International Symposium on Bioinformatics and its Application

Tuesday, September 30, 2014. 13:00 - 18:00. Jointly hosted by Tokyo Institute of Technology and Niigata University

Invited Speakers:

13:10 - 13:40

J.B. BROWN
Graduate School of Medicine, Kyoto University
"Pharmacogenomics and Life Science Informatics - what is done and where we are going"

13:40 - 14:10

Vachiranee LIMVIPHUVADH
Agency for Science, Technology and Research (A*STAR)
Singapore
"Workflow for selecting SNPs in pathways linked to defined phenotype"

14:10 - 14:40

Sayaka MIZUTANI
Bioinformatics Center, Kyoto University
"Pharmacoepidemiological characterization of drug-induced adverse reaction clusters towards understanding of their mechanisms"

15:00 - 15:30

Kousuke HASHIMOTO
RIKEN Center for Life Science Technologies (CLST)
"Activation of LTR derived non-coding RNAs in liver cancer" (肝細胞がんにおいて発現上昇するLTR由来のnon-coding RNA)

15:30 - 16:00

Daichi SHIGEMIZU
RIKEN Center for Integrative Medical Sciences
"Analysis for disease-causing mutations using whole-exome sequencing data"

Venue:


Google Map (https://maps.google.co.jp/maps/place?saferoff&espv=2&bav=on.2,or.r_cp.r_qf.&bvm=bv.72938740,d.cGU,pv.xs.s;j
緑が丘駅&fb=1&gl=ja&cid=0)

Participation Fee:

Free of charge

Mixer:

Around 19:00, near Midorigaoka or Jiyugaoka Station
（懇親会は予定していますが時間・場所・参加費とも未定です）

Co-chair:

Masaaki KOTERA, Associate Professor, Tokyo Institute of
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<tr>
<th>Time</th>
<th>Speaker</th>
<th>Institution</th>
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<tr>
<td>16:00</td>
<td>Yoshihiro YAMANISHI</td>
<td>Medical Institute of Bioregulation, Kyushu University</td>
<td>&quot;Analysis and inference of drug-target interaction networks&quot;</td>
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<tr>
<td>16:50</td>
<td>Ai MUTO</td>
<td>Nara Institute of Science and Technology (NAIST)</td>
<td>&quot;Characterization of Genetic Interactions in E.coli based on Database Information&quot;</td>
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<td>17:20</td>
<td>Katsuhisa OZAKI</td>
<td>JT Biohistory Research Hall</td>
<td>&quot;Identification of chemoreceptor genes involved in host selection in swallowtail butterflies&quot;</td>
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