AGR7306 MULTI-OMIC INTEGRATION FOR APPLIED PREDICTION BREEDING

Graduate Level – 3 credit hours
Spring 2026

Instructor: Dr. Diego Jarquin
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Office hours: Tuesday and Thursday 3:00PM – 4:00 PM. Please feel free to talk to me about any issue relating to the course and start this process early in the semester (350 Complex).

TAs: Sehijpreet Kaur (skaur4@ufl.edu), Shatabdi Proma (shatabdi.proma@ufl.edu), & Julian Garcia-Abadillo (garciaabadillo.j@ufl.edu).

Office hours: Tuesday & Thursday 11:30AM – 12:30PM (350 Complex).

Lecture time: Tuesdays periods 6-7 (12:50PM - 2:45PM); and Thursdays period 6 (12:50PM - 1:40PM)

Location: Tuesday in Weimer Hall 1070 and Thursday in MAEB 0234 (to be discussed).

Course Description

This course focuses on the development and implementation of prediction and estimation models in private and public sector plant breeding programs. Students will learn the basis for modeling trait performance of genotypes assisted by the integration of multiple data types 'omics' under different approaches (parametric, non-parametric AI).

Intended Audience

The course is designed for MS and PhD graduate students in the following disciplines: plant breeding, agronomy, horticultural sciences, environmental horticulture, forestry, and animal breeding.

Learning Objectives.

- Identify the underlying foundations of the different prediction paradigms (parametric [frequentist, Bayesian], non-parametric Artificial Intelligence AI).

- Write R scripts replicating the results of elaborated functions implemented under parametric and non-parametric frameworks.
- Identify the best strategy to adopt according to the needs of the trait(s) under study.
- Identify the presence of genotype-by-environment G×E interaction and leverage it in prediction models.
- Integrate different 'Omics' of information in prediction models to outperform conventional models.
- Develop sophisticated prediction pipelines for plant and animal breeding.
- Identify and analyze when and how to implement the different cross-validation scenarios in breeding pipelines.
- Deploy complex prediction pipelines using parallel computing capabilities of the High-Throughput Computing (HTC) and High-Performance (HPC) Computing facilities such as HiPerGator.

Course Objectives

This course is designed to build onto concepts learned in plant breeding, quantitative genetics, and statistical genetics courses. At the end of this course, students will be able to distinguish the differences between the prediction paradigms assisting in the selection of superior cultivars, integrate multiple layers or 'Omics' (genomics, enviromics/weather, soil, high-throughput phenotyping, etc.) of information in the prediction models, apply quality control on the data, data collection, and data alignment. In addition, students will also be able to estimate the genotype-by-environment (G×E) interaction and leverage it in prediction models, exploit genetic correlation by considering multi-trait analysis, and achieve hybrid prediction based on the General Combining Ability GCA and Specific Combining Ability SCA terms using the marker information of the parents in interaction with environments. The students will be able to write their own modules to conduct customized analyses adapted to the needs of specific breeding programs (annual crops, perennial crops including tree species, repeated measures, time-related traits). Finally, the students will be able to develop complex prediction pipelines using parallel computing capabilities of High-Throughput Computing (HTC) and High-Performance Computing (HPT) facilities such as HiPerGator.

Evaluation

Quizzes

Three quizzes will happen randomly during lectures (3 in classroom and 2 on canvas). These will consist of questions pertinent to the topics being discussed in class. Make up for quizzes will be possible due to justified medical or religious absences. Answers will be reviewed and discussed in class after completion to provide comprehensive feedback. Full points will be provided to concise and correct responses. Partial points will be assigned to responses providing a vague answer. No points to question left in blank. Feedback will be provided in two manners. We will discuss the answers in class, and I will make notes in the exams prior to returning these to the class.

Breeding pipeline development.

Teams of two students will develop a genomic prediction pipeline including at least two different omics or layers of information (genomics plus another [soil, weather, proximal and remote sensing - high-throughput phenotyping, satellite-image data, etc.]) as part of the final project.

The pipeline development will be divided into three parts:

Part 1. Due on Thursday, January 29, by 5 PM (ET) in Canvas. Identification of a suitable multi-environments data set containing phenotypic data and at least two data 'omics' to be used as covariates (marker SNPs and any other layer [weather, soil, proximal and/or remote sensing - high-throughput phenotypic, etc.]) Describe the dataset: the source, trait(s) of interest, and the objective of the study (limited to 200 words). Each student will receive feedback from the instructor and TAs. Well described proposals will receive full points (3/3), and these should mention the dataset to analyze, omics of information involved in the analyses, and stablish clear objectives. Each one of these three sections accounts for 1/3 of the grade. Partial points will be provided according to the complete information of each one of these three sections (0/3, 1/3, or 2/3). After the students or team turn out their proposals, the TAs and will meet with them to provide feedback.

Part 2. Due on Tuesday, April 7, by 5 PM (ET) in Canvas. It should include the information presented in Part 1, plus the following components of a prediction pipeline: (1) quality control on the data, (2) compute the covariance structures to model main effects of the covariates and the interactions between these and environments and/or environmental covariates, (3) and the simulation of training testing prediction scenarios: prediction of *i*) tested genotypes in observed environments, *ii*) untested genotypes in observed environments, *iii*) tested genotypes in unobserved environments, *iv*) untested genotypes in unobserved environments). Each student will receive feedback from the instructor and TAs. Each one of the three sections accounts for 1/3 of the grade. Points will be provided according to the complete information of each one of these three sections (0/3, 1/3, 2/3, or 3/3). After the students or team submit their proposals, the TAs and will meet with them to provide feedback.

Part 3. Due on Tuesday, April 21, by 5 PM (ET) in Canvas. It should include all the sections presented in Part 1 and Part 2, plus the prediction stage using different paradigms (parametric [frequentist, and Bayesian], and non-parametric [Artificial Intelligence, and kernels]). Each student will receive feedback from the instructor and TAs. Full points (2/2) will be provided to those cases where both parametric and AI methods are employed for model fitting. Partial points will be assigned according to the methods implemented (0/2, or 1/2). After the students or team submit their proposals, the TAs and will meet with them to provide feedback.

Oral presentation. Each student or team will present their project during a 15-minute oral presentation in class on Thursday (April 24) or Tuesday (April 29) (the order of the students will be randomly assigned to these dates). The presentation format is open, and the students are encouraged to use their preferred delivery method. Each student will receive feedback from the instructor and TAs. Full points will be granted to the students or teams than provide a comprehensive overview of project including (1) the goals and objectives of the project, (2) the pipeline overview, (3) data analyses flow chart, (4) high quality set of slides, (5) show confidence during the presentation, (6) and quality of the responses to questions from the audience. Points will be granted according to the components presented (i.e., 0/6, 1/6, 2/6, 3/6, 4/6, 5/6, and 6/6).

At the end, after all of the students or teams finished their presentations, the TAs and I will meet with the students or teams to provide feedback.

Exam

There will be a final take-home exam starting on Saturday April 25, and it is due on Thursday April 30 by 11:59 PM.

The take-home exam comprises of the analysis of a data set mimicking the scenario of deliverables for a breeding program from a company. The tree main components are: (1) alignment and implementation of quality control to the data, and imputation, (2) performing the analyses using three prediction models for two cross-validations schemes, and (3) elaborate a report to answer the question that a breeder from the company is interested on. Points will be granted according to the components the student present in the exam (i.e., 0/3, 1/3, 2/3, and 3/3). Feedback will be provided meeting with each student and review their exam.

Homework/bonus points

Extra points will be assigned to homework exercises I will assign during the class (4), each one will account for 1 bonus point. To receive the points, the students should submit the scripts, and conclusions/answers within a period of a week.

Participation in class

This is a class that requires an active participation from all the students in the class. It is expected that the students will volunteer to participate and answer questions from the instructor and are also welcome to answer questions from other students. Participation in class will count for 10 points toward the final grade. Missing class could affect the expected levels of participation in class too.

Activity	Number	Points/activity	Total
Quizzes	5 (3 in classroom and 2 on canvas)	3	15
Pipeline development	3 stages	10	30
Oral presentation	1	20	20
Participation in class		10	10
Final Take-home Exam	1	35	25

A > 91 B+ 85 to 90.9 B 80 to 84.9 C+ 75 to 79.9 C 70 to 74.9 D+ 65 to 69.9 D 60 to 64.9 E < 60

UF grading policies

For information on how UF assigns grade points, visit: https://catalog.ufl.edu/UGRD/academic-regulations/grades-grading-policies/

Software and computer

You will need to use your own laptop for data analyses demos and homework. Different software will be used during the semester. Specific instructions about where and how to obtain them will be given in class. All analysis will be conducted using R-CRAN statistical software (standalone version only).
To access the High-Throughput Computing facilities (e.g., HiperGator), OSX and Windows users can use the terminal (command line); however, I strongly recommend Windows users to install Putty. To exchange files between personal computers and the HTC facilities, Windows users are encouraged to install WinSCP while OSX users can install Cyberduck. There are free versions for all the mentioned software; no need to pay for these.

Recommended Literature – specific scientific papers will be assigned as the semester progresses.

Montesinos López OA, Montesinos López A, Crossa J. Multivariate statistical machine learning methods for genomic prediction. Cham: Springer; 2022.
https://link.springer.com/book/10.1007/978-3-030-89010-0
Ahmadi N, Bartholome J. Genomic Prediction of Complex 2022. Humana, New York, NY.
https://link.springer.com/book/10.1007/978-1-0716-2205-6

Course Schedule and Topics (Tentative)

Week	Description
1 Jan 13-Jan 15	**Theme: Software overview and connectivity.** Day 1: Tuesday, January 13. a. Introductions, reviewing the syllabus, and assessment of expectations. b. Review of the software to use in the class (R, WinSCP, Putty, Cyberduck, etc.) c. Quick review of useful commands in R. Day 2: Thursday, January 15. a. Accessing the high-throughput computing facilities HTC using the command line (terminal, Putty). b. Review of basic commands useful to navigate in the cluster.
2 Jan 20 - Jan 22	**Theme: Genomic Selection and Statistical learning - Basic concepts.** Day 1: Tuesday, January 20 (**Plant Sciences Symposium**). a. Introduction to Genomic Selection and Genomic Prediction. b. Current paradigms, approaches, and models. c. Cross-validation schemes and Assessment of predictive ability.

	Day 2. Thursday, January 22. a. Prediction versus Inference b. Statistical Machine Learning Models – Basic ideas c. Data types and types of learning (unsupervised, supervised, semi-supervised).
3 Jan 27 - Jan 29	**Theme: Data preparation for implementing prediction models.** Day 1: Tuesday, January 27. a. Fixed vs Random effects. b. BLUEs and BLUPs. Day 2: Thursday, January 29 (**Due date for Part 1 of the breeding pipeline development project**). c. Quality Control on the genomic data. d. Methods for computing genomic covariance structures.
4 Feb 3 - Feb 5	**Theme: Basic elements for building supervised statistical Machine learning models.** Day 1: Tuesday, February 3. a. Linear Multiple Regression Model LMRM. b. Fitting LMRM using Ordinary Least Squares (OLS). c. Fitting LMRM using Maximum Likelihood (ML). d. Fitting LMRM using Gradient Descent Method (GD). Day 2: Thursday, February 5. a. Pros and cons of standard LMRM. b. Regularization parameters to overcome the curse of dimensionality. c. Ridge regression, LASSO regression. d. Logistic regression, Logistic Ridge regression, and LASSO logistic regression.
5 Feb 10 - Feb 12	**Theme: Overfitting, Model tunning, and evaluation of Prediction.** Day 1. Tuesday, February 10. a. Overfitting and Underfitting. b. Prediction accuracy vs. Model interpretability. c. Cross-validation. Day 2. Thursday, February 12. a. Model tunning. b. Evaluating model performance for prediction.

6 Feb 17 - Feb 19	**Theme: Linear Mixed Models.** Day 1. Tuesday, February 17. a. Intro to Linear Mixed Models. b. Estimation Methods. Day 2. Thursday, February 19. a. Linear Mixed Models in Genomic Prediction. b. Multi-trait Genomic Linear Mixed-Effects Models.
7 Feb 24 - Feb 26	**Theme: Bayesian Genomic Linear Regression.** Day 1. Tuesday, February 24. a. Bayes Theorem and Bayesian Linear Regression. b. Bayesian Genome-Based Ridge Regression. c. Bayesian GBLUP Genomic Model. Day 2. Thursday, February 26. a. Genomic-Enabled Prediction Bayes A Model. b. Genomic-Enabled Prediction Bayes B and C Models. c. Genomic-Enabled Bayesian LASSO Model.
8 March 3 - March 5	**Theme: Estimation of Covariance Structures and Multi-Trait Prediction Models.** Day 1. Tuesday, March 3. a. Bayesian Factor Analytic Model and other Co-variance structures. Day 2. Thursday, March 5. a. Genomic Prediction Models using structured Co-variances. b. Multi-trait methods for Genomic Prediction.
9 March 10 - March 12	**Theme: Estimation of Genotype-by-Environment Interaction.** Day 1. Tuesday, March 10. a. Additive Main-effects and Multiplicative Interaction Model AMMI. b. Singular Value Decomposition SVD. c. Estimation of AMMI model parameters (OLS). Day 2. Thursday, March 12. a. Bayesian AMMI model. b. General Bayesian AMMI model. c. Hierarchical Bayesian AMMI model.

10 March 17 - 19	**No class due to Spring Break**
11 March 24 - March 26	**Theme: G×E Genomic Prediction models.** Day 1. Tuesday, March 24. a. Genomic Prediction including interactions between markers and environments. b. Genomic Prediction including interactions between markers and weather covariates. c. Practical G×E. d. Practical G×W. Day 2. Thursday, March 26. a. Practical G×E. b. Practical G×W.
12 March 31 - April 2	**Theme: G×E Genomic Prediction models.** Day 2. Tuesday, March 31. a. Multi -omics integration using co-variance structures. b. General and Specific Combining Ability (GCA and SCA) in interaction with environments. c. Sparse Testing Designs. d. Prediction of time-related traits. e. Pipeline development for Genomic Selection. **Theme: Artificial Intelligence Methods for Genomic Prediction.** Day 2: Thursday, April 2. a. The RKHS. b. Generalized Kernel model.
13 April 7 - April 9	**Theme: Artificial Intelligence Methods for Genomic Prediction.** Day 1. Tuesday, April 7 (**Due date for Part 2 of the breeding pipeline development project**). a. Linear Mixed Model with Kernels. b. Hyperparameter Tunning. c. Bayesian Kernel Methods. Day 2. Thursday, April 9. a. Fundamentals of Artificial Neural Networks and Deep Learning.
14 April 14 - April 16	**Theme: Artificial Intelligence Methods for Genomic Prediction.**

	Day 1. Tuesday, April 14. a. Artificial Neural Networks and Deep Learning for Genomic Prediction. Day 2. Thursday, April 16. a. Convolutional Neural Networks.
15 April 21 - April 23	**Theme: Artificial Intelligence Methods for Genomic Prediction.** Day 1. Tuesday, April 21 (**Due date for Part 3 of the breeding pipeline development project**) a. Introduction to Convolutional Neural Networks. b. Random Forest for Genomic Prediction. **Theme: Presentations** Day 2. Thursday, April 23. a. Oral Presentation.
17 April 28 – April 30	**a. Exam due on Thursday, April 30 at 11:59 PM.**

ADDITIONAL REFERENCES

Acosta-Pech, R., Crossa, J., de los Campos, G., Teyssedre, S., Claustres, B., Pérez-Elizalde, S., et al. (2017). Genomic models with genotype × environment interaction for predicting hybrid performance: an application in maize hybrids. Theor. Appl. Genet. 130, 1431–1440. DOI: 10.1007/s00122-017-2898-0 - **To be reviewed in week 12, March 31, 2026**.

Crossa J., Perez-Elizalde S., Jarquin D., Miguel Cotes, J., Viele, K., Liu, G., and Cornelius, P. (2011) Bayesian Estimation of the Additive Main Effects and Multiplicative Interaction Model. Crop Science, 51:1468-1469. doi.org/10.2135/cropsci2010.06.0343 - **To be reviewed in week 9, March 10 and 12, 2026**.

Jarquin D., Pérez-Elizalde S., Burgueno J., Crossa J*. (2016) A Hierarchical Bayesian Estimation Model for Multienvironment Plant Breeding Trials in Successive Years. Crop Science, 56(5): 2260-2276. doi:10.2135/cropsci2015.08.0475. - **To be reviewed in week 9, March 10 and 12, 2026**.

Jarquin D., Crossa J., Lacaze X., Pérez P., Cheyron P.D., Daucourt J., Lorgeou J., Piraux F., Guerreiro L., Burgueno J., de los Campos G*. (2014) A Reaction Norm Model for Genomic Selection Using High-Dimensional Genomic and Environmental Data. Theoretical and Applied Genetics, 127(3):595-607. doi:10.1007/s00122-013-2243-1. - **To be reviewed in week 11, March 24 and 26, 2026**.

Jarquin D., Howard R., Xavier A., Choudhury S.D. (2018). Increasing Predictive Ability by Modeling Interactions between Environments, Genotype and Canopy Coverage Image Data for Soybeans. Agronomy, 8(4), 51. doi:10.3390/agronomy8040051. **To be reviewed in week 12, March 31, 2026**.

Jarquin D., Kajiya-Kanegae H. Taishen C., Persa R.,Yabe S., Iwata H. Coupling Day Length Data and Genomic Prediction tools for Predicting Time-Related Traits under Complex Scenarios. Scientific Reports. Sci Rep 10, 13382 (2020). doi.org/10.1038/s41598-020-70267-9. - **To be reviewed in week 12, March 31, 2026**.

Jarquin D., de Leon N., Romay C., Bohn M., Buckler E.S, Ciampitti I., Edwards J., Ertl D., Flint-Garcia S., Gore M.A, Graham C., Hirsch C.N, Holland J.B., Hooker D., Kaeppler S.M., Knoll J., Lee E.C., Lawrence-Dill C.J, Lynch J.P., Moose S.P, Murray S.C, Nelson R., Rocheford T., Schnable J.C., Schnable P.S., Smith M., Springer N., Thomison P., Tuinstra M., Wisser R.J., Xu W., Yu J., Lorenz A. Utility of Climatic Information via Combining Ability Models to Improve Genomic Prediction for Yield within the Maize Genomes to Fields Project. Front. Genet., 08 March 2021 | https://doi.org/10.3389/fgene.2020.592769. - **To be reviewed in week 12, March 31, 2026**.

Meuwissen TH, Hayes BJ, Goddard ME. Prediction of total genetic value using genome-wide dense marker maps. Genetics. 2001;157:1819–1829. DOI: 10.1093/genetics/157.4.1819. - **To be reviewed in week 7, February 24 and 26, 2026**.

Perez-Elizalde S., Jarquin D., Crossa J. (2011) A General Bayesian Estimation Method of Linear-Bilinear Models Applied to Plant Breeding Trials with Genotype by Environment Interaction. Journal of Agricultural, Biology and Environmental Statistics, 17 (1): 15-37. doi:10.1007/s13253-011-0063-9. - **To be reviewed in week 9, March 10 and 12, 2026**.

Persa R., Grondona M., Jarquin D. (2021). Development of a Genomic Prediction Pipeline for Maintaining Comparable Sample Sizes in Training and Testing Sets across Prediction Schemes Accounting for the Genotype-by-Environment Interaction. Agriculture 2021, 11(10), 932; doi.org/10.3390/agriculture11100932. - **To be reviewed in week 9, March 10 and 12, 2026**.

Ray S., Jarquin D., Howard R (2022). Comparing Artificial Intelligence Techniques with State-of-the-Art Parametric Prediction Models for Predicting Soybean Traits. The Plant Genome. - **To be reviewed in week 2, January 20, 2026**.

VanRaden PM. Efficient methods to compute genomic predictions. J Dairy Sci. 2008;91:4414–4423. doi: 10.3168/jds.2007-0980. - **To be reviewed in week 7, February 24 and 26, 2026**.

Viera C.C., Persa R., Chen P., Jarquin D. (2022) Incorporation of Soil-derived Covariates in Progeny Testing and Line Selection to Enhance Genomic Prediction Accuracy in Soybean Breeding. Front. Genet., 08 September 2022 Sec. Plant Genomics. https://doi.org/10.3389/fgene.2022.905824. - **To be reviewed in week 12, March 31, 2026**.

Materials and Supplies Fees: n/a

Attendance and Make-Up Work

"Requirements for class attendance and make-up exams, assignments, and other work in this course are consistent with university policies. Those can be found at: https://catalog.ufl.edu/UGRD/academicregulations/
attendance-policies/

Online Course Evaluation Process

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, located in the Canvas course menu under GatorEvals, or via https://ufl.bluera.com/ufl/. Summaries of course evaluation results are available to students at https://gatorevals.aa.ufl.edu/public-results/.

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.

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). 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.
If you have any questions or concerns, please consult with the instructor or TAs in this class.

Services for Students with Disabilities

"Students with disabilities requesting accommodations should first register with the Disability Resource Center (352-392-8565; https://disability.ufl.edu/get-started/) by providing appropriate documentation. Once registered, students will receive an accommodation letter which must be presented to the instructor when requesting accommodation. Students with disabilities should follow this procedure as early as possible in the semester."

Campus 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, https://counseling.ufl.edu/

Counseling Services
Groups and Workshops
Outreach and Consultation
Self-Help Library
Wellness Coaching

U Matter, We Care: If you or someone you know is in distress, please contact umatter@ufl.edu, 352-392-1575, or visit U Matter, We Care website to refer or report a concern and a team member will reach out to the student in distress.

Counseling and Wellness Center: Visit the Counseling and Wellness Center website or call 352-392-1575 for information on crisis services as well as non-crisis services.

Student Health Care Center: Call 352-392-1161 for 24/7 information to help you find the care you need, or visit the Student Health Care Center website.

University Police Department: Visit UF Police Department website or call 352-392-1111 (or 9-1-1 for emergencies).

UF Health Shands Emergency Room / Trauma Center: For immediate medical care call 352-733-0111 or go to the emergency room at 1515 SW Archer Road, Gainesville, FL 32608; Visit the UF Health Emergency Room and Trauma Center website.

GatorWell Health Promotion Services: For prevention services focused on optimal wellbeing, including Wellness Coaching for Academic Success, visit the GatorWell website or call 352-273-4450.

Academic Resources
E-learning technical support: Contact the UF Computing Help Desk at 352-392-4357 or via e-mail at
helpdesk@ufl.edu

Career Connections Center: Reitz Union Suite 1300, 352-392-1601. Career assistance and counseling services.

Library Support: Various ways to receive assistance with respect to using the libraries or finding resources.

Teaching Center: Broward Hall, 352-392-2010 or to make an appointment 352- 392-6420. General study skills and tutoring.

Writing Studio: 2215 Turlington Hall*,* 352-846-1138. Help brainstorming, formatting, and writing papers.
Student Complaints On-Campus: Visit the Student Honor Code and Student Conduct Code webpage for more information.

On-Line Students Complaints: Visit the Distance Learning Student Complaint Process.

In-Class Recording
Students are allowed to record video or audio of class lectures. However, the purposes for which these recordings may be used are strictly controlled. The only allowable purposes are (1) for personal educational use, (2) in connection with a complaint to the university, or (3) as evidence in, or in preparation for, a criminal or civil proceeding. All other purposes are prohibited. Specifically, students may not publish recorded lectures without the written consent of the instructor.
A "class lecture" is an educational presentation intended to inform or teach enrolled students about a particular subject, including any instructor-led discussions that form part of the presentation, and delivered by any instructor hired or appointed by the University, or by a guest instructor, as part of a University of Florida course. A class lecture does not include lab sessions, student presentations, clinical presentations such as patient history, academic exercises involving solely student participation, assessments (quizzes, tests, exams), field trips, private conversations between students in the class or between a student and the faculty or lecturer during a class session.

Publication without permission of the instructor is prohibited. To "publish" means to share, transmit, circulate, distribute, or provide access to a recording, regardless of format or medium, to another person (or persons), including but not limited to another student within the same class section. Additionally, a recording, or transcript of a recording, is considered published if it is posted on or uploaded to, in whole or in part, any media platform, including but not limited to social media, book, magazine, newspaper, leaflet, or third-party note/tutoring services. A student who publishes a recording without written consent may be subject to a civil cause of action instituted by a person injured by the publication and/or discipline under UF Regulation 4.040 Student Honor Code and Student Conduct Code.

Privacy statement

Our class sessions may be audio visually recorded for students in the class to refer back and for enrolled students who are unable to attend live. Students who participate with their camera engaged or utilize a profile image are agreeing to have their video or image recorded. If you are unwilling to consent to have your profile or video image recorded, be sure to keep your camera off and do not use a profile image. Likewise, students who un-mute during class and participate orally are agreeing to have their voices recorded. If you are not willing to consent to have your voice recorded during class, you will need to keep your mute button activated and communicate exclusively using the "chat" feature, which allows students to type questions and comments live. The chat will not be recorded or shared. As in all courses, unauthorized recording and unauthorized sharing of recorded materials is prohibited.

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, https://disability.ufl.edu/

The instructor reserves the right to make changes in the assignments and syllabus as needed. Notification will be made via E-Learning, e-mail or class announcements

“Instructional materials for this course consist of only those materials specifically reviewed, selected, and assigned by the instructor(s). The instructor(s) is only responsible for these instructional materials.”