

## AGRI5710 Module : Complex genomes Module 1

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Schedule: October-November, 2014; 5 week period, class sessions of 1.5 hours /week  
Location and time to be determined in consultation with interested students

Evaluation: Participation: 20%, essay 40%, written exam 40%

Prerequisite: no specific course requirements, but a working knowledge of genetics and genomics is desirable

The genomes of complex species contain a variety of genetic elements, some of which are considered essential to the development and maintenance of the organism while others are not. In fact, when the first draft of the human genome was released in 2001, less than 5% of the genome was considered 'essential' and the remaining 95% 'non-essential'. Approximately half of the non-essential portion of the genome was comprised of repetitive DNA, and the other half a mixture of intergenic DNA and DNA of unknown function and origin.

Over the past decade, a number of studies have reshaped our thinking on essential vs non-essential DNA in complex genomes. In particular, a series of 30 papers published by the ENCODE (Encyclopedia of DNA Elements) consortium in 2012 was widely quoted as implicating over 80% of the human genome in functions of relevance to host cells. This conclusion has since been widely criticized because it is based on the assumption that every DNA element in our genomes that is expressed is essential for our health and survival.

This module is designed to explore the landscape of complex genomes, and to take a critical look at the data on both sides of the essential vs non-essential DNA argument, particularly in light of the ongoing debate triggered by the ENCODE papers. It is laid out roughly as follows:

1. Historical perspective on genome sizes and complexity
2. Reference genome sequences (human, mouse, chicken)
3. Structural genomics
4. Essential vs non-essential DNA elements – pre-ENCODE
5. The ENCODE project
6. The post-ENCODE fallout
7. A practical guide to complex genomes