

Tentative Outline

Special Issue for "Current Genomics"

Systems Genomics in the Age of Next Generation sequencing

Guest Editor: Dr. Prashanth Suravajhala

Aims & Scope:

With the advent of next generation sequencing (NGS) technologies, there arose a need to identify the candidate mutations for causality. A challenge often seen in identifying and inferring the causal SNPs from sequence data is that different methods need to be preferentially used to predict the effect of mutations for checking the bona fide. In this thematic issue, we encourage authors to submit the articles that ascertain methods to find mutations from coding and non-coding regions. With genetic variation best seen in non-coding regions, we expect submissions in the areas of, but not limited to non-coding RNAs from NGS, genome wide studies, high-throughput RNA-Sequencing approaches, exome based analysis, targeted sequencing etc. The articles could focus on a wide array of highly sensitive, if not less-stringent methods that the NGS has had delivered in the recent past using systems genomic integration.

Subtopics:

Systems Genomics
Next Generation Sequencing
Functional Genomics
Prioritizing mutations

Schedule:

Call for submissions: January 28, 2019
Submissions close: August 31, 2019
Notification of acceptance: September 30, 2019
Online first: October 30, 2019.

Contacts:

Guest Editor: Dr. Prashanth Suravajhala, Ph.D.
Research Scientist, Systems Biology
Department of Biotechnology and Bioinformatics
Birla Institute of Scientific Research
Statue Circle, Jaipur 302001 RJ, India
Telephone: (work) +91-141-2385094. Extension 308
E mail: prash[AT]biser[DOT]res[DOT]in
Home page: <http://www.bioinformatics.org/wiki/Prash>