제3회
생물정보 연구 교류회

연구 동향 및 개발 분석 도구 소개

2017. 4. 3.(월) | 서울대학교 박물관 강당

PROGRAM

10:00~10:10	*Registration*	
10:10~10:40	Literature based analysis of omics data	김 선(서울대)
10:40~11:10	Speeding up all-pairs suffix-prefix matching	박근수(서울대)
11:10~11:40	Towards accurate detection of somatic variations in contaminated tumor samples	백대현(서울대)
11:40~12:10	High-confidence coding and non-coding transcriptome maps	남진우(한양대)
12:10~13:10	*Lunch*	
13:10~13:40	Genome-based taxonomic framework for bacteria	천종식(서울대)
13:40~14:10	Literature mining, drug repurposing and precision medicine	강재우(고려대)
14:10~14:40	Neural universal discrete denoiser	윤성로(서울대)
14:40~15:10	Recent advances in reference-assisted genome assembly	김재범(건국대)

문의 : SNU Bioinformatics Institute 생물정보연구소 (02-880-2858~9, snubioinfo@gmail.com)

주관 : 서울대학교 생물정보연구소 후원 : 한국연구재단

주최 : 서울대학교 생물정보연구소, 생명공학공동연구원
유전체 정보분석 기술개발 사업단, 서울대학교 BIT 융합 연계교육팀

Towards accurate detection of somatic variations in contaminated tumor samples

Somatic substitutions are the most frequent type of mutations that are known to drive most human cancers. It has been key interest of the cancer genomicists and clinicians to reliably and accurately detect such somatic substitutions in tumor samples. Major efforts have been used to develop such tools for the past several years and as a result, many software tools have been reported. However, it is still difficult to obtain pure tumor samples from most cancer patients, a problem that continues to remain as a major challenge for all the existing mutation detection tools. In this talk, we will briefly discuss about a benchmark result for the currently available software tools for detecting somatic substitutions and about our recent efforts to improve the detection accuracy of somatic variations in contaminated tumor samples.