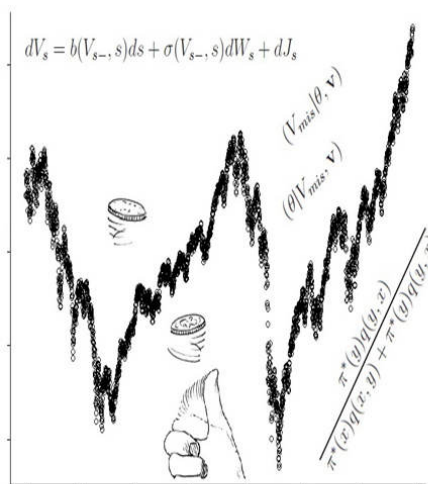


Quarta-feira, 15 de abril de 2015

Programa

14:00 - 15:20 – **Flávio B. Gonçalves (UFMG)**

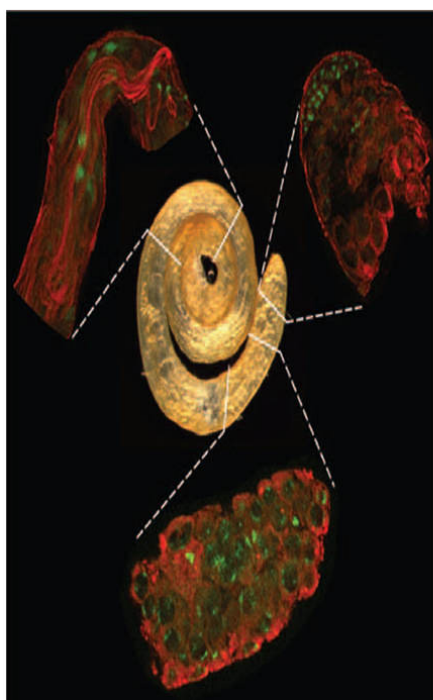
An infinite-dimensional MCMC for exact Bayesian inference in jump-diffusion processes



Jump-diffusions have considerable appeal as flexible families of stochastic models. Making statistical inference based on discrete observations of such processes is a complex and challenging problem. Its infinite-dimensional nature has required from existing inference methodologies the use of discrete approximations that naturally represent a considerable source of error. In this talk, we rely on a novel algorithm to perform exact simulation of jump-diffusions bridges as the basis to develop an MCMC algorithm to make inference for jump-diffusion processes. The resulting infinite-dimensional Markov chain has the exact posterior distribution of the parameters and missing paths as its invariant distribution. More specifically, it is a Gibbs Sampling with Barker's steps. The methodology is exact in the sense that it is free of discretisation error and Monte Carlo error is the only source of inaccuracy. The exactness feature is related to the simulation of events of unknown probability.

15:40 - 17:00 – **Maria D. Vibranovski (USP)**

The use of genomic and gene expression large-scale data for the analyses of sexual evolution



Although more than a decade has passed since the first eukaryotic genome was sequenced, the molecular basis of genome organization and complexity remains a largely unresolved problem. The relationship of genotype to phenotype has proven particularly challenging. I use gametogenesis in *Drosophila* as a model system to study the evolution and phenotypic expression of genomic features. Gametogenesis is a fascinating biological process; it varies temporally throughout development, and has profound evolutionary impact in that it provides the raw material for the next generation - the gamete. To date, gametogenesis research has primarily focused on single gene studies of fertility. In contrast, I apply a genomic perspective to the overall process of gametogenesis to understand the role sexual selection plays in genome evolution. In my research on genome evolution in *Drosophila melanogaster*, I have combined bioinformatics and statistics with experimental genomic and molecular genetic methods to obtain large-scale gene expression data on gametogenesis, or spermatogenic-stage-specific transcriptome (SpermPress). The results help to solve two classical problems that have puzzled biologists for decades: evidence for Meiotic Sex Chromosome inactivation and for Post-meiotic transcription. In this talk, I present the results obtained through the application of advanced Bayesian statistics to Gene Chip microarray data. I also introduce another puzzle yet to be solved in the evolutionary biology field related to the role of sperm haploid selection in the evolution of new genes.

17:00 – Discussão e lanche

Local

Centro de Tecnologia – UFRJ
Sala C-116 - Bloco C
Ilha do Fundão

Contatos

Augusto Teixeira (IMPA)
Evaldo M. F. Curado (CBPF)
Fábio D. A. Aarão Reis (UFF)
Maria Eulália Vares (UFRJ)
Mariane B. Alves (UFRJ)
Patrícia Gonçalves (PUC-Rio)

augusto@impa.br
evaldo@cbpf.br
reis@if.uff.br
eulalia@im.ufrj.br
mariane@im.ufrj.br
patricia@mat.puc-rio.br

Realização:



Apoio:

