<table>
<thead>
<tr>
<th>Date, Day</th>
<th>Lecture Topic</th>
<th>Lecturer</th>
</tr>
</thead>
<tbody>
<tr>
<td>January 8, M</td>
<td>The structure of genomes</td>
<td>Sen</td>
</tr>
<tr>
<td>January 10, W</td>
<td>Expression of the genome</td>
<td>Barton</td>
</tr>
<tr>
<td>January 12, F</td>
<td>Chromosomes &amp; aneuploidy</td>
<td>Cole</td>
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<tr>
<td>January 15, M</td>
<td><strong>Holiday - No Class</strong></td>
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<tr>
<td>January 17, W</td>
<td>The nature of mutations</td>
<td>Mattox</td>
</tr>
<tr>
<td>January 19, F</td>
<td>Classic genetic screen strategies</td>
<td>Mattox</td>
</tr>
<tr>
<td>January 22, M</td>
<td>Genetic interactions &amp; sensitized screens</td>
<td>Van Hoof</td>
</tr>
<tr>
<td>January 24, W</td>
<td>Genetic model organisms</td>
<td>Eisenhoffer</td>
</tr>
<tr>
<td>January 26, F</td>
<td>Transgenic animals</td>
<td>Behringer</td>
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<tr>
<td>January 29, M</td>
<td>Active genetics</td>
<td>Behringer</td>
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<tr>
<td>January 31, W</td>
<td>RNAi screens</td>
<td>Li</td>
</tr>
<tr>
<td>February 2, F</td>
<td><strong>Exam 1</strong></td>
<td>-</td>
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<tr>
<td>February 5, M</td>
<td>RNA-seq workshop</td>
<td>Liu</td>
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<tr>
<td>February 7, W</td>
<td>RNA-seq workshop</td>
<td>Liu</td>
</tr>
<tr>
<td>February 9, F</td>
<td>RNA-seq workshop</td>
<td>Liu</td>
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<tr>
<td>February 12, M</td>
<td>RNA splicing mechanisms &amp; consequences</td>
<td>Cote</td>
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<tr>
<td>February 14, W</td>
<td>Introduction to human genetics &amp; patterns of single gene inheritance</td>
<td>Fornage</td>
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<tr>
<td>February 16, F</td>
<td>Complex inheritance and multifactorial disorders</td>
<td>Fornage</td>
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<tr>
<td>February 19, M</td>
<td><strong>Holiday - No Class</strong></td>
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<tr>
<td>February 21, W</td>
<td>Genetic variability</td>
<td>Hixson</td>
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<tr>
<td>February 23, F</td>
<td>Molecular basis of disease phenotype-genotype</td>
<td>Hixson</td>
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<tr>
<td>February 26, M</td>
<td>Next generation Sequencing</td>
<td>Krahe/Fornage</td>
</tr>
<tr>
<td>February 28, W</td>
<td>Genetic basis of cancer</td>
<td>Huff/ Krahe</td>
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<tr>
<td>March 2, F</td>
<td>Case study: Chronic myeloid leukemia</td>
<td>Huff/ Krahe</td>
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<tr>
<td>March 5, M</td>
<td>Tumor suppressor genes</td>
<td>Huff/ Krahe</td>
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<tr>
<td>March 7, W</td>
<td>Case study: Colorectal cancer</td>
<td>Huff/ Krahe</td>
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<tr>
<td>March 9, F</td>
<td><strong>Exam 2</strong></td>
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<td>March 12-16</td>
<td><strong>Spring Break - No Class</strong></td>
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<tr>
<td>March 19, M</td>
<td>Application of Mendelian genetics to clinical care</td>
<td>Daiger</td>
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<tr>
<td>March 21, W</td>
<td>Medical genetics services and genetic counseling</td>
<td>Singletary</td>
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<tr>
<td>March 23, F</td>
<td>Functional validation of cancer</td>
<td>Huff</td>
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<tr>
<td>March 26, M</td>
<td>The microbiome in human disease</td>
<td>Hanis</td>
</tr>
<tr>
<td>March 28, W</td>
<td>Clinical risk assessment with case studies</td>
<td>Singletary</td>
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<tr>
<td>March 30, F</td>
<td>Gene precision therapies and stem cell therapeutics</td>
<td>McDonnell</td>
</tr>
<tr>
<td>April 2, M</td>
<td>Epigenetics</td>
<td>Cheng</td>
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<tr>
<td>Date</td>
<td>Topic</td>
<td>Instructor</td>
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<tr>
<td>April 4, W</td>
<td>Histone code (writers &amp; erasers)</td>
<td>Lee</td>
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<tr>
<td>April 6, F</td>
<td>Histone code (readers)</td>
<td>Bedford</td>
</tr>
<tr>
<td>April 9, M</td>
<td>Histone variants</td>
<td>Bartholomew</td>
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<tr>
<td>April 11, W</td>
<td>ATP-dependent chromatin remodelers</td>
<td>Bartholomew</td>
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<tr>
<td>April 13, F</td>
<td>Epigenetics &amp; cancer</td>
<td>Bedford</td>
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<tr>
<td>April 16, M</td>
<td>DNA methylation</td>
<td>Chen</td>
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<tr>
<td>April 18, W</td>
<td>Imprinting &amp; X inactivation</td>
<td>Chen</td>
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<tr>
<td>April 20, F</td>
<td>Non-coding RNAs</td>
<td>Calin</td>
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<tr>
<td>April 23, M</td>
<td>Epigenetics &amp; therapeutics</td>
<td>Bedford</td>
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<tr>
<td>April 25, W</td>
<td>Epigenetics techniques: bench skills</td>
<td>Jain</td>
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<tr>
<td>April 27, F</td>
<td>Epigenetics techniques: bioinformatics analysis</td>
<td>Xu</td>
</tr>
<tr>
<td>May 4, F</td>
<td>Exam 3</td>
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</tbody>
</table>
**Course**

The course is organized into three general sections: 1. Experimental Genetics, 2. Human Genetics, and 3. Epigenetics. There will also be a one-week hands-on bioinformatics workshop to learn how to process and analyze RNA-seq data.

This course fulfills a requirement of the Genetics and Epigenetics Graduate Program.

**RNA-Seq Workshop**

This hands-on workshop will teach you how to process and analyze sequence data to assess and compare transcriptomes. You can use your own sequence data, use datasets in public repositories, or we will provide sequence datasets.

**Exams**

There will be 3 exams of 100 points each.

A = 85%
B = 75%
C = 65%
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