

Monday 8.10	Tuesday 9.10	Wednesday 10.10	Thursday 11.10	Friday 12.10
<p>9.30 - 10.45: Intro Unix I</p> <p>11.00 - 12.30: Intro Unix II / Software installation</p> <p>12.30 – 13.30: Lunch</p> <p>13.30 – 15.00: Unix commands</p> <p>15.15 - 17.00: HTS file formats</p>	<p>09.00 – 09.45: Introduction to Next Generation Sequencing</p> <p>10.00 - 11.00: Applications of Next Generation Sequencing</p> <p>11.15 – 12.00: Sequencing File formats</p> <p>12.00 - 12.45: Lunch</p> <p>12.45 – 15.15 FastQC and read trimming practical</p> <p>15.30 – 17.00 Assembly: introduction</p>	<p>09.00 - 10.30: Assembly</p> <p>10.45 - 12.00: Assembly</p> <p>12.00 - 12.45: Lunch</p> <p>12.45 - 15.15: Assembly</p> <p>15.30 - 17.00: Assembly</p>	<p>09.00 - 10.30: Assembly</p> <p>10.45 - 12.00: Assembly</p> <p>12.00 - 12.45: Lunch</p> <p>12.45 - 15.15: Assembly</p> <p>15.30 - 17.00: Assembly</p>	<p>09.00 – 12.00: miRNA-seq Pt I</p> <p>12.00 - 12.45: Lunch</p> <p>12.45 - 17.00: miRNA-seq Pt II</p>
<p>Presenting (P)/assisting (A):</p> <p>Merete (P)</p> <p>Daniel (P)</p> <p>Morten (A)</p> <p>Karin (A)</p>	<p>Presenting (P)/assisting (A):</p> <p>Leonardo (P) - NGS</p> <p>Lex (P) – File formats, FastQC and read trimming, assembly</p> <p>Karin (A)</p> <p>Merete (A)</p>	<p>Presenting (P)/assisting (A):</p> <p>Lex (P)</p> <p>Karin (A)</p>	<p>Presenting (P)/assisting (A):</p> <p>Lex (P)</p> <p>Karin (A)</p>	<p>Presenting (P)/assisting (A):</p> <p>Merete (P)</p> <p>Daniel (A)</p> <p>Line (A)</p>

Monday 15.10	Tuesday 16.10	Wednesday 17.10	Thursday 18.10	Friday 19.10
<p>09.30 – 10.00: mRNA-seq technology</p> <p>10.15 – 12.15: RNA-seq analysis theory</p> <p>12.15 – 13.00: Lunch</p> <p>13.00 - 17.00: RNA-seq analysis hands-on</p>	<p>09.00 - 09.30: mRNA-seq technology</p> <p>09.45 - 11.45: RNA-seq analysis theory</p> <p>11.45 - 12.30: Lunch</p> <p>12.30 - 17.00: RNA-seq analysis hands-on</p>	<p>09.00 - 17.00: Basic variant calling</p>	<p>09.00 - 17.00: Advanced variant calling</p> <p>Functional annotation and filtering of VCF files</p>	<p>09.00 - 10.30: Statistical genome analysis</p> <p>10.45 - 12.15: Statistical genome analysis</p> <p>12.15 - 13.00: Lunch</p> <p>13.00 – 14.00: Galaxy and reproducibility</p> <p>14.15 - 15.15: Galaxy and reproducibility</p> <p>15.30 - 17.00: Course evaluation, Instructions for exam</p>
<p>Presenting (P)/assisting (A):</p> <p>Susanne (P)</p> <p>Amine (P)</p> <p>Jan Christian (A)</p> <p>Daniel (A)</p>	<p>Presenting (P)/assisting (A):</p> <p>Amine (P)</p> <p>Susanne (P)</p> <p>Daniel (A)</p> <p>Jan Christian (A)</p>	<p>Presenting (P)/assisting (A):</p> <p>Tim (P)</p> <p>Yvan Strahm (A)</p> <p>Ying Sheng (A)</p> <p>Pubudu Samarakoon (A)</p> <p>Tony Håndstad (A)</p>	<p>Presenting (P)/assisting (A):</p> <p>Tim (P)</p> <p>Yvan Strahm (A)</p> <p>Ying Sheng (A)</p> <p>Pubudu Samarakoon (A)</p> <p>Tony Håndstad (A)</p>	<p>Presenting (P)/assisting (A):</p> <p>Sveinung (P)</p> <p>Geir Kjetil (P)</p> <p>Merete (A)</p> <p>Daniel (A)</p> <p>Kai (A)</p>