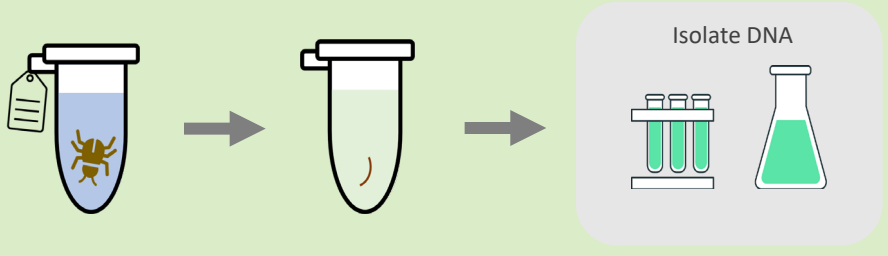
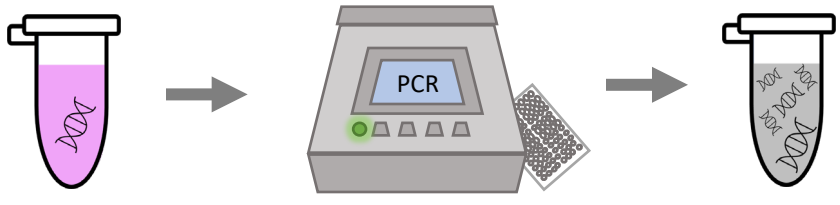
Genetic laboratory workflow



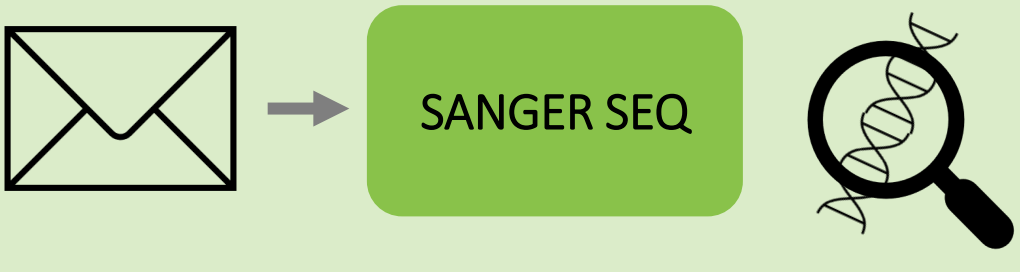
Isolate DNA

DNA can be isolated from a small part of the sample, i.e. an appendage. Carefully store the rest of sample, you may need it later! DNA ISOLATON differ between labs and development of techniques; it employs commercial EXTRACTION KITS.
TIP: Pay attention to database and collection management: keep the information on the sampling site and date, sequenced individual and DNA sequence in one place.



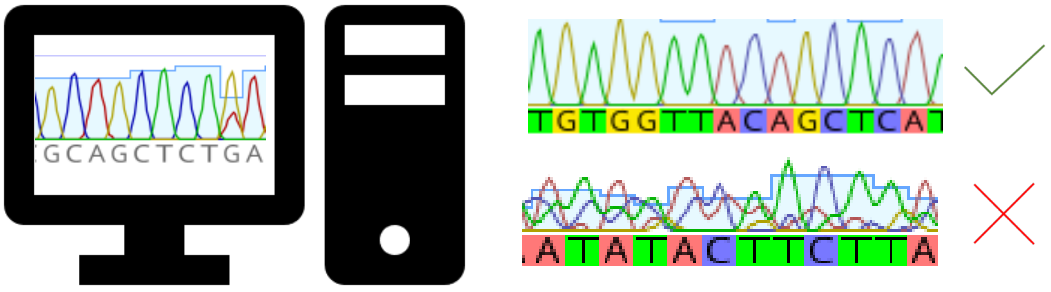
Amplify molecular markers

You have probably already heard of gene amplification or **Polymerase chain reaction,** or shorter **PCR**.
PCR is a method that allows DNA segments to be amplified in billions of copies using suitable molecular primers and the enzyme DNA polymerase.
TIP: keep a laboratory diary, it may be priceless to reconstruct potential mistakes or contaminations.



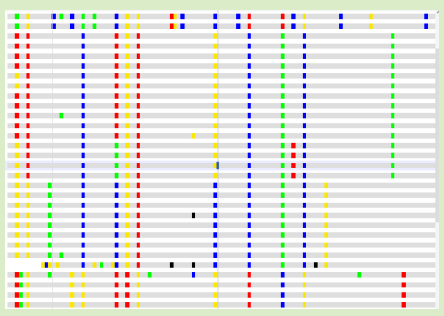
Acquire DNA sequences

DNA sequencing is a laboratory method, used to determine the exact order of nucleotides in a DNA molecule.
TIP: If only possible, request both direction-sequencing; it will tremendously improve the quality of your data and save your time when you interpret the results.



Check and trim sequences

Check your sequences and trim if needed. Assemble reads from from both primers into the so called contigs.
Discard low quality reads, they tend to cause issues in later analyses.
TIP: Use NCBI Blast tool for a fast recognition of sequences on taxa level and checking for possible contaminations.



Align sequences

Align newly acquired sequences with sequences from SubbioCode database or other sources as Genebank.
Aligned sequences can be further used in phylogenetic analysis.
TIP: There is a lot of free software or web tools available for this step, such as MEGA, MAFFT, ClustalW..

Upload sequences

Contribute your data to bigger data bases, like Genebank, Bold…
TIP: Remember, the quality of data you return to community determines, whether the public databases will be increasingly more powerful tool that will serve all of us, or will they become a source of error and mismatch.

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