

Name and NetID: _____

BIO 311, READING HOMEWORK
DUE 23 MARCH 2017

Read these papers:

1. Spellman et al., (1998). Comprehensive identification of cell cycle-regulated genes of the yeast *Saccharomyces cerevisiae* by microarray hybridization. *Molecular Biology of the Cell*. 9 3273–3297.
2. Lee et al., (2002). Transcriptional regulatory networks in *Saccharomyces cerevisiae*. *Science*. 298(5594):799-804.

Answer the questions below. Provide your answers in a separate file, numbered according to questions listed below. Submit your file on Sakai by the start of class on March 23. Be sure to write in your own words. If you use verbiage from the paper, be sure to put it in quotes!

1. (10 points) Note that the Lee et al. paper, published in the high profile journal “Science”, is in a much different format than that of the Spellman et al. paper. Answer the following questions regarding this format difference.
 1. (3 point) Describe how the format is different between the Spellman and Lee papers.
 2. (2 point) Where do you find the Materials and Methods section of the Lee et al. paper? (Hint: read the fine print!)
 3. (2 points) Find another paper in Science. Give the citation in the format of Science. Is this other paper also formatted like the Lee et al. paper?
 4. (3 points) Go to the website of the journal “Science” and read the detailed instructions for authors for preparation of manuscripts for submission to the journal. Do the same for where the Spellman et al. paper was published. Based on this comparison, describe why you think the format might be so different between the journals that published the Lee and Spellman papers.
2. (15 points) After reading the Lee et al., paper, answer the following questions below and note where in the paper you found the answer (use “Exercise 2” in the in-class workshop on the Spellman paper as a guide for how to answer this question). Answer each question in 2-3 sentences in your own words.
 1. (3 points) What main scientific question did this paper address?
 2. (3 points) What are the main conclusions?
 3. (3 points) What evidence supports these conclusions?
 4. (3 points) Why are these conclusions important based on the cutting edge of the field at the time?
 5. (3 points) Are you convinced that the data support the conclusions? Why or why not?
3. (5 points) If you analyzed the data sets of the Lee et al. and Spellman et al. papers together, what conclusions might you be able to make about the transcription regulatory network that controls cell cycle gene expression? List and describe these conclusions in 2-3 sentences.
4. (2 points) Skim through this paper:

- Harbison et al. 2004. Transcriptional regulatory code of a eukaryotic genome. *Nature* 431, 99-104. <http://www.nature.com/nature/journal/v431/n7004/full/nature02800.html>

Note that the objectives and methods of the study were very similar to those of the Lee et al paper. Why did Harbison et al conduct this follow-up study? Choose one of the options below.

- A. Because Lee et al. was not technically sound.
- B. Because Harbison et al. wanted to know how transcription factors bound to the genome under varying growth conditions.
- C. Because Lee et al. only tested the binding sites of a few transcription factors.
- D. In order to determine the source(s) of technical variability in the data and correct for them.