

Combine many imputation directories for meta-analysis.

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Please also refer to this document:

<https://docs.google.com/document/d/1uD0VBFr-9UeALZ4rVssJcJG9855nQ7tgX6B-zoamosg>

Ricopili imputation directories can be combined for meta-analysis by using the *'my.joinimp2'* module of the pipeline.

```
- bash:~> my.joinimp2 DIR1 DIR2 DIR3
```

[DIR1](#), [DIR2](#), [DIR3](#) are full path of the imputation directory (no relative paths).

If successful, you will get this message:

```
-----  
Success: joined the named directories, see joininfo.txt for detailed information  
-----
```

This collates best guess genotypes and dosage data for each distinct imputation directory into one directory for further common analysis.

Be aware that you will get warnings if you try to merge imputations done with distinct imputation references. Please handle with care in these cases.

Please see *"joininfo.txt"* file for all the directories that have been merged.

After success you might want to start with a common PCAer run to identify and exclude cross-cohort overlap.

Note: Starting point is after successful imputation of all the dataset (imputed in distinct directory).
(<https://sites.google.com/a/broadinstitute.org/ricopili/imputation>)