Basic Statistics with R

**Objective**
To familiarise participants with the foundations of practical biostatistics.

**Description**
The course addresses the following topics:

- **Sampling theory:**
  Obtaining information about a population via sampling. Sample characteristics (location, dispersion, skewness), estimation of the mean, standard error of the mean
- **Discrete and continuous probability distributions:**
  Central limit theorem
- **Hypothesis testing:**
  Basic principles, one- and two-sided testing, types of errors, power calculations
- **“Cookbook of tests”:**
  Location testing, normality, variance comparisons, counting statistics, contingency tables, regression tests

**Methodology**
Instructor-led lectures plus hands-on exercises using the R programming language (accessed via a dedicated web server).

**Conditions**

- Basic familiarity with the R programming language is required.
- In particular the following skills are necessary:
  - Using the R interpreter, either the command-line program or in R Studio
  - How to invoke R functions, pass optional/named parameters
  - Some familiarity with simple plotting commands

**Organizational Information**

<table>
<thead>
<tr>
<th>Language</th>
<th>English</th>
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<tbody>
<tr>
<td>Target group</td>
<td>Doctoral Candidates at all stages and Postdocs from Natural and Life Sciences</td>
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<tr>
<td>Date</td>
<td>Thursday–Friday, 7–8 November 2019, 9:00 – 13:00</td>
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<td>Registration</td>
<td>For registration click here</td>
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