

Epigenetics

Biosciences 704: Topics in Biosciences
Biology 695: Seminar in Molecular, Microbial, and Cellular Biology
Fall, 2011

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This course meets on the Prince William campus, in Bull Run Hall room 253, at 4:30 pm to 7:10 pm. This is a one credit course, but was scheduled for a 3 hr time slot, so we will meet at this time in alternate weeks (see schedule below). Note that we will meet on the Tuesday following Columbus Day, and on the Monday before Thanksgiving. There is no final exam in this course.

Monday, August 29 – Introduction & topic assignments

Monday, September 12 – student presentations

Monday, September 26 – student presentations

Tuesday, October 11 – student presentations (on Tuesday because of Columbus Day)

Monday, October 24 – student presentations.

Monday, November 7 – student presentations.

Monday, November 21 – student presentations.

Monday, December 5 – student presentations (last class meeting).

Grades in this seminar are based on your presentations (60%), participation in class discussions (10%), attendance (10%), and written answers to brief (in-class, open book) quiz questions (20%). Quizzes will be given at the end of class and will cover the material presented that day. To accommodate schedule conflicts, we will drop one absence and one quiz for each student. Beyond that, you are expected to attend this class in order to receive credit for it, and to arrange your schedule accordingly. We will not have make-up sessions or final exams.

MS student presentations should last about 30 min, including the relevant definitions and background from other papers. Typically this means 30 slides or less. You will also be expected to lead the class discussion (about 15 min) following your presentation.

Ph.D. students will generally be expected to present somewhat longer papers (including the review papers so identified in the reading list), as well as including more background from other papers. PhD student presentations are expected to last 45-60 min, including the relevant definitions and background from other papers. This should be sufficient time for an in-depth presentation of a review paper (but not necessarily every detail). You will also be expected to lead the class discussion (about 15 min) following your presentation.

The class schedule will typically include 2-3 presentations per class meeting. The detailed presentation schedule will be posted on the course web site after the papers are assigned.

Introduction

Bonasio, R., Tu, S., and Reinberg, D. (2010). Molecular signals of epigenetic states. *Science (New York, NY)* *330*, 612-616.

Reviews (Ph.D. students)

1. Bourc'his, D., and Voinnet, O. (2010). A small-RNA perspective on gametogenesis, fertilization, and early zygotic development. *Science (New York, NY)* *330*, 617-622.
2. Feng, S., Jacobsen, S.E., and Reik, W. (2010b). Epigenetic reprogramming in plant and animal development. *Science (New York, NY)* *330*, 622-627.
3. Ho, L., and Crabtree, G.R. (2010). Chromatin remodelling during development. *Nature* *463*, 474-484.

Histones

4. Araki, Y., Wang, Z., Zang, C., Wood, W.H., 3rd, Schones, D., Cui, K., Roh, T.Y., Lhotsky, B., Wersto, R.P., Peng, W., *et al.* (2009). Genome-wide analysis of histone methylation reveals chromatin state-based regulation of gene transcription and function of memory CD8+ T cells. *Immunity* *30*, 912-925.
5. Jin, C., Zang, C., Wei, G., Cui, K., Peng, W., Zhao, K., and Felsenfeld, G. (2009). H3.3/H2A.Z double variant-containing nucleosomes mark 'nucleosome-free regions' of active promoters and other regulatory regions. *Nature genetics* *41*, 941-945.
6. Wang, Z., Zang, C., Cui, K., Schones, D.E., Barski, A., Peng, W., and Zhao, K. (2009). Genome-wide mapping of HATs and HDACs reveals distinct functions in active and inactive genes. *Cell* *138*, 1019-1031.
7. Soppe, W.J., Jasencakova, Z., Houben, A., Kakutani, T., Meister, A., Huang, M.S., Jacobsen, S.E., Schubert, I., and Fransz, P.F. (2002). DNA methylation controls histone H3 lysine 9 methylation and heterochromatin assembly in Arabidopsis. *EMBO J* *21*, 6549-6559.

DNA demethylation

8. Bhutani, N., Brady, J.J., Damian, M., Sacco, A., Corbel, S.Y., and Blau, H.M. (2010). Reprogramming towards pluripotency requires AID-dependent DNA demethylation. *Nature* *463*, 1042-1047.
9. Guo, J.U., Su, Y., Zhong, C., Ming, G.L., and Song, H. (2011). Hydroxylation of 5-methylcytosine by TET1 promotes active DNA demethylation in the adult brain. *Cell* *145*, 423-434.
10. Popp, C., Dean, W., Feng, S., Cokus, S.J., Andrews, S., Pellegrini, M., Jacobsen, S.E., and Reik, W. (2010). Genome-wide erasure of DNA methylation in mouse primordial germ cells is affected by AID deficiency. *Nature* *463*, 1101-1105.

de novo methylation of DNA

11. Feng, J., Zhou, Y., Campbell, S.L., Le, T., Li, E., Sweatt, J.D., Silva, A.J., and Fan, G. (2010a). Dnmt1 and Dnmt3a maintain DNA methylation and regulate synaptic function in adult forebrain neurons. *Nat Neurosci* *13*, 423-430.
12. Law, J.A., Vashisht, A.A., Wohlschlegel, J.A., and Jacobsen, S.E. (2011). SHH1, a Homeodomain Protein Required for DNA Methylation, As Well As RDR2, RDM4, and Chromatin Remodeling Factors, Associate with RNA Polymerase IV. *PLoS Genet* *7*, e1002195.

Chromatin remodeling complexes

13. Lessard, J., Wu, J.I., Ranish, J.A., Wan, M., Winslow, M.M., Staahl, B.T., Wu, H., Aebersold, R., Graef, I.A., and Crabtree, G.R. (2007). An essential switch in subunit composition of a chromatin remodeling complex during neural development. *Neuron* *55*, 201-215.
14. Yoo, A.S., Staahl, B.T., Chen, L., and Crabtree, G.R. (2009). MicroRNA-mediated switching of chromatin-remodelling complexes in neural development. *Nature* *460*, 642-646.

Methylomes

15. Lister, R., Pelizzola, M., Downen, R.H., Hawkins, R.D., Hon, G., Tonti-Filippini, J., Nery, J.R., Lee, L., Ye, Z., Ngo, Q.M., *et al.* (2009). Human DNA methylomes at base resolution show widespread epigenomic differences. *Nature* 462, 315-322.
16. Wu, H., D'Alessio, A.C., Ito, S., Wang, Z., Cui, K., Zhao, K., Sun, Y.E., and Zhang, Y. (2011). Genome-wide analysis of 5-hydroxymethylcytosine distribution reveals its dual function in transcriptional regulation in mouse embryonic stem cells. *Genes & development* 25, 679-684.

Inheritance of epigenetic states

17. Jacobsen, S.E., and Meyerowitz, E.M. (1997). Hypermethylated SUPERMAN epigenetic alleles in *Arabidopsis*. *Science* (New York, NY 277, 1100-1103.