Please describe your expectations for the seminar topic in a few sentences:

* **16S rRNA gene cloning:** Refers to the procedure (methods) we will apply in the practical. Please describe the steps involved, starting from DNA extraction from microbial communities, PCR of the 16S rRNA gene, cloning of the gene into a vector, transformation into *E.coli* with subsequent plasmid preparation.
* **Methods for 16S rRNA gene analysis:** This topic deals with methods for 16S rRNA gene analysis, e.g. starting with gel-based methods (DGGE, SSCP, RFLP), simple Sanger sequencing and high-throughput, next-generation sequencing approaches (e.g. Illumina Miseq, Ion Torrent). Please do not work on metagenomics, cause this is another topic.
* **Food webs of freshwater ecosystems:** Provide examples of typical freshwater food webs with a focus on the role of microbes and related bottom-up processes (microbial loop, primary production). How can such food web be affected by environmental change or human influence (e.g. eutrophication)?
* **Ecology of freshwater phytoplankton:** Which are the major algae groups in freshwater ecosystems and their ecological functions? What type of phytoplankton would you expect in the Uni pond? Which environmental conditions are key to influence phytoplankton dynamics and how does it work? How could you study phytoplankton communities?
* **SLIMEs (Subsurface Lithoautotrophic Microbial Ecosystems):** What type of ecosystems exist (in regards to energy source)? What are SLIMEs and why can you only find lithoautotrophic ecosystems in the subsurface/oxygen-poor environments? How does carbon fixation work in these ecosystems? Highlight how they can function based on an example for a chemolithoautotrophic community!
* **Microbes with limited metabolic capacities:** Which microbe groups exist with limited metabolic capacities (-> CPR/DPANN as pointers) and what characterizes them? How can they survive despite their limited metabolism? (How would you go about cultivating them? -> only if Abi doesn’t cover this)
* **Statistical evaluation of enumeration data:** What is enumeration data and how do you evaluate it? What peculiarities does it have (distribution? / no negative values / only integers) and how does this affect the statistical evaluation? How do you do hypothesis testing with enumeration data and how do you test for the prerequisites of said testing methods?
* **The emergence of FISH** how did FISH evolve, which inventions/technical developments where necessary, what are important milestones to improve the method.
* **Coupling FISH to othe methods** Give examples of techniques that can be coupled to FISH and point out advantages and difficulties
* **Electron microscopy** should be specified due to preferences of the student either technical principals (for examples differences of SEM and TEM) or important sample preparation methods. In the end, some linkages to microbial samples should be made.
* **Methods for enumeration of cells**: Which methods are currently known? What are the advantages and disadvantages? Please describe also the methods we are using in the practical (Thoma, DAPI counts, BacLight etc.)
* **Light Microscopy:** What is the principal behind this technique? Which other methods do you know?
* **Detection of viruses in environmental samples:** With which methods are you able to detect viruses in **environmental samples**? Name also briefly the advantages and disadvantage of these techniques. Please also describe a workflow from the sample to virus detection (hint: virus purification)
* **Virus-host arms races:** Every host cell try to prevent itself from parasites such as viruses but how does that work? Describe some “mechanisms” for evading phage infection and killing.
* **Cultivation and cultivation-independent approaches**

The student will give an overview of basic cultivation techniques as well as new techniques developed recently. And explain how cultivation can be improved (and coupled) with genomic information of the organism in question.

* **Anaerobes, characteristics and cultivation**

Overview of anaerobes, their general metabolism (specially energy), cultivation (anaerobic media characteristics, Hungate technique, etc) and an example of an organism the student finds interesting.

* **Functional (meta)proteomics**

Explain how (meta)proteomics (e.g. protein-SIP) helps investigate role of organisms in a microbial community.

* **Elucidating microbial dark matter**

Overview of what we know about the "uncultivated majority" based on different studies/techniques, how cultivation-independent techniques have helped to unravel these organisms.

* **Shotgun Metagenomics**

It is expected, that the term shotgun metagenomics is defined and an introduction into the field of application as well as an metagenomic workflow is given. Additionally, at least 2 different sequencing methods should be described.

* **Genomes from metagenomes**

The student should in general describe what a genome is and how completeness and contamination of a genome is defined in metagenomics. The methods ESOM and uBIN and 1 additional methodical tool should be described. What is the advantage of binning genomes?

* **Proteomics of viruses**

What is the definition of a virus and give a short introduction of different virus types and morphologies of viruses specific to prokaryotes? What are typical proteins of viruses and are viral sequences detectable in metagenomic analyses? Please explain shortly the lysogenic and the lytic viral infection in prokaryotic cells.

* **CRISPR systems**

How is a CRISPR system structured and how does it work? Describe and compare different CRISPR types and explain the advantage of a CRISPR system for prokaryotic cells.