

Group work Monday

1. Present yourself and what you are working on. Why do you follow the course? Are you experience with DNA-metabarcoding and R? Are you planning to use DNA-metabarcoding in your further work?
2. What do you think are the most problematic step(s) during DNA metabarcoding analyses when it comes to introduction of errors and biases?
3. In practice, what do you think are the most difficult parts and most severe obstacles when it comes to carry out DNA-metabarcoding analyses? How can that be solved?
4. Which topics would you like to have some extra emphasis on during the course?

Each group should submit answers for questions 2-4 here: <https://nettskjema.no/a/201071>