

PROPS-CLF

A program to compute Biodiversity Critical Loads
based on the PROPS model

User Manual

Version 1.3 – November 2016

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Changes since version 1.2:

-More information is written out in 'Probsfil'.

Changes since version 1.1:

-The input variable 'thick' is not needed explicitly (but see Note below Table 1).

-The data in 'HSoutfil' are now comma-separated (instead of blank-separated).

-In an Annex the method for deriving the CL function is explained.

Introduction

This manual describes how to use the program *PROPS-CLF*, which allows computing biodiversity critical loads (CLs) using (isolines of) the Habitat Suitability Index (HSI) derived for a given set of plant parameters of the PROPS model (generated by *PROPSselect*, see Reinds 2016) and abiotic parameters of the site under consideration.

PROPS-CLF can be run on all (32-bit or higher) PCs under Windows by starting it in a CMD-box (DOS-window). *PROPS-CLF* also runs under 'Virtual PC/Windows OS' on Apple computers. The program is written in Fortran and compiled in Visual Fortran 6.1A.

Installing *PROPS-CLF*

Installing *PROPS-CLF* means copying the executable *PROPS-CLF.exe* into a directory of your choice.

Running *PROPS-CLF*

PROPS-CLF is run by executing the following command:

PROPS-CLF[.exe] i:Parfile

i:Parfile specifies the input file *Parfile*, which holds the parameters and names of input/output files needed (see below). If no *Parfile* is specified, the program terminates with a useful message.

Typing ‘**PROPS_CLs -h[elp]**’ displays the command-line option(s) available.

PROPS-CLF computes the 4 values of critical loads that define the N-S critical load function (CLF; see Fig. 1) for a defined set of plants (defined under ‘*PROPSfil*’; see below). Those CLs are derived from the HSI-values for an array of N_{dep} - S_{dep} -values, computed from plant species probabilities obtained with the PROPS model (for details see Chapters 3 and 4 in Slootweg et al. 2015).

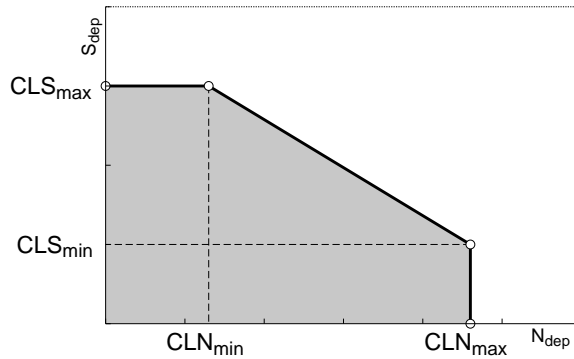


Figure 1: The 4 values CLN_{min} , CLS_{max} , CLN_{max} , and CLS_{min} defining the N-S critical load function.

Together with *PROPS-CLF.exe* the program *iso.exe* is distributed with which HSI-isolines can be plotted. It is executed by typing **iso[.exe] iso.par**, where *iso.par* is a parameter-file produced by *PROPS-CLF* (see ‘HSisopar’ in Table 1).

Input Data and Model Output

The input data are provided in a single file (i.e. *Parfile*, see above) that, in turn, may refer to other files (see below). Every input parameter is preceded by a keyword. After the keyword, on the same line, one (or more) parameters are expected. These can be numbers or character strings (e.g. filenames). The order of the keywords (i.e. records) is irrelevant; in addition, there can be comment lines, i.e. lines starting with an exclamation mark (!), anywhere in the file; they are ignored when reading the input data.

Table 1 summarises all input parameters. Many of them are optional, and if they are not specified (e.g. commented out) default values are used (given in column 4).

Table 1: Input parameters for *PROPS-CLF*. Note: Keywords are case sensitive, and all files are written as ASCII files.

Keyword	Description	Unit	Default
PROPSfil	file with PROPS parameters of selected plants (from <i>PROPSselect</i>) (max 128 chars)	–	a)
CNref	C:N ratio of the soil compartment	g/g	20 ^{b)}
Precip	annual precipitation	m/yr	0.7 ^{b)}
TempC	annual average soil temperature	°C	8 ^{b)}
percol	percolation (precipitation surplus) at bottom of rooting zone	m/yr	0.3
expAl	exponent a (>0) in $[Al]=K_{Al_{lox}} \cdot [H]^a$	–	3
lgKAl _{lox}	log ₁₀ of gibbsite equilibrium constant $K_{Al_{lox}}$	(mol/l) ^{1-a}	8
pCO ₂ fac	CO ₂ pressure in soil solution (multiple of pCO ₂ [atm] in air)	–	15
BcDpWeUp	net input (source) of base cations: $BC_{dep} - Cl_{dep} + z \cdot BC_{we} - Bc_{upt}$	eq/m ²	0
NiNu	net sink of nitrogen: $N_{imm} + N_{upt} - N_{fix}$	eq/m ²	0
f_de	denitrification fraction ($0 \leq f_{de} < 1$)	–	0
cOrg	total concentration of organic acids (m*DOC)	mol/m ³	0

RCOOpars	3 parameters for (Oliver-type) mono-protic organics model: $pK = \text{par}(1) + \text{par}(2) \cdot \text{pH} - \text{par}(3) \cdot \text{pH}^2$	–	4.5 0 0
Maxima	=2, 3 or 5: dimensions of maxima used: pH, Ndep [, C:N] or all	–	3
plim4CLs	limit for deriving CLs (fraction of maximum) (0-1)	–	0.8
CLoutfil	file into which CLs are written (if blank or missing, written to screen)	–	‘ ‘
Ndepmax	maximum N deposition for CL-computation/display	eq/ha/yr	3000
Sdepmax	maximum S deposition for CL-computation/display	eq/ha/yr	3000
Additional output/ parameters:			
HSoutfil	comma-separated file into which HSI-array (e.g. for isoline drawing) is written (if blank or missing, not produced)	–	‘ ‘ ^{c)}
HSisopar	file with parameters for running <i>iso.exe</i> (if no HSoutfil defined, or if blank or missing, not produced)	–	‘ ‘ ^{c)}
PSfile	file name of EPS-plot of isolines to be produced by <i>iso.exe</i>	–	‘ ‘ ^{c)}
intx	number of intervals on Ndep-axis of isoline plot	–	6
inty	number of intervals on Sdep-axis of isoline plot	–	6
Probsfil	file into which individual species probabilities are written for (pHref, CNref, Ndepref, Precip, TempC) (if blank or missing, not produced)	–	‘ ‘
pHref	pH for which Probsfil is made	–	d)
Ndepref	Ndep for which Probsfil is made	eq/m ² /yr	d)

^{a)} If not specified the program terminates with a message to the screen;

^{b)} This parameter might (also) be needed to compute the maxima in the HSI (see ‘Maxima’);

^{c)} Needed if *iso.exe* to be used (to produce ‘PSfile’);

^{d)} If missing, no ‘Probsfil’ is produced.

Note: The thickness of the soil compartment considered (rooting zone) is not an explicit input; however, it is needed for deriving ‘percol’, ‘BcDpWeUp’ and ‘NiNu’.

The following is an example of an input data file (say ‘testA.par’; containing about the minimum input to run *PROPS-CLF*):

```
PROPSfil testA.plants
CNref 17
f_de 0.1
BcDpWeUp 0.16
cOrg 0.01
plim4CLs 0.667
CLoutfil testA.clf
HSoutfil testA.out
HSisopar testA.iso
PSfile testA.eps
Probsfil testA.probs
pHref 5.6
Ndepref 0.06
```

Running *PROPS-CLF* with this parameter file, the 4 CL values are computed and written into the file ‘CLoutfil’ (see Annex A on how the CLF is derived). The computations are defined by the value of ‘plim4CLs’, which is the fraction of the HSI-maximum which should be approximated by the CL-function (see Fig.2 below). For the above parameters, the ‘CLoutfil’ looks like this:

```
!Made by: PROPS-CLF
!... using: testA.par
 767.64 CLNmin (eq/ha/yr)
2534.60 CLSmax (eq/ha/yr)
1494.06 CLNmax (eq/ha/yr)
```

240.92 CLSmin (eq/ha/yr)

For calculating the HSI, the maximum probabilities for the individual plants are also needed. The way to calculate them is defined by the parameter 'Maxima'. If Maxima=5, the overall maximum of the 5-dimensional PROPS-probability function is taken; if Maxima=3 (default), the user-supplied 'Precip' and 'TempC' values (i.e. for a given 'climate') are used, and the maxima are computed in the resulting 3-dimensional subspace; and if Maxima=2, also the C:N ratio is fixed at 'CNref', and the maxima are computed in the pH-Ndep subspace only.

Running the isoline program *iso.exe* with the parameter file 'testA.iso' – created by *PROPS-CLF* – computes the HSI-isolines from the 101×101 HSI-matrix in defined in 'HSoutfil' (if defined) and produces the EPS-file 'testA.eps' shown in Fig.2. Note that the values 'HSoutfil' are normalised to one, i.e. all values are divided by the maximum HSI (the value of which is reported at the top of 'HSoutfil').

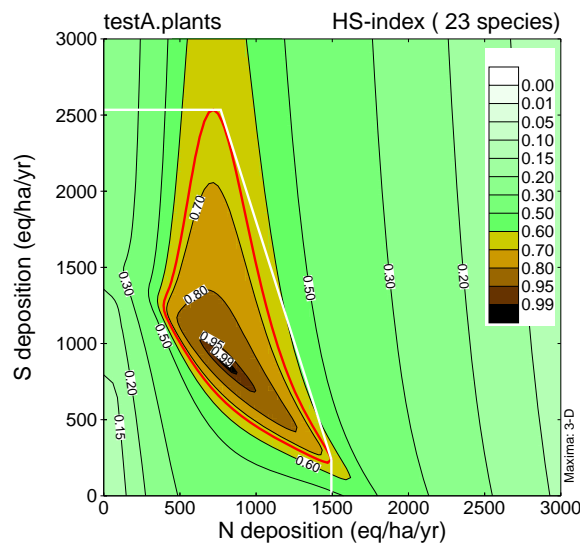


Figure 2: Example of an isoline plot ('testA.eps') and CLF, produced by running 'iso.exe testA.iso', with 'testA.iso' produced by *PROPS-CLF* using the parameter file 'testA.par' given above. The red isoline is the one defined by 'plim4CLs'.

Furthermore, by specifying a 'Probsfil' (and values for pHref, Ndepref, e.g. observed values for the site) the HSI and the probabilities of the individual plants (listed in 'PROPSfil') are written to that file for the input parameters pHref, CNref, Ndepref, Precip, TempC. (From pHref and Ndepref and the abiotic parameters provided in 'testA.par' the corresponding S-deposition, Sdepref, is computed and written out.) Also their maximum probabilities (computed according to 'Maxima') and the values at which the maximum occurs are written out. The first lines of the file 'testA.probs' look like:

```
!Made by: PROPS-CLF
!... using: testA.par
!... for pHref,CNref,Ndepref,Precip,TempC = 5.6 17.0 0.060 0.700 8.000
!pHref & Ndepref ==> Sdepref = 0.090 (= 14.4 kg/ha/yr)
!resulting HSI: 0.39603
! prob 3D-probmax pHmax CNmax Ndepmax 23 species
0.00427 0.00728 5.04 15.59 0.020 Antennaria_dioica
0.00078 0.00266 4.38 20.55 0.092 Arnica_montana
0.00000 0.00001 5.04 17.45 0.114 Campanula_barbata
...
```

References:

- Reinds GJ, 2016. PROPSelect – A tool to select species from the PROPS database. User Manual, Alterra WUR, Wageningen, Netherlands, 3 pp
- Slootweg J, Posch M, Hettelingh J-P (eds), 2015. Modelling and mapping the impacts of atmospheric deposition of nitrogen and sulphur: CCE Status Report 2015. RIVM Report 2015-0193, Coordination Centre for Effects, Bilthoven, Netherlands, 182 pp; www.wge-cce.org

Annex A: Derivation of the Biodiversity CL Function

There is no obvious way to derive a biodiversity CL function (CLF) from the PROPS-model output (HSI-isolines).

Two methods have earlier been suggested by the CCE:

- (1) Compute the HSI-isoline defined by 'plim4CLs' and determine the point with the highest N-dep value (P1 in Fig.A1) and the highest S-dep value (P2); and these two points define a CLF (see Chap.3 in the 2014 CCE Status Report).
- (2) Determine the location of the maximum HSI (point M in Fig.A1) and go 'eastwards' until you reach the value 'plim4CLs' (point Q1), and 'northwards' till you reach Q2; and these two points define a CLF (see Chap.3 in the 2015 CCE Status Report).

There are cases in which either one of those methods yields 'better' results; the following procedure was chosen in an attempt to capture the advantages of both methods.

The executable 'PROPS-CLF.exe' (and the R-script 'isoCLs.R') compute the CLF by combining the two methods in the following way: (a) the N-dep value of P1 and the S-dep value of P2 define CLN_{max} and CLS_{max} , resp.; (b) intersecting the straight line defined by Q1 and Q2 (dashed line in Fig.A1) with those values gives the points R1 and R2; (c) CLN_{min} is then the greater of the N-dep values of P2 and R2, and CLS_{min} the greater of the S-dep values of P1 and R1; thus in the example of Fig.A1 the CLF is defined by the points R2 and P1.

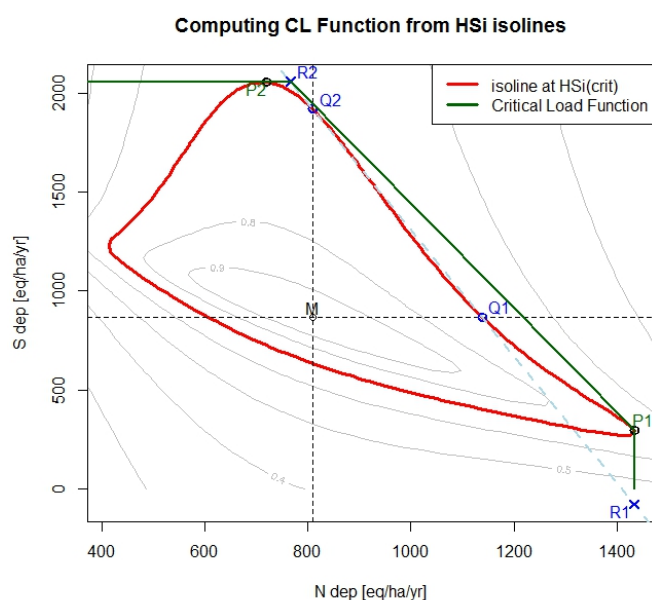


Figure A1: Geometry involved in deriving the biodiversity CLF.