Using Mamba to install Conda packages

[Mamba](#) is an alternative to Conda package manager. The main advantage is its speed regarding dependency resolution.

Setting up Mamba

The proposed installation is based on `micromamba` and doesn't require any installation or module loading on the cluster. You just have to add the following 2 lines to your `~/.bashrc` file:

```
export PATH="$PATH:/dcsrsoft/spack/external/micromamba"
export MAMBA_ROOT_PREFIX="/work/FAC/INSTITUTE/PI/PROJECT/mamba_root"
```

Of course, replace `/work/FAC/INSTITUTE/PI/PROJECT` with the path corresponding to your project.

Then, you just have to run the initialization process with the following command:

```
micromamba shell init
```

Finally, you have to logout from the cluster and the environment will be properly configured at the next login.

Using Mamba

Instead of using `conda` commands, you can replace `conda` with `micromamba`. For instance:

```
micromamba create --prefix ./my_mamba_env
micromamba activate ./my_mamba_env
micromamba install busco -c conda-forge -c bioconda
busco -v
micromamba deactivate
```

Restriction

You cannot use Mamba with virtual environment created previously with Conda. Such environments must be recreated.

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