<table>
<thead>
<tr>
<th>Date, Day</th>
<th>Lecture Topic</th>
<th>Lecturer</th>
</tr>
</thead>
<tbody>
<tr>
<td>January 7, T</td>
<td>The structure of the genome</td>
<td>Sen</td>
</tr>
<tr>
<td>January 9, Th</td>
<td>Chromosomes and aneuploidy</td>
<td>Cole</td>
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<tr>
<td>January 14, T</td>
<td>Next generation DNA sequencing</td>
<td>Fornage/Krahe</td>
</tr>
<tr>
<td>January 16, Th</td>
<td>Molecular basis of disease phenotype-genotype</td>
<td>Hixson</td>
</tr>
<tr>
<td>January 21, T</td>
<td>Genetic screens</td>
<td>Mattox</td>
</tr>
<tr>
<td>January 23, Th</td>
<td>RNA interference</td>
<td>Arur</td>
</tr>
<tr>
<td>January 28, T</td>
<td>Transgenic animals</td>
<td>Behringer</td>
</tr>
<tr>
<td>January 30, Th</td>
<td>Conditional genetic manipulations</td>
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<tr>
<td>February 4, T</td>
<td>Current human genetic approaches to gene discovery for multifactorial disorders</td>
<td>Fornage</td>
</tr>
<tr>
<td>February 6, Th</td>
<td>Applications of genetic information to health outcomes in multifactorial disorders</td>
<td>Fornage</td>
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<tr>
<td>February 11, T</td>
<td>Medical genetics services &amp; clinical risk assessment</td>
<td>Singletary</td>
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<tr>
<td>February 13, Th</td>
<td>Genetic basis of cancer</td>
<td>Huff/Krahe</td>
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<tr>
<td>February 18, T</td>
<td>Case study: Cancer genetics</td>
<td>Huff/Krahe</td>
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<tr>
<td>February 20, Th</td>
<td>Functional validation of cancer genes</td>
<td>Huff</td>
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<tr>
<td>February 25, T</td>
<td>Gene precision therapies and stem cell therapeutics</td>
<td>McDonnell</td>
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<tr>
<td>February 27, Th</td>
<td>The microbiome in human disease</td>
<td>Hanis</td>
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<tr>
<td>March 3, T</td>
<td>RNA-Seq Workshop</td>
<td>Liu/Behringer</td>
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<tr>
<td>March 5, Th</td>
<td>RNA-Seq Workshop</td>
<td>Liu/Behringer</td>
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<tr>
<td>March 10, T</td>
<td>RNA-Seq Workshop</td>
<td>Liu/Behringer</td>
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<tr>
<td>March 12, T</td>
<td>RNA-Seq Workshop</td>
<td>Liu/Behringer</td>
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<tr>
<td>March 16-20</td>
<td><strong>Spring Break - No Class</strong></td>
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<tr>
<td>March 24, T</td>
<td>Epigenetics &amp; expression of the genome</td>
<td>Cheng</td>
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<tr>
<td>March 26, Th</td>
<td>Epigenetics techniques: bench skills</td>
<td>Jain</td>
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<tr>
<td>March 31, T</td>
<td>Histone code (writers &amp; erasers)</td>
<td>Lee</td>
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<tr>
<td>April 2, Th</td>
<td>Histone code (readers)</td>
<td>Barton</td>
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<tr>
<td>April 7, T</td>
<td>DNA methylation</td>
<td>Huang</td>
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<tr>
<td>April 9, Th</td>
<td>Imprinting &amp; X inactivation</td>
<td>Chen</td>
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<tr>
<td>April 14, T</td>
<td>Histone variants</td>
<td>Bartholomew</td>
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<tr>
<td>April 16, Th</td>
<td>ATP-dependent chromatin remodelers</td>
<td>Bartholomew</td>
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<tr>
<td>April 21, T</td>
<td>Non-coding RNAs</td>
<td>Calin</td>
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<tr>
<td>April 23, Th</td>
<td>Epigenetics and cancer therapeutics</td>
<td>Santos</td>
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<tr>
<td>April 27-May 1</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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