Command Reference: CheckPenmanMonteith()

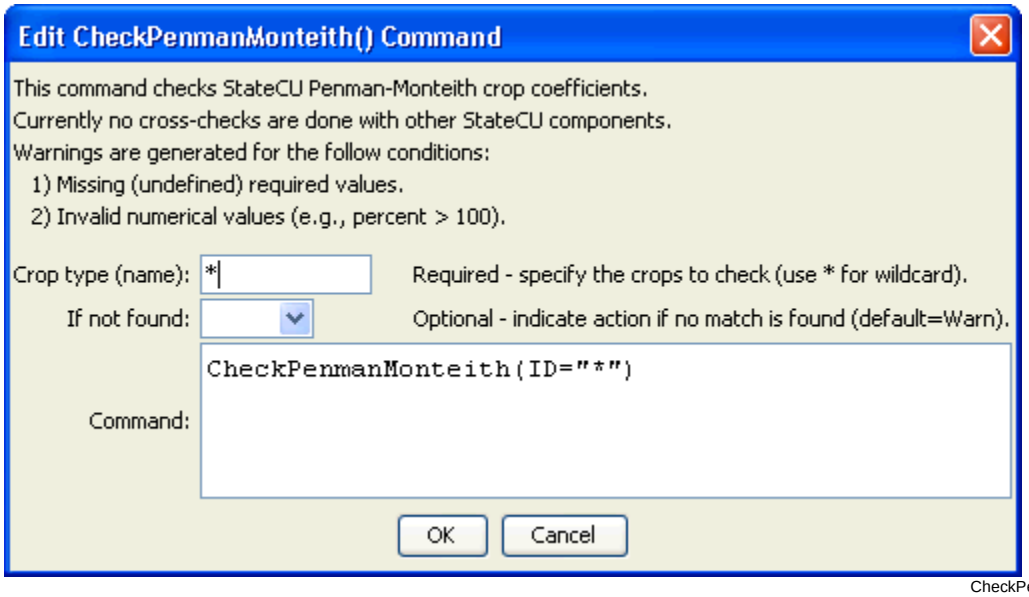
Check Penman-Monteith data for problems

StateCU Command

Version 3.10.00, 2010-04-02

The `CheckPenmanMonteith()` command checks the Penman-Monteith crop coefficient data for problems. The command should usually be used with a `WriteCheckFile()` command at the end of a command file.

The following dialog is used to edit the command and illustrates the syntax of the command.



CheckPenmanMonteith

CheckPenmanMonteith() Command Editor

The command syntax is as follows:

```
CheckPenmanMonteith(Parameter=Value,…)
```

Command Parameters

Parameter	Description	Default
`ID`	The name of the crop(s) to check. Use `*` to match a pattern.	None – must be specified.
`IfNotFound`	One of the following: • `Fail` – generate a failure message if the identifier is not matched • `Ignore` – ignore (don't generate a message) if the identifier is not matched • `Warn` – generate a warning message if the identifier is not matched	`Warn`

The following example command file illustrates how Penman-Monteith coefficients can be defined, checked, and written to a StateCU file:

```
StartLog(LogFile="Crops_KPM.StateDMI.log")
#
# StateDMI commands to create the Penman-Monteith crop coefficients file
#
# Step 1 - read data from HydroBase
#
# Read the general ASCE standardized coefficients
ReadPenmanMonteithFromHydroBase(PenmanMonteithMethod="PENMAN-MONTEITH_ALFALFA")
#
# Step 3 - write the file
#
SortPenmanMonteith()
WritePenmanMonteithToStateCU(OutputFile="rg2007.kpm")
#
# Check the results
#
CheckPenmanMonteith(ID="*")
WriteCheckFile(OutputFile="Crops_KPM.StateDMI.check.html")
```