

Cover Sheet: Request 14427

PCB 4XXX – Synthetic Biology and Comparative Genomics

Info

Process	Course New Ugrad/Pro
Status	Pending at PV - University Curriculum Committee (UCC)
Submitter	Edward Braun ebraun68@ufl.edu
Created	11/6/2019 10:15:15 PM
Updated	2/1/2021 12:35:26 PM
Description of request	Request to create a new advanced undergraduate (4000-level) course entitled "Synthetic Biology and Comparative Genomics".

Actions

Step	Status	Group	User	Comment	Updated
Department	Approved	CLAS - Biology 16900300	Marta Wayne		11/7/2019
SynthBiology.Syllabus.ELB_v3.pdf					11/6/2019
UCC-ewtriplett.pdf					11/6/2019
College	Recycled	CLAS - College of Liberal Arts and Sciences	Joseph Spillane	The College Curriculum Committee recycles this request, with the following changes needed: 1) please rework the Transcript Title to include some indication of Genomics; 2) please revise the course description to be consistent with university style guidelines for the catalog (see https://gov.clas.ufl.edu/files/CorProblems-Checklist.pdf); 3) Please re-do the prerequisites to use the format specified in the instructions; 4) please include the grading scheme explanation on the form as well as the syllabus; in addition, please describe how participation will be assessed.	1/24/2020
No document changes					
Department	Approved	CLAS - Biology 16900300	Marta Wayne		1/22/2021
No document changes					
College	Approved	CLAS - College of Liberal Arts and Sciences	Joseph Spillane		2/1/2021
No document changes					
University Curriculum Committee	Pending	PV - University Curriculum Committee (UCC)			2/1/2021
No document changes					
Statewide Course Numbering System					
No document changes					

Step	Status	Group	User	Comment	Updated
Office of the Registrar					
No document changes					
Student Academic Support System					
No document changes					
Catalog					
No document changes					
College Notified					
No document changes					

Course|New for request 14427

Info

Request: PCB 4XXX – Synthetic Biology and Comparative Genomics

Description of request: Request to create a new advanced undergraduate (4000-level) course entitled "Synthetic Biology and Comparative Genomics".

Submitter: Edward Braun ebraun68@ufl.edu

Created: 11/6/2019 10:18:05 PM

Form version: 2

Responses

Recommended Prefix

Enter the three letter code indicating placement of course within the discipline (e.g., POS, ATR, ENC). Note that for new course proposals, the State Common Numbering System (SCNS) may assign a different prefix.

Response:
PCB

Course Level

Select the one digit code preceding the course number that indicates the course level at which the course is taught (e.g., 1=freshman, 2=sophomore, etc.).

Response:
4

Number

Enter the three digit code indicating the specific content of the course based on the SCNS taxonomy and course equivalency profiles. For new course requests, this may be XXX until SCNS assigns an appropriate number.

Response:
XXX

Category of Instruction

Indicate whether the course is introductory, intermediate or advanced. Introductory courses are those that require no prerequisites and are general in nature. Intermediate courses require some prior preparation in a related area. Advanced courses require specific competencies or knowledge relevant to the topic prior to enrollment.

Response:
Advanced

- 1000 and 2000 level = Introductory undergraduate
- 3000 level = Intermediate undergraduate
- 4000 level = Advanced undergraduate
- 5000 level = Introductory graduate
- 6000 level = Intermediate graduate
- 7000 level = Advanced graduate

4000/5000 and 4000/6000 levels = Joint undergraduate/graduate (these must be approved by the UCC and the Graduate Council)

Lab Code

Enter the lab code to indicate whether the course is lecture only (None), lab only (L), or a combined lecture and lab (C).

Response:
None

Course Title

Enter the title of the course as it should appear in the Academic Catalog.

Response:
Synthetic Biology and Comparative Genomics

Transcript Title

Enter the title that will appear in the transcript and the schedule of courses. Note that this must be limited to 21 characters (including spaces and punctuation).

Response:
Synth Comp Biol

Degree Type

Select the type of degree program for which this course is intended.

Response:
Baccalaureate

Delivery Method(s)

Indicate all platforms through which the course is currently planned to be delivered.

Response:
On-Campus

Co-Listing

Will this course be jointly taught to undergraduate, graduate, and/or professional students?

Response:
No

Co-Listing Explanation

Please detail how coursework differs for undergraduate, graduate, and/or professional students. Additionally, please upload a copy of both the undergraduate and graduate syllabus to the request in .pdf format.

Response:
Course will be offered at the advanced undergraduate level only.

Effective Term

Select the requested term that the course will first be offered. Selecting "Earliest" will allow the course to be active in the earliest term after SCNS approval. If a specific term and year are selected, this should reflect the department's best projection. Courses cannot be implemented retroactively, and therefore the actual effective term cannot be prior to SCNS approval, which must be obtained prior to the first day of classes for the effective term. SCNS approval typically requires 2 to 6 weeks after approval of the course at UF.

Response:
Earliest Available

Effective Year

Select the requested year that the course will first be offered. See preceding item for further information.

Response:
Earliest Available

Rotating Topic?

Select "Yes" if the course can have rotating (varying) topics. These course titles can vary by topic in the Schedule of Courses.

Response:
No

Repeatable Credit?

Select "Yes" if the course may be repeated for credit. If the course will also have rotating topics, be sure to indicate this in the question above.

Response:
No

Amount of Credit

Select the number of credits awarded to the student upon successful completion, or select "Variable" if the course will be offered with variable credit and then indicate the minimum and maximum credits per section. Note that credit hours are regulated by Rule 6A-10.033, FAC. If you select "Variable" for the amount of credit, additional fields will appear in which to indicate the minimum and maximum number of total credits.

Response:
3

S/U Only?

Select "Yes" if all students should be graded as S/U in the course. Note that each course must be entered into the UF curriculum inventory as either letter-graded or S/U. A course may not have both options. However, letter-graded courses allow students to take the course S/U with instructor permission.

Response:
No

Contact Type

Select the best option to describe course contact type. This selection determines whether base hours or headcount hours will be used to determine the total contact hours per credit hour. Note that the headcount hour options are for courses that involve contact between the student and the professor on an individual basis.

Response:

Regularly Scheduled

- Regularly Scheduled [base hr]
- Thesis/Dissertation Supervision [1.0 headcount hr]
- Directed Individual Studies [0.5 headcount hr]
- Supervision of Student Interns [0.8 headcount hr]
- Supervision of Teaching/Research [0.5 headcount hr]
- Supervision of Cooperative Education [0.8 headcount hr]

Contact the Office of Institutional Planning and Research (352-392-0456) with questions regarding contact type.

Weekly Contact Hours

Indicate the number of hours instructors will have contact with students each week on average throughout the duration of the course.

Response:

3

Course Description

Provide a brief narrative description of the course content. This description will be published in the Academic Catalog and is limited to 50 words or fewer. See course description guidelines.

Response:

Synthetic biology is a field that merges genetics and engineering to: 1) redesign and fabricate existing biological systems; and 2) design and fabricate unnatural biological systems. This course has a strong focus on the use of comparisons among existing organisms to understand the results of synthetic biology experiments

Prerequisites

Indicate all requirements that must be satisfied prior to enrollment in the course. Prerequisites will be automatically checked for each student attempting to register for the course. The prerequisite will be published in the Academic Catalog and must be formulated so that it can be enforced in the registration system. Please note that upper division courses (i.e., intermediate or advanced level of instruction) must have proper prerequisites to target the appropriate audience for the course.

Response:

A grade of C in BSC 2010, passing grades in PCB 3063 or AGR 3303 or PCB 4522

Completing Prerequisites on UCC forms:

- Use "&" and "or" to conjoin multiple requirements; do not use commas, semicolons, etc.
- Use parentheses to specify groupings in multiple requirements.
- Specifying a course prerequisite (without specifying a grade) assumes the required passing grade is D-. In order to specify a different grade, include the grade in parentheses immediately after the course number. For example, "MAC 2311(B)" indicates that students are required to obtain a grade of B in Calculus I. MAC2311 by itself would only require a grade of D-.
- Specify all majors or minors included (if all majors in a college are acceptable the college code is sufficient).
- "Permission of department" is always an option so it should not be included in any prerequisite or co-requisite.

*Example: A grade of C in HSC 3502, passing grades in HSC 3057 or HSC 4558, and major/minor in PPHP should be written as follows:
HSC 3502(C) & (HSC 3057 or HSC 4558) & (HP college or (HS or CMS or DSC or HP or RS minor))*

Co-requisites

Indicate all requirements that must be taken concurrently with the course. Co-requisites are not checked by the registration system.

Response:
None

Rationale and Placement in Curriculum

Explain the rationale for offering the course and its place in the curriculum.

Response:

The field of synthetic biology is extremely new, having emerged as a major research area in the past decade, after the technologies to synthesize and assemble large segments of DNA and methods to alter DNA have become both relatively inexpensive and reliable. Comparative genomics is a slightly older field, having emerged in the early 2000s after DNA sequencing became inexpensive enough to generate genome assemblies for many different organisms.

Both of these fields are revolutionizing the field of genetics and the science of biology more broadly, but students get little focused exposure to the fields in other courses. This course is necessary to expose students to these very new fields and build on their knowledge of genetics. This course is appropriate for advanced undergraduates that have already mastered basic genetics.

Course Objectives

Describe the core knowledge and skills that student should derive from the course. The objectives should be both observable and measurable.

Response:

After completing this course students should be able to:

1. Describe technologies used to construct synthetic organisms
2. Design biological systems using "parts" (genes) available in biological systems
3. Distinguish different types of biological "parts" (e.g., essential vs non-essential genes, orthologs and paralogs)
4. Describe the ways that novel engineered systems (e.g., expanded versions of the genetic code) differ from evolved biological systems

Understanding of these concepts will be assessed using the assignments

Course Textbook(s) and/or Other Assigned Reading

Enter the title, author(s) and publication date of textbooks and/or readings that will be assigned. Please provide specific examples to evaluate the course.

Response:

Textbook: Synthetic Biology - A Primer: Revised Edition, by Geoff Baldwin et al., Imperial College Press; Revised edition (October 25, 2015), ISBN-13: 978-1783268795

Examples of additional readings from the peer-reviewed literature:

Burns, N., Grimwade, B., Ross-Macdonald, P. B., Choi, E. Y., Finberg, K., Roeder, G. S., & Snyder, M. (1994). Large-scale analysis of gene expression, protein localization, and gene disruption in *Saccharomyces cerevisiae*. *Genes & development*, 8(9), 1087-1105. (example of large-scale gene disruption using TE insertions, a method used to identify essential genes)

Calles, J., Justice, I., Brinkley, D., Garcia, A., & Endy, D. (2019). Fail-safe genetic codes designed to intrinsically contain engineered organisms. *Nucleic Acids Res*, gkz745. doi: 10.1093/nar/gkz745 (computational methods to redesign the genetic code to ensure fidelity)

Chin, J. W., Cropp, T. A., Anderson, J. C., Mukherji, M., Zhang, Z., & Schultz, P. G. (2003). An expanded eukaryotic genetic code. *Science*, 301(5635), 964-967. (adding "unnatural" amino acids to the genetic code)

DeFeo-Jones, D., Tatchell, K., Robinson, L. C., Sigal, I. S., Vass, W. C., Lowy, D. R., & Scolnick, E. M. (1985). Mammalian and yeast ras gene products: biological function in their heterologous systems. *Science*, 228(4696), 179-184. (first example of "swapping" orthologs between yeast and mammals, near functional equivalence demonstrated)

Gustafsson, C., Govindarajan, S., & Minshull, J. (2004). Codon bias and heterologous protein expression. *Trends in Biotechnology*, 22(7), 346-353. (importance of codon bias for gene expression)

Hershberg, R., & Petrov, D. A. (2008). Selection on codon bias. *Annual review of genetics*, 42, 287-299. (importance of codon bias for expression)

Hutchison, C. A., Chuang, R. Y., Noskov, V. N., Assad-Garcia, N., Deerinck, T. J., Ellisman, M. H., et al. (2016). Design and synthesis of a minimal bacterial genome. *Science*, 351(6280), 1414 (aad6253). (first example of designed minimal organism)

Kachroo, A. H., Laurent, J. M., Akhmetov, A., Szilagyi-Jones, M., McWhite, C. D., Zhao, A., & Marcotte, E. M. (2017). Systematic bacterialization of yeast genes identifies a near-universally swappable pathway. *Elife*, 6, e25093. (example of gene swapping using CRISPR-Cas9)

Kachroo, A. H., Laurent, J. M., Yellman, C. M., Meyer, A. G., Wilke, C. O., & Marcotte, E. M. (2015). Systematic humanization of yeast genes reveals conserved functions and genetic modularity. *Science*, 348(6237), 921-925. (example of gene swapping using other methods)

Khorana, H. G. (1979). Total synthesis of a gene. *Science*, 203(4381), 614-625. (first example of complete gene synthesis)

Koonin, E. V. (2000). How many genes can make a cell: the minimal-gene-set concept. *Annu Rev Genomics Hum Genet*, 1, 99-116. (review of efforts to define the minimal cell using comparative and functional genomics)

Mitchell, L. A., Wang, A., Stracquandano, G., Kuang, Z., Wang, X., Yang, K., et al. (2017). Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. *Science*, 355(6329), eaaf4831. (introduces the idea of the need to "debug" a synthetic yeast chromosome to make it work)

Mnaimneh, S., Davierwala, A. P., Haynes, J., Moffat, J., Peng, W. T., Zhang, W., et al. (2004). Exploration of essential gene functions via titratable promoter alleles. *Cell*, 118(1), 31-44. (description of large-scale placement of engineered tet promoters that can be controlled using doxycycline)

Nehring, S., Budisa, N., & Wiltschi, B. (2012). Performance analysis of orthogonal pairs designed for an expanded eukaryotic genetic code. *PloS one*, 7(4), e31992. (building orthogonal sets of proteins and tRNAs to expand the genetic code)

Neumann, H., Wang, K., Davis, L., Garcia-Alai, M., & Chin, J. W. (2010). Encoding multiple unnatural amino acids via evolution of a quadruplet-decoding ribosome. *Nature*, 464(7287), 441-444. (alternative method for expanding the amino acid set)

Plotkin, J. B., & Kudla, G. (2011). Synonymous but not the same: the causes and consequences of codon bias. *Nature Reviews Genetics*, 12(1), 32-42. (comparative genomics of codon bias)

Richardson, S. M., Mitchell, L. A., Stracquadanio, G., Yang, K., Dymond, J. S., DiCarlo, J. E., et al. (2017). Design of a synthetic yeast genome. *Science*, 355(6329), 1040-1044. (overview of the "yeast 2.0" redesign project)

Shen, Y., Wang, Y., Chen, T., Gao, F., Gong, J., Abramczyk, D., et al. (2017). Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. *Science*, 355(6329), eaaf4791. (use of synthetic biology to analyze a yeast chromosome)

Windram, O. P., Rodrigues, R. T., Lee, S., Haines, M., & Bayer, T. S. (2017). Engineering microbial phenotypes through rewiring of genetic networks. *Nucleic acids research*, 45(8), 4984-4993. (illustrates the use of synthetic biology to perturb yeast expression system to maximize production of a compound)

Wishart, J. A., Hayes, A., Wardleworth, L., Zhang, N., & Oliver, S. G. (2005). Doxycycline, the drug used to control the tet-regulatable promoter system, has no effect on global gene expression in *Saccharomyces cerevisiae*. *Yeast*, 22(7), 565-569. (illustrates the importance of controls – in this case the need to determine whether the doxycycline used to control the tet promoter has undesirable off-target effects)

Zhang, Y., Lamb, B. M., Feldman, A. W., Zhou, A. X., Lavergne, T., Li, L., & Romesberg, F. E. (2017). A semisynthetic organism engineered for the stable expansion of the genetic alphabet. *Proceedings of the National Academy of Sciences*, 114(6), 1317-1322. (description of system to expand the number of DNA nucleotides from four to six in vivo)

Weekly Schedule of Topics

Provide a projected weekly schedule of topics. This should have sufficient detail to evaluate how the course would meet current curricular needs and the extent to which it overlaps with existing courses at UF.

Response:

Weak, followed by topic and associated readings:

- 1 Review of Genetics and Molecular Biology – Textbook (chapter 1)
- 2 Conceptual Foundations of Biological Engineering, Orthogonality – Textbook (chapter 2)
- 3 Foundational technologies – Textbook (chapter 3; also material in Appendix)
Reading the Peer-Reviewed Scientific Literature – handout focusing on the best ways to see the "big picture" in scientific publications, using the Khorana (1979) paper as an example
- 4 Definition of Essential Genes; Identifying and Characterizing Essential Genes – Burns et al. (1994); Mnaimneh et al. (2004); Wishart et al. (2005)
- 5 Definition of Minimal Genomes via Comparative Genomics – Koonin (2000)
Yeast 2.0 – Richardson et al. (2017); Mitchell et al. (2017); Shen et al. (2017)
- 6 Yeast 2.0 continued, Removal of "Selfish" Genetic Elements – continue material from Richardson et al. (2017); Mitchell et al. (2017); Shen et al. (2017)
Perturbing Metabolic Systems – Windram et al. (2017)
- 7 "Swapability" of Orthologous Genes – DeFeo-Jones et al. (1985); Kachroo et al. (2015); Kachroo et al. (2017)
- 8 "Swapability" of Orthologous Genes continued – DeFeo-Jones et al. (1985); Kachroo et al. (2015); Kachroo et al. (2017)
Design and Synthesis of Minimal Organisms – Hutchison et al. (2015)

9 Skills for Comparative Genomics – Handout
Review Concepts for Minimal Organisms, Essential Genes, and Ortholog Swapping – begin class project

10 Importance of Codon Bias for Expression –Gustafsson et al. 2004; Hershberg & Petrov (2008); Plotkin & Kudla (2011)
Gene Design Software – Handout

11 Redesigning the Genetic Code (also discussion of the need to contain synthetic organisms, which can be facilitated by unnatural codes) – Calles et al. (2019)

12 “Non-natural” (Non-canonical) Amino Acids and Modified Genetic Codes – Chin et al. (2003); Neumann et al. (2010); Nehring et al. (2012)

13 Expanding the Genetic Alphabet – Zhang et al. (2017)

14 Complete Project; Presentations

15 Complete Presentations

Links and Policies

Consult the syllabus policy page for a list of required and recommended links to add to the syllabus. Please list the links and any additional policies that will be added to the course syllabus.

Please see: syllabus.ufl.edu for more information

Response:

All of the following material is included in the syllabus:

Course policies

* Academic dishonesty will not be tolerated. If cheating or plagiarism is suspected, all persons involved will receive a zero on the affected assignment and it will be reported to the Dean of Students Office.

* If you notice another student engaging in activities to you believe to constitute academic dishonesty please report the potential violation. I take all allegations seriously. However, remember that you are bound by the UF honor code, which states that “in reporting an alleged Student Honor Code violation, a student shall not intentionally or in bad faith make a false or misleading statement.” In other words, I view intentional false allegations as a type of academic dishonesty.

*Attendance in class is required. However, if you cannot attend on specific days just email with the subject line “UNABLE TO ATTEND CLASS ON <DATE>” and provide a brief explanation. If you have concerns at any time just discuss them with me. My goal is to make the course enjoyable and informative so you will want to attend!

University support services

Resources are available on campus to help students meet academic goals and solve personal problems, which interfere with their academic performance. Resources include:

1. UF Counseling and Wellness Center, 301 Peabody Hall and Radio Rd Facility, 392-1575, personal and career counseling.
2. Career Resource Center, Reitz Union, 392-1601, career development assistance and counseling.
3. CLAS Academic Advising Center, Farrison Hall, 100 Fletcher Drive, 392-1521, provides advise on course selection and course planning to meet graduation requirements

Disability Notice

Students with disabilities enrolled in this course and who may need disability-related classroom accommodations are encouraged to make an appointment to see me before the end of the second week of the term. All discussions will remain confidential, although the Student Accessibility Services office may be consulted to discuss appropriate implementation of any accommodation requested.

Grading Scheme

List the types of assessments, assignments and other activities that will be used to determine the course grade, and the percentage contribution from each. This list should have sufficient detail to evaluate the course rigor and grade integrity. Include details about the grading rubric and percentage breakdowns for determining grades.

Response:

There will be three types of assignments: Class participation, a class project, and take home exercises. Full details are included on the sample syllabus.

Grading scale

The following grading scale will be used (values are percentages):

91-100 A

88-90.9 A-

85-87.9 B+

81-84.9 B

78-80.9 B-

75-77.9 C+

68-74.9 C

65-67.9 C-

62-64.9 D+

58-61.9 D

Below 58 is failing (E).

Instructor(s)

Enter the name of the planned instructor or instructors, or "to be determined" if instructors are not yet identified.

Response:

Edward L Braun

Synthetic Biology and Comparative Genomics
PCB XXXX — Class Number: XXXX (Fall Semester 20XX)

Instructor Information:

Prof. Edward L. Braun
Office Hours: By appt. (514 Carr)
(352) 846-1124
ebraun68@ufl.edu

Brief Course Description:

Synthetic biology is a field that merges genetics and engineering to: 1) redesign and fabricate existing biological systems; and 2) design and fabricate unnatural biological systems. This course has a strong focus on the use of comparisons among existing organisms to understand the results of synthetic biology experiments

Textbook:

Synthetic Biology - A Primer: Revised Edition, by Geoff Baldwin et al.

- **Publisher:** Imperial College Press; Revised edition (October 25, 2015)
- **Language:** English
- **ISBN-10:** 1783268794
- **ISBN-13:** 978-1783268795

<https://books.google.com/books?id=mTK6CgAAQBAJ>

Note: this is a relatively inexpensive textbook (approx. \$35 from various sources)

We will also do a number of readings from the peer-reviewed scientific literature. I provide examples in a selected bibliography at the end of this document.

Additional Readings and Expanded Course Description:

Synthetic Biology and Comparative Genomics is a stimulating and challenging survey of the field of synthetic biology. Synthetic biology is a diverse field that merges genetics and engineering and use methods from those fields to: 1) redesign and fabricate existing biological systems; and 2) design and fabricate biological systems that do not exist in the natural world. This course has a strong focus on the use of comparisons among existing organisms to understand the results of synthetic biology experiments. This course will comprise lectures, discussions, readings from the scientific literature, and a class project.

In addition to *Synthetic Biology - A Primer* we will read a number of papers from the peer-reviewed scientific literature. I vary the precise set of papers we read each year, but the general foci are: papers molecular genetics that illustrate principles important for synthetic biology (sometimes older than the “synthetic biology” era); and 2) papers on comparative and evolutionary genomics that can inspire the design of biological systems. A third focus is papers focused on the addition of “letters” to the two genetic “alphabets” (nucleic acids and proteins). Much of the discussion in class will focus on the yeast (*Saccharomyces cerevisiae*) as a “chassis” for building synthetics, augmented with examples from a variety of other organisms. The final topic has important implications for the early evolution of life and therefore a direct connection to the comparative and evolutionary foci of the course.

Course Assignments and Grading:

Course component	Proportion of grade
Participation	35%
Class project	35%
Take home exercises	30%

Class participation

I expect regular attendance. If you are sick, have a family emergency, or plan to participate in a university-sanctioned event just let me know; those absences are excused. Likewise, I will consider excusing you for any reasonable professional development activities; just discuss them with me. But otherwise I expect to see you in class and you will lose 1% of this portion of the grade for unexcused absences. Although some classes will be lectures many will include discussions; I expect everybody to participate. We will also be learning how to use specific computer programs during some classes and participating in those activities is important.

Class project

We will work on project to understand and analyze minimal genome projects, where synthetic biology is used to answer the question of “what is the minimum set of genes necessary for life?” This will involve extracting information from recent scientific papers, learning about the functions of specific proteins that appear to be necessary for life, and preparing a poster about your findings.

Take home exercises

There will be no tests, but I will expect you to produce short (1-2 paragraph) summaries of assigned readings.

Grading scale

The following grading scale will be used (values are percentages):

91-100 A	88-90.9 A-	
85-87.9 B+	81-84.9 B	78-80.9 B-
75-77.9 C+	68-74.9 C	65-67.9 C-
62-64.9 D+	58-61.9 D	

Below 58 is failing (E).

Course policies

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Schedule

NOTE: an example bibliography is provided below; this is a fast-moving field and I anticipate changes in the readings over time

Week	Topic and Reading
1	<i>Review of Genetics and Molecular Biology</i> – Textbook (chapter 1)
2	<i>Conceptual Foundations of Biological Engineering, Orthogonality</i> – Textbook (chapter 2)
3	<i>Foundational technologies</i> – Textbook (chapter 3; also material in Appendix) <i>Reading the Peer-Reviewed Scientific Literature</i> – handout focusing on the best ways to see the “big picture” in scientific publications, using the Khorana (1979) paper as an example
4	<i>Definition of Essential Genes; Identifying and Characterizing Essential Genes</i> – Burns et al. (1994); Mnaimneh et al. (2004); Wishart et al. (2005)
5	<i>Definition of Minimal Genomes via Comparative Genomics</i> – Koonin (2000) <i>Yeast 2.0</i> – Richardson et al. (2017); Mitchell et al. (2017); Shen et al. (2017)
6	<i>Yeast 2.0 continued, Removal of “Selfish” Genetic Elements</i> – continue material from Richardson et al. (2017); Mitchell et al. (2017); Shen et al. (2017) <i>Perturbing Metabolic Systems</i> – Windram et al. (2017)
7	<i>“Swapability” of Orthologous Genes</i> – DeFeo-Jones et al. (1985); Kachroo et al. (2015); Kachroo et al. (2017)
8	<i>“Swapability” of Orthologous Genes continued</i> – DeFeo-Jones et al. (1985); Kachroo et al. (2015); Kachroo et al. (2017) <i>Design and Synthesis of Minimal Organisms</i> – Hutchison et al. (2015)
9	<i>Skills for Comparative Genomics</i> – Handout <i>Review Concepts for Minimal Organisms, Essential Genes, and Ortholog Swapping</i> – begin class project
10	<i>Importance of Codon Bias for Expression</i> –Gustafsson et al. 2004; Hershberg & Petrov (2008); Plotkin & Kudla (2011) <i>Gene Design Software</i> – Handout
11	<i>Redesigning the Genetic Code (also discussion of the need to contain synthetic organisms, which can be facilitated by unnatural codes)</i> – Calles et al. (2019)

12	<i>“Non-natural” (Non-canonical) Amino Acids and Modified Genetic Codes – Chin et al. (2003); Neumann et al. (2010); Nehring et al. (2012)</i>
13	<i>Expanding the Genetic Alphabet – Zhang et al. (2017)</i>
14	<i>Complete Project; Presentations</i>
15	<i>Complete Presentations</i>

Annotated Bibliography

Burns, N., Grimwade, B., Ross-Macdonald, P. B., Choi, E. Y., Finberg, K., Roeder, G. S., & Snyder, M. (1994). Large-scale analysis of gene expression, protein localization, and gene disruption in *Saccharomyces cerevisiae*. *Genes & development*, 8(9), 1087-1105. *(example of large-scale gene disruption using TE insertions, a method used to identify essential genes)*

Calles, J., Justice, I., Brinkley, D., Garcia, A., & Endy, D. (2019). Fail-safe genetic codes designed to intrinsically contain engineered organisms. *Nucleic Acids Res*, gkz745. doi: 10.1093/nar/gkz745 *(computational methods to redesign the genetic code to ensure fidelity)*

Chin, J. W., Cropp, T. A., Anderson, J. C., Mukherji, M., Zhang, Z., & Schultz, P. G. (2003). An expanded eukaryotic genetic code. *Science*, 301(5635), 964-967. *(adding “unnatural” amino acids to the genetic code)*

DeFeo-Jones, D., Tatchell, K., Robinson, L. C., Sigal, I. S., Vass, W. C., Lowy, D. R., & Scolnick, E. M. (1985). Mammalian and yeast *ras* gene products: biological function in their heterologous systems. *Science*, 228(4696), 179-184. *(first example of “swapping” orthologs between yeast and mammals, near functional equivalence demonstrated)*

Gustafsson, C., Govindarajan, S., & Minshull, J. (2004). Codon bias and heterologous protein expression. *Trends in Biotechnology*, 22(7), 346-353. *(importance of codon bias for gene expression)*

Hershberg, R., & Petrov, D. A. (2008). Selection on codon bias. *Annual review of genetics*, 42, 287-299. *(importance of codon bias for expression)*

Hutchison, C. A., Chuang, R. Y., Noskov, V. N., Assad-Garcia, N., Deerinck, T. J., Ellisman, M. H., et al. (2016). Design and synthesis of a minimal bacterial genome. *Science*, 351(6280), 1414 (aad6253). *(first example of designed minimal organism)*

Kachroo, A. H., Laurent, J. M., Akhmetov, A., Szilagyijones, M., McWhite, C. D., Zhao, A., & Marcotte, E. M. (2017). Systematic bacterialization of yeast genes identifies a near-universally swappable pathway. *Elife*, 6, e25093. (example of gene swapping using CRISPR-Cas9)

Kachroo, A. H., Laurent, J. M., Yellman, C. M., Meyer, A. G., Wilke, C. O., & Marcotte, E. M. (2015). Systematic humanization of yeast genes reveals conserved functions and genetic modularity. *Science*, 348(6237), 921-925. (example of gene swapping using other methods)

Khorana, H. G. (1979). Total synthesis of a gene. *Science*, 203(4381), 614-625. (first example of complete gene synthesis)

Koonin, E. V. (2000). How many genes can make a cell: the minimal-gene-set concept. *Annu Rev Genomics Hum Genet*, 1, 99-116. (review of efforts to define the minimal cell using comparative and functional genomics)

Mitchell, L. A., Wang, A., Stracquadanio, G., Kuang, Z., Wang, X., Yang, K., et al. (2017). Synthesis, debugging, and effects of synthetic chromosome consolidation: synVI and beyond. *Science*, 355(6329), eaaf4831. (introduces the idea of the need to "debug" a synthetic yeast chromosome to make it work)

Mnaimneh, S., Davierwala, A. P., Haynes, J., Moffat, J., Peng, W. T., Zhang, W., et al. (2004). Exploration of essential gene functions via titratable promoter alleles. *Cell*, 118(1), 31-44. (description of large-scale placement of engineered tet promoters that can be controlled using doxycycline)

Nehring, S., Budisa, N., & Wiltschi, B. (2012). Performance analysis of orthogonal pairs designed for an expanded eukaryotic genetic code. *PloS one*, 7(4), e31992. (building orthogonal sets of proteins and tRNAs to expand the genetic code)

Neumann, H., Wang, K., Davis, L., Garcia-Alai, M., & Chin, J. W. (2010). Encoding multiple unnatural amino acids via evolution of a quadruplet-decoding ribosome. *Nature*, 464(7287), 441-444. (alternative method for expanding the amino acid set)

Plotkin, J. B., & Kudla, G. (2011). Synonymous but not the same: the causes and consequences of codon bias. *Nature Reviews Genetics*, 12(1), 32-42. (comparative genomics of codon bias)

Richardson, S. M., Mitchell, L. A., Stracquadanio, G., Yang, K., Dymond, J. S., DiCarlo, J. E., et al. (2017). Design of a synthetic yeast genome. *Science*, 355(6329), 1040-1044. (overview of the "yeast 2.0" redesign project)

Shen, Y., Wang, Y., Chen, T., Gao, F., Gong, J., Abramczyk, D., et al. (2017). Deep functional analysis of synII, a 770-kilobase synthetic yeast chromosome. *Science*, 355(6329), eaaf4791. (use of synthetic biology to analyze a yeast chromosome)

Windram, O. P., Rodrigues, R. T., Lee, S., Haines, M., & Bayer, T. S. (2017). Engineering microbial phenotypes through rewiring of genetic networks. *Nucleic acids research*, 45(8), 4984-4993. *(illustrates the use of synthetic biology to perturb yeast expression system to maximize production of a compound)*

Wishart, J. A., Hayes, A., Wardleworth, L., Zhang, N., & Oliver, S. G. (2005). Doxycycline, the drug used to control the *tet*-regulatable promoter system, has no effect on global gene expression in *Saccharomyces cerevisiae*. *Yeast*, 22(7), 565-569. *(illustrates the importance of controls – in this case the need to determine whether the doxycycline used to control the tet promoter has undesirable off-target effects)*

Zhang, Y., Lamb, B. M., Feldman, A. W., Zhou, A. X., Lavergne, T., Li, L., & Romesberg, F. E. (2017). A semisynthetic organism engineered for the stable expansion of the genetic alphabet. *Proceedings of the National Academy of Sciences*, 114(6), 1317-1322. *(description of system to expand the number of DNA nucleotides from four to six in vivo)*

External Consultation Results (departments with potential overlap or interest in proposed course, if any)

Department Microbiology & Cell Science	Name and Title Eric W. Triplett, Professor and Chair <i>EW Triplett</i>
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Comments <i>Does not conflict with our proposed courses. Budget Dept has agreed to approve our course as well.</i>	

Department	Name and Title
Phone Number	E-mail
Comments	

Department	Name and Title
Phone Number	E-mail
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