CBMG688G: Evolution of Transcriptional regulation – A computational perspective

Instructor: Sridhar Hannenhalli (Sridhar at umiacs dot umd dot edu)
Time: Tues, Thurs 10 – 12pm
Location: Biomolecular Sciences Building 3118
Office hour: Thurs 10-11am, Biomolecular Sciences Building 3104G

Credits – 2 (no project) or 3 (project)

Course description – Motivation, Form, and Goal

Transcription is one of the most important control points at which the expression of the ultimate gene product is regulated, and as such, is critical for understanding the genetic basis of phenotypic diversity and evolution. Transcriptional regulation is an extremely complex process, details of which are continually refined. In this course, we will review the rich literature on the evolution of various aspects of transcriptional regulation and how they may inform phenotypic evolution. Our focus will be on Eukaryotes. Although, the underlying questions we will study will be biological, the approaches will be computational and model-based. The course will be instructor-coordinated but student-driven, and is meant to provide a broad conceptual understanding of evolutionary processes and models as it pertains to eukaryotic transcriptional regulation.

Course material

The course will be based entirely on primary literature. A broad (but far from complete) list of papers is provided below for prospective students as a guide. Students are encouraged to suggest additional papers of their interest.

Grading

	2-credits	**3-credits**
Class participation	40%	20%
Presentation	60%	40%
Project		40%

For project (3 credit) option, each student (or small group) will design a project during first 3 weeks, work on it through the semester, and prepare a 2 page report and present the results at the end of the course.

Tentative list of topics (and a highly biased and incomplete list of papers)

- *Fundamentals of transcriptional regulation (covered by instructor)*
- *Comparative genomic analysis of regulatory regions [1-9]*
- *Natural selection acting on regulatory regions [10-19]*
- *Evolution / Turnover of TF binding sites [20-29]*
- *Comparative transcriptomic analysis [30-37]*
- *Regulatory network evolution [38-50]*
- *Review articles [51-58]*

Expected student background/interest

This course is meant for students with reasonable intuition of how transcriptional regulation works and evolution in general. Beyond this biological pre-requisite, a certain level of computational sophistication is expected because the majority of papers we will discuss employ computational approaches. However, it is difficult to enumerate specific computational approaches because it varies a lot depending on specific analysis.

Tentative schedule

Date	Content
1/27	Logistics – paper selection by weekend
2/3	Overview based on selected papers
2/10	Student presentation (preliminary project proposal)
2/17	Student presentation (projects finalized)
2/24	Student presentation
3/3	Student presentation
3/10	Student presentation
SPR BREAK	
3/24	Student presentation
3/31	Student presentation
4/7 **	Student presentation
4/14	Student presentation
4/21	Student presentation
4/28	Student presentation
5/5	Student presentation
5/12	Project presentation
5/19	Project presentation

** We may have a guest on this day (and/or some other days)

References

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