# Installation

# UNIX/Linux

unzip pamilo.zip
cd pamilo
cmake .
make

### Windows

This is how I've got pamilo to run:

- Unzip pamilo.zip and go into the directory it is unzipped into.
- Run <path to cmake>\cmake.exe . . If you have a standard installation of CPLEX this should suffice, but sometimes it does not. Refer to the CMake section below. I have not testet CDD on Windows.
- Start Visual Studio and build pamilo\_cli in Release mode.
- Go to <path to pamilo>\Release and run pamilo\_cli.exe (for detailed usage see below).

As I am no expert in Windows whatsoever, please feel free to let me know if the configuration and compilation process can be made more efficient or the descriptions more precise.

## **CMake**

Version 3.18 or higher is needed.

## **CPLEX**

Version 12.9 or higher is needed, as we rely on the multiobjective optimization features introduced in in 12.9.

If CPLEX is installed in a default location (/opt/ibm/ILOG/CPLEX\_Studio12<9-10> or C:/Program Files/IBM/ILOG/CPLEX\_Studio12<9-10>), it should be found automaticly. If it is installed in such a way that the directories <path to cplex>/concert and <path to cplex>/cplex are present you can set CPLEX to the <path to cplex>. Otherwise you have to set CONCERT\_INCLUDE\_DIR and CPLEX\_INCLUDE\_DIR to the directories containing ilconcert/iloenv.h and ilcplex/ilocplex.h respectively and CONCERT\_LIB, CPLEX\_LIB, and ILOCPLEX\_LIB to the corresponding static libraries. Furthermore, on UNIX CPLEX needs the libraries dl and pthread.

### CDD

For four or more objectives the vertex enumeration can be sped up by using the cddlib. This is done by activating the CMake flag USE\_CDD and (if they are not found automatically) providing libcdd.a in CDD\_LIB and the directory containing cdd.h in CDD\_INCLUDE\_PATH. The cddlib can be found at https://github.com/cddlib/cddlib.

### Usage

<pamilo\_cli> = ./pamilo\_cli on UNIX and <pamilo\_cli> = Release\pamilo\_cli.exe
on Windows.

<pamilo\_cli> [<parameters>] <instance>

Important parameters are:

- -o <output> The basename for all output files. This defaults to on UNIX and an empty string on Windows.
- -e <epsilon> Epsilon to be used in floating point calculations.

<pamilo\_cli> -h shows all available parameters.

### Instance format

An instance is to be in CPLEX .1p format with multiple objective functions. All multiobjective parameters (Priority, Weight, AbsTol, and RelTol) are ignored. If the demand is there this could be changed for the tolerances.

#### Output

A list of all extreme points is printed to the command line. Every line is one point, where the coordinates are separated by spaces. <output>\_log logs the running time, the vertex enumeration time and the time that CPLEX took. If you want anything else to be logged, let me know. <output>\_sol stores all extreme points with their corresponding variable assignment. Every line has the form:

```
[ <obj1> <obj2> ... ] <var1>=<val1> <var2>=<val2> ...
```

This format is the one used by PolySCIP. If you prefer any other solution format (e.g. xml or json based, like CPLEX's .sol), let us know.