Course advertisement

Bioinformatics and Next Generation Sequencing

Within this course you will learn important bioinformatic concepts and tools and in particular focus on the analysis of Next Generation Sequencing datasets with many examples and exercises.

The course is open to all PhD students. Students of the PhD Program Biomedicine (BioMed) have priority.

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<tr>
<th>Date</th>
<th>Topic</th>
<th>Time</th>
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<tbody>
<tr>
<td>Mon 1st Nov 2021</td>
<td>Introduction to R</td>
<td>09:30-17:00 GMT</td>
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<tr>
<td>Mon 8th Nov 2021</td>
<td>Introduction to Unix</td>
<td>09:30-12:30 GMT</td>
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<tr>
<td>Mon 8th Nov 2021</td>
<td>Sequencing QC</td>
<td>13:30-17:00 GMT</td>
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<tr>
<td>Mon 15th Nov 2021</td>
<td>RNA Seq Data Analysis</td>
<td>09:30-17:00 GMT</td>
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<tr>
<td>Mon 22nd Nov 2021</td>
<td>ChIP Seq Data Analysis</td>
<td>09:30-17:00 GMT</td>
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<tr>
<td>Mon 29th Nov 2021</td>
<td>10X single cell RNA Seq Data Analysis</td>
<td>09:30-17:00 GMT</td>
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<tr>
<td>Mon 6th Dec 2021</td>
<td>Extracting Biological Information from Gene Lists</td>
<td>09:30-17:00 GMT</td>
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Room                                      via Zoom, details to follow
Type                                       Interactive Course with many hands-on exercises
Requirement                                Basic bioinformatics knowledge is recommended
Recommendation                             PhD students that will work with NGS datasets
Maximum participants                       20

Further information                        BioMed Coordinating Office (andrea.schmitz@uzh.ch)
                                          and here https://www.bioinformatics.babraham.ac.uk/training.html

Credit points                              3 ECTS (exercises within the course)
Registration                               By e-mail to andrea.schmitz@uzh.ch until Friday 1st October 2021 including the registration form.
                                          If the number of applications exceeds the maximum number of possible participants, priority will be given to BioMed students and those working with NGS datasets.