

<b>Day/Time</b>	<b>Mon 11.8.</b>	<b>Tue 12.8.</b>	<b>Wed 13.8.</b>	<b>Thu 14.8.</b>	<b>Fri 15.8.</b>
<b>Morning</b>	<p><b>Introduction to Environmental Bioinformatics</b></p> <p><b>Theme I: Identifying and differentiating pure cultures</b> (Kristina Lindström, Leena Räsänen, Hannu Rita)</p> <ul style="list-style-type: none"> <li>- What is a strain-species-genus?</li> <li>- Genetic and phenetic fingerprinting techniques</li> </ul>	<p><b>Theme II: Studying single genes</b> (German Jurgens, Lars Paulin)</p> <ul style="list-style-type: none"> <li>- Introduction to genes</li> <li>- Databases</li> <li>- PCR primer design</li> <li>- Phylogenetic trees with <i>Archaea</i> as example</li> </ul>	<p><b>Theme III: Fingerprinting environmental samples</b> (Maarit Niemi, Anu Mikkonen)</p> <ul style="list-style-type: none"> <li>- Fingerprinting - what for?</li> <li>- Genetic and phenetic fingerprinting techniques for complex communities</li> </ul>	<p><b>Theme IVa: Data mining from large sequence pools - genomes</b> (Peter Young &amp; Lars Paulin)</p> <ul style="list-style-type: none"> <li>- Producing massive sequence data</li> <li>- Sequencing and studying whole genomes, comparative genomics</li> </ul>	<p><b>Theme IVb: Data mining from large sequence pools - metagenomes</b> (Lars Paulin &amp; Peter Young)</p> <ul style="list-style-type: none"> <li>- Environmental metagenomics</li> </ul>
<b>Afternoon</b>	<ul style="list-style-type: none"> <li>- Evolutionary aspects</li> <li>- Principles of some clustering techniques</li> <li>- Principal Component Analysis</li> </ul> <p>Hands on work in the computer class (Hannu Rita, Kristina Lindström)</p> <ul style="list-style-type: none"> <li>- manual clustering</li> <li>- PCA with MatLab</li> </ul>	<p>Hands on work in the computer class (German Jurgens, Lars Paulin)</p> <ul style="list-style-type: none"> <li>- primer design</li> <li>- BLAST</li> <li>- sequence alignment</li> </ul>	<p>Hands on work in the computer class (Anu Mikkonen, Leena Räsänen)</p> <ul style="list-style-type: none"> <li>- using BioNumerics Platform for all steps of biological data analysis</li> </ul>	<p>Hands on work in the computer class</p> <ul style="list-style-type: none"> <li>- work with BioNumerics continued</li> </ul>	<p>Conclusions</p>