Introduction to Conda and Conda environments

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# [Lecture](https://docs.google.com/presentation/d/12iTVQh5mjZ8KfzXUaVo9sW9hwHYVzeqieGhR_dho0-s/edit?usp=sharing)

# Practical

1. Install miniconda
   1. Follow instructions [here](https://conda.io/projects/conda/en/latest/user-guide/install/linux.html).
   2. Hint - Ensure that you’ve activated the `base` environment. Your command prompt should include `(base)`
2. Install mamba
   1. Need help? Click [here](https://letmegooglethat.com/?q=install+mamba+using+conda).
3. Use mamba to install samtools into base environment
   1. Need help? Click [here](https://anaconda.org/bioconda/samtools).
   2. Hint - don’t forget to use `mamba` instead of `conda`.
4. Make a conda environment and install something into it
   1. `mamba create -n test -c bioconda prokka`
5. Deactivate the environment
6. Re-activate the environment
7. Install a new package into the same environment
8. Export all the packages from a conda environment, and make a new conda environment based on that
   1. `conda env export > my\_env.yaml`
   2. `conda env create -f my\_env.yaml` (you may need to change the name specified in the yaml file).