<table>
<thead>
<tr>
<th>Date, Day</th>
<th>Lecture Topic</th>
<th>Lecturer</th>
</tr>
</thead>
<tbody>
<tr>
<td>January 14, M</td>
<td>The structure of the genome</td>
<td>Sen</td>
</tr>
<tr>
<td>January 16, W</td>
<td>Chromosomes and aneuploidy</td>
<td>Cole</td>
</tr>
<tr>
<td>January 21, M</td>
<td><strong>Holiday - No Class</strong></td>
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</tr>
<tr>
<td>January 23, W</td>
<td>Next generation DNA sequencing</td>
<td>Fornage/Krahe</td>
</tr>
<tr>
<td>January 28, M</td>
<td>Molecular basis of disease phenotype-genotype</td>
<td>Hixson</td>
</tr>
<tr>
<td>January 30, W</td>
<td>Genetic screens</td>
<td>Mattox</td>
</tr>
<tr>
<td>February 4, M</td>
<td>RNAi/CRISPR screens</td>
<td>Arur</td>
</tr>
<tr>
<td>February 6, W</td>
<td>Transgenic animals</td>
<td>Behringer</td>
</tr>
<tr>
<td>February 11, M</td>
<td>Single gene inheritance &amp; application of Mendelian genetics to clinical care</td>
<td>Daiger</td>
</tr>
<tr>
<td>February 13, W</td>
<td>Current human genetic approaches to multifactorial disorders</td>
<td>Fornage</td>
</tr>
<tr>
<td>February 18, M</td>
<td><strong>Holiday - No Class</strong></td>
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<tr>
<td>February 20, W</td>
<td>Medical genetics services &amp; clinical risk assessment</td>
<td>Singletary</td>
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<tr>
<td>February 25, M</td>
<td>Genetic basis of cancer</td>
<td>Huff/Krahe</td>
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<tr>
<td>February 27, W</td>
<td>Case study: Cancer genetics</td>
<td>Huff/Krahe</td>
</tr>
<tr>
<td>March 4, M</td>
<td>Functional validation of cancer genes</td>
<td>Huff</td>
</tr>
<tr>
<td>March 6, W</td>
<td>Gene precision therapies and stem cell therapeutics</td>
<td>McDonnell</td>
</tr>
<tr>
<td>March 11, M</td>
<td>The microbiome in human disease</td>
<td>Hanis</td>
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<tr>
<td>March 13, W</td>
<td>RNA-Seq Workshop</td>
<td>Liu/Behringer</td>
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<tr>
<td>March 18-22</td>
<td><strong>Spring Break - No Class</strong></td>
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<tr>
<td>March 25, M</td>
<td>RNA-Seq Workshop</td>
<td>Liu</td>
</tr>
<tr>
<td>March 27, W</td>
<td>RNA-Seq Workshop</td>
<td>Liu</td>
</tr>
<tr>
<td>April 1, M</td>
<td>RNA-Seq Workshop</td>
<td>Liu</td>
</tr>
<tr>
<td>April 3, W</td>
<td>Epigenetics &amp; expression of the genome</td>
<td>Cheng</td>
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<tr>
<td>April 8, M</td>
<td>Epigenetics techniques: bench skills</td>
<td>Jain</td>
</tr>
<tr>
<td>April 10, W</td>
<td>Histone code (writers &amp; erasers)</td>
<td>Lee</td>
</tr>
<tr>
<td>April 15, M</td>
<td>Histone code (readers)</td>
<td>Bedford</td>
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<tr>
<td>April 17, W</td>
<td>DNA methylation, imprinting &amp; X inactivation</td>
<td>Chen</td>
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<tr>
<td>April 22, M</td>
<td>Epigenetics &amp; cancer therapeutics</td>
<td>Bedford</td>
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<tr>
<td>April 24, W</td>
<td>Histone variants</td>
<td>Bartholomew</td>
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<tr>
<td>April 29, M</td>
<td>ATP-dependent chromatin remodelers</td>
<td>Bartholomew</td>
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<tr>
<td>May 1, W</td>
<td>Non-coding RNAs</td>
<td>Calin</td>
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<tr>
<td>May 6-10</td>
<td><strong>Finals Week</strong></td>
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</tbody>
</table>
Course Description

The course is organized into three general sections: 1. Experimental Genetics, 2. Human Genetics, and 3. Epigenetics. There will also be a 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.
**Course Directors**

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