CUPID's Output

How to get started

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Purpose

- From the CUPID's sensitivity analysis, I guess you are familiarise how CUPID's input influence the the output
- Here, I am presenting you two methods making the output becomes prettier

Two methods

It comprises of two methods:

1. `cup2rdb`
2. `cuprd3`

`cup2rdb` will be relatively easier than `cuprd3`

Before you get started...

Before you even start this process, you must have these tools on your computer.

1. Terminal (MacOS or Linux) or Command Line, known as CMD (WindowOS)
2. `gfortran` (I installed this on your computer previously)
3. CUPID folder made by Hieu Le

How to check - Terminal or CMD

1. Search for "Terminal" or "CMD" and open it
2. Type `gfortran --version` to show the version [1]

Now thing get a bit complicated, I will demonstrate this on the video...

[1] On WindowOS, type "`bash`" to open UNIX environment before implementing this step. Meanwhile, on MacOS and Linux, you don't need to do this.

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cup2rdb

The first type of compiler I want to mention is cup2rdb.
The command line construct like this

```
./cup2rdb cupfile.rd outputfile.org | somecondition ...
```

The output can be further strip down and seen in
https://soils.wisc.edu/facstaff/wayne/cupid/cup2rdb.html

Trimmed output

DOY	Time	Layer	Depth	Soil water potential	Water content
222	26	1	2.00	17.60	43.19
222	26	2	1.60	17.96	43.62
222	26	3	1.30	18.33	44.04
222	26	4	1.00	18.85	44.61
222	26	5	0.70	19.72	45.53
⋮	⋮	⋮	⋮	⋮	⋮

Table: Strip output sample

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cuprd3

The second method requires a bit more involvement of command line, meaning you have to work with Terminal and CMD
This has been well documented in CUPID's documentation `cuprd3.docx`