., Orlando D.A., Hnisz D., Abraham B.J., Lin C.Y., Kagey M.H., Rahl P.B., Lee T.I., Young R.A. 2013. Master transcription factors and mediator establish super-enhancers at key cell identity genes. *Cell* **153**: 307-319. <https://doi.org/10.1016/j.cell.2013.03.035>.
- Hnisz D., Abraham B.J., Lee T.I., Lau A., Saint-André V., Sigova A.A., Hoke H.A., Young R.A. 2013. Super-enhancers in the control of cell identity and disease. *Cell* **155**: 934-947. <https://doi.org/10.1016/j.cell.2013.09.053>.
- Skene P.J., Henikoff S. 2017. An efficient targeted nuclease strategy for high-resolution mapping of DNA binding sites. *Elife* **6**: e21856. <https://doi.org/10.7554/eLife.21856>.
- Meers M.P., Bryson T.D., Henikoff J.G., Henikoff S. 2019. Improved CUT&RUN chromatin profiling tools. *Elife* **8**: e46314. <https://doi.org/10.7554/eLife.46314>.

Week 14:

- Dixon JR, Gorkin DU, Ren B. 2016. Chromatin Domains: The Unit of Chromosome Organization. *Mol Cell* **62**, 668-80. <https://doi.org/10.1016/j.molcel.2016.05.018>.
- Sexton T, Cavalli G. 2015. The role of chromosome domains in shaping the functional genome. *Cell* **160**: 1049-1059. <https://doi.org/10.1016/j.cell.2015.02.040>.

Grades and Grade Points:

For information on current UF policies for assigning grade points, see <https://catalog.ufl.edu/UGRD/academic-regulations/grades-grading-policies/>.

The course grading is based on a total of 800 points, distributed as follows:

- **Weekly or Biweekly Quizzes (100 points, 10% of final grade):** Weekly or biweekly quizzes will be administered through the Canvas course website. These quizzes are designed to reinforce your understanding of lectures and course materials.
- **Post-Class Assignments (400 points, 40% of final grade):** Regular assignments will be provided after class to reinforce your practice of computational approaches covered in lectures. Late submissions will incur a 5% penalty per day.
- **Midterm (120 points, 12% of the final grade) and final exam (180 points, 18% of the final grade):** Both exams will focus exclusively on material presented in class, assessing your understanding of fundamental concepts and techniques in computational genomics and epigenomics.

Submission Methods: You need to submit your assignment through our class Canvas website.

930 – 1000	points	93% - 100%	A
900 – 929	points	90% - 92.9%	A-
870 – 899	points	87% - 89.9%	B+
830 – 869	points	83% - 86.9%	B
800 – 829	points	80% - 82.9%	B-
770 – 799	points	77% - 79.9%	C+
730 – 769	points	73% - 76.9%	C
700 – 729	points	70% - 72.9%	C-
670 – 699	points	67% - 69.9%	D+
630 – 669	points	63% - 66.9%	D
600 – 629	points	60% - 62.9%	D-
Less than 600 points		<60%	E

Attendance and Make-Up Work

Requirements for class attendance and make-up exams, assignments and other work are consistent with university policies that can be found at:

<https://catalog.ufl.edu/UGRD/academic-regulations/attendance-policies/>.

Tentative Course Schedule

Week	Date	Topic	Quizzes and Assignments
Weeks 1-2	Jan 12-25	UNIX Basics: 1. Course information 2. Introduction of supercomputer 3. Overview of the UNIX operating system 4. Introduction and hands-on UNIX for shell and command lines 5. Hands-on UNIX for module and running batch jobs 6. Introduction to awk	Quiz 1 Assignment 1, due by 11:59 PM Feb 2
Week 3	Jan 23-Feb 1	Sequencing technologies and sequences: 1. Brief history of genomics and epigenomics 2. DNA sequencing (sequencing technologies, FASTA and FASTQ sequences, and tools) 3. Human genome project	Quiz 2
Week 4	Jan 30-Feb 8	Sequence mapping and alignment: 1. Sequence alignment (Dynamic programming, local and global alignments)	Quiz 3

		2. Sequence mapping (SAM/BAM, Samtools, BWA, and Bowtie2) 3. Sequence alignment (MUSCLE, ClustalW, and T-coffee)	Assignment 2, due by 11:59 PM Feb 16
Week 5	Feb 6-15	Variant identification and GWAS analysis: 1. Single nucleotide polymorphism calling (SNPs) 2. Structural variant analysis (InDel) 3. VCF annotation and interpretation (GATK, picard, bcftools and vcftools toolkits) 4. Genotyping by sequencing and genome-wide association studies (plink)	Quiz 4 Assignment 3, due by 11:59 PM Feb 23
Week 6	Feb 13-22	Genome assembly and annotation: 1. Genome assembly (<i>de novo</i> genome assembly & pan genome) 2. Genome annotation (gene finding) 3. Genome annotation (transposable elements finding) 4. PacBio assembly and gene prediction (canu, circulator, prokka)	Quiz 5 Assignment 4, due by 11:59 PM Mar 2
Week 7	Feb 21-Mar 2	Midterm exam (Weeks 1-6)	
Week 7-9	Feb 20-Mar 16	RNA-sequencing and differentially expressed genes: 1. RNA-seq experimental design 2. RNA-seq reads quality control, trimming, mapping, and qualification (FASTQC, Trimmomatic, HISAT2, and HTSeq) 3. Identification of differentially expressed genes (DESeq2) 4. R and RStudio 5. Gene ontology (GO) analysis 6. Clustering (Heatmap, K means, and others)	Quiz 6 Assignment 5, due by 11:59 PM Mar 23
	Mar 14-22	No classes, spring break.	
Week 10	Mar 20-29	Single-cell RNA-seq: 1. Single cell RNA-seq technologies 2. Preprocessing and quality control 3. Read alignment and quantification 4. Dimension reduction and visualization 5. Clustering and annotation 6. Single cell RNA-seq data analysis (Seurat)	Quiz 7
Week 11	Mar 27-Apr 5	Small RNAs: 1. Biogenesis and function of small RNAs (microRNAs, small interfering RNAs, and piwi-interacting RNA) 2. Small RNA identification and analyses 3. Target site prediction of small RNAs 4. bedtools	Quiz 8 Assignment 6, due by 11:59 PM Apr 13
Week 12	Apr 3-12	DNA methylation in plants and animals: 1. DNA methylation (Initiation and maintenance of DNA methylation) 2. Techniques to measure DNA methylation 3. Identification of differentially methylated regions (DMRs) 4. Integrative analysis of DEGs, small RNAs and DMRs	Quiz 9 Assignment 7, due by 11:59 PM Apr 20
Week 13	Apr 10-19	Histone modification: 1. Chromosome structure and histone tail modifications	Quiz 10

		2. Histone marks (H3K9me2, H3K27me3, H3K4me3, etc.) 3. ChIP-seq principles and analysis (MACS2, IDR, and IGV) 4. Cut&Run principles	
Week 14	Apr 17-22	Chromatin interaction: 1. Chromatin accessibility (DNase-seq, ATAC-seq including single-cell ATAC-seq, and MNase-seq) 2. 3D chromatin interaction (HiC, chromatin loops, topologically associating domains, A/B compartments, chromosome territories, and HiC-Pro analysis)	
	Apr 25-May 1	Final exam	

Note: Exact schedule may be changed based on the progress of the class.

Online Course Evaluation Process

Student assessment of instruction is an important part of efforts to improve teaching and learning. At the end of the semester, students are expected to provide feedback on the quality of instruction in this course using a standard set of university and college criteria. Students are expected to provide professional and respectful feedback on the quality of instruction in this course by completing course evaluations online via GatorEvals. Guidance on how to give feedback in a professional and respectful manner is available at:

<https://gatorevals.aa.ufl.edu/students/>. Students will be notified when the evaluation period opens and can complete evaluations through the email they receive from GatorEvals, in their Canvas course menu under GatorEvals, or via <https://ufl.bluer.com/ufl/>. Summaries of course evaluation results are available to students at: <https://gatorevals.aa.ufl.edu/public-results/>.

University Policy and Support Resources

The most up-to-date university-wide policies and support resources on academic policies, grading, attendance, accommodations, and wellness service can be found at the UF Syllabus Policy page:

👉 <https://syllabus.ufl.edu/syllabus-policy/uf-syllabus-policy-links/>

Academic Honesty

As a student at the University of Florida, you have committed yourself to uphold the Honor Code, which includes the following pledge: *"We, the members of the University of Florida community, pledge to hold ourselves and our peers to the highest standards of honesty and integrity."* You are expected to exhibit behavior consistent with this commitment to the UF academic community, and on all work submitted for credit at the University of Florida, the following pledge is either required or implied: *"On my honor, I have neither given nor received unauthorized aid in doing this assignment."*

It is assumed that you will complete all work independently in each course unless the instructor provides explicit permission for you to collaborate on course tasks (e.g. assignments, papers, quizzes, exams). Furthermore, as part of your obligation to uphold the Honor Code, you should report any condition that facilitates academic misconduct to appropriate personnel. It is your individual responsibility to know and comply with all university policies and procedures regarding academic integrity and the Student Honor Code. Violations of the Honor Code at the University

of Florida will not be tolerated. Violations will be reported to the Dean of Students Office for consideration of disciplinary action. For more information regarding the Student Honor Code, please see: <http://www.dso.ufl.edu/sccr/process/student-conduct-honor-code>.

Software Use

All faculty, staff and students of the university are required and expected to obey the laws and legal agreements governing software use. Failure to do so can lead to monetary damages and/or criminal penalties for the individual violator. Because such violations are also against university policies and rules, disciplinary action will be taken as appropriate.

Services for Students with Disabilities

The Disability Resource Center coordinates the needed accommodations of students with disabilities. This includes registering disabilities, recommending academic accommodations within the classroom, accessing special adaptive computer equipment, providing interpretation services and mediating faculty-student disability related issues. Students requesting classroom accommodation must first register with the Dean of Students Office. The Dean of Students Office will provide documentation to the student who must then provide this documentation to the instructor when requesting accommodation

0001 Reid Hall, 352-392-8565, www.dso.ufl.edu/drc/

Campus Helping Resources

Students experiencing crises or personal problems that interfere with their general well-being are encouraged to utilize the university's counseling resources. The Counseling & Wellness Center provides confidential counseling services at no cost for currently enrolled students. Resources are available on campus for students having personal problems or lacking clear career or academic goals, which interfere with their academic performance.

- *University Counseling & Wellness Center, 3190 Radio Road, 352-392-1575, www.counseling.ufl.edu*
Counseling Services
Groups and Workshops
Outreach and Consultation
Self-Help Library
Wellness Coaching
- U Matter We Care, www.umatter.ufl.edu/
- *Career Connections Center, First Floor JWRU, 392-1601, <https://career.ufl.edu/>.*
- Student Success Initiative, <http://studentsuccess.ufl.edu>.

Student Complaints

- Residential Course: <https://sccr.dso.ufl.edu/policies/student-honor-code-student-conduct-code/>.
- Online Course: <http://www.distance.ufl.edu/student-complaint-process>