

CRANCOD

A Program for the Analysis and Reconstruction of Spatial Forest Structure



Manual

<http://www.crancod.org>

To grant me a vision of Nature's forces
That bind the world, all its seeds and sources.
Goethe, Faust, 382

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1. Introduction

It is widely acknowledged that spatial forest structure is a driving factor for growth, competition and birth & death processes which, in return, influence the structural composition of woodlands. Also any impact on forests – whether natural or human-induced - is primarily a change of spatial forest structure.

In the last few decades an impressive number of structural indices (also referred to as nearest neighbour summary statistics [NNSS]) have been developed to quantify spatial forest structure and it has also been suggested that they can be used as surrogate measures for quantifying biodiversity (Pommerening, 2002). Of particular interest in this regard is the development of a family of individual tree neighbourhood-based indices, which are measures of small-scale variations in tree positions, species and dimensions, developed by Gadow and colleagues (Gadow and Hui, 2002). Especially when expressed as frequency distributions these indices offer valuable information on spatial woodland structure.

The CRANCOD program is a scientific laboratory for analysing and experimenting with nearest neighbour summary statistics and second-order characteristics (see section 15.1). CRANCOD has been designed for use with large research plots with full enumeration of trees and in addition offers the opportunity to analyse forest inventory data (see section 7) consisting of multiple sample plots of circular or rectangular shape and varying plot size based on a systematic grid. The program has inbuilt flexibility with the user able to select the number of neighbour trees and choose between six different methods of edge correction. CRANCOD can, of course, also be used to analyse research and sample plots without spatial information. The integrated sampling simulator Isis allows the simulation of systematic inventories with varying plot geometry (see section 8). Saving individual tree results (see section 6) in addition to the summary files enables you to carry out individual tree based follow-up investigations. A special visualisation tool (see section 10) allows the user to visually explore structural indices. Tree species codings and colours can be flexibly edited externally (see sections 11 and 15.3). A number of language options allow optimal adaptation of the program in different countries (see section 12). The table below summarises the main computation types of CRANCOD 1.4 which are public domain.

Computation type	Plot shapes
Non-spatial analysis	Rectangular, circular (with fixed and variable radii)
Spatial analysis	Rectangular, circular (with fixed and variable radii)
Sampling simulation	Rectangular, circular (with fixed and variable radii), relascope sample plots
Visualisation	Rectangular, circular (with fixed and variable radii)

The reconstruction functionality (Pommerening and Stoyan, 2008) is currently not public domain and can be activated on request.

As with any Java application CRANCOD can be used on MS Windows, Macintosh and Linux computers. However, the software was only optimised for use on MS Windows and Macintosh computers. The philosophy and objectives of the program are described in greater detail in the papers provided in the references (see section 16).

This core version of CRANCOD is a public domain software. However, the program is protected by intellectual property rights and users are expected to acknowledge CRANCOD and its author when publishing results.

The programming work of CRANCOD has been optimised towards the efficient and correct computation of scientifically interesting summary statistics. In order to achieve this less importance has been given to creating user-friendly interfaces, messages and warnings. The manual shares the same philosophy. This, however,

could change in the future as part of collaborations with interested partners or companies.

2. Loading the program

You will have received or downloaded an executable file entitled “CranCOD.jar”. Copy this file onto the desktop of your computer or into an arbitrary folder, e.g. C:\CranCOD (in MS Windows). Make sure that MS Windows, Mac OS or another program has not added any additional extension such as *.txt or *.zip. The correct file name is “CranCOD.jar”.

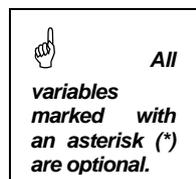
If necessary you now need to download the Java Runtime Environment (JRE) at <http://www.java.com> into your program files folder. Go to the downloads menu on that page and follow the link to the download site of the current version of Java. Follow the links to find and download the JRE. You will have to select the version suitable for your operating system. The JRE is all you need to run CRANCOD successfully, and there is no need to install the Java Development Kit (JDK), a programming environment or anything else you might come across on that web site. However, in most cases the JRE is already installed on your computer and there is no need to download any additional resources.

You can now double click on the file “CranCOD.jar” to start the CRANCOD program. The same procedure will also work on Macintosh computers.

3. Input files

Two input files in ASCII format are required, a tree data file with the compulsory extension *.dat (e.g. SamplePlot.dat) and a geometry file (e.g. SamplePlot.geo). CRANCOD can analyse rectangular or circular sample plots but no other geometric shapes. The different shaped plot files require different input files which can easily be created in MS EXCEL.

For the tree data input file for **rectangular sample plots** you have to create a minimum of seven columns (A-G in MS EXCEL) with the variables



- plot number (integer, column A),
- tree number (integer, column B),
- tree species (integer, column C),
- x-coordinate or easting of trees (float, in metres, column D),
- y-coordinate or northing of trees (float, in metres, column E),
- DBH (float, in centimetres, column F) and
- tree height (float, in metres, column G)*.

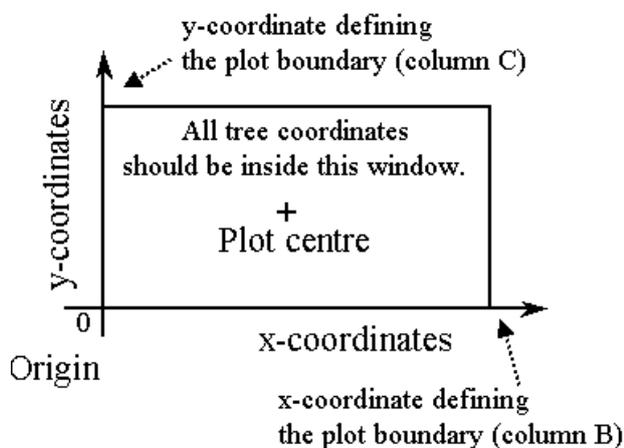
The program assumes that the stand boundaries of rectangular sample plots are true and parallel to the x and y axes of the system of coordinates. It is essential, therefore, to have the origin of the coordinate system correspond to the lower left hand corner of the *rectangular* sample plot (see figure below). This is achieved by transforming the original tree coordinates. The transformation of coordinates is easily done in MS EXCEL using the *min()* function to find the minimum x and minimum y coordinates of the data set. The minima are rounded down and subtracted from all tree coordinates and the bottom left corner of the plot put at the origin (0, 0). All tree coordinates specified in columns B and C should be within the plot boundaries.

For the geometry input file for rectangular sample plots you have to create a minimum of five columns (A-E in MS EXCEL) with the variables

- plot number (integer, column A),
- x-dimension of the sample plot (float, in metres, column B),
- y-dimension of the sample plot (float, in metres, column C),
- x-coordinate or easting of the sample plot centre (float, in metres, column D) and
- y-coordinate or northing of the sample plot centre (float, in metres, column E).



The plot numbers in column A of the geometry file have to have a corresponding plot number in column A in the tree data file, otherwise the geometry information cannot be related to the tree data and the analysis will not be performed.



For the tree data input file of **circular sample plots** you have to create a minimum of seven columns (A-G in MS EXCEL) with the variables

- plot number (integer, column A),
- tree number (integer, column B),
- tree species (integer, column C),
- azimuth of trees from plot centre (float, in degrees, column D),
- distance of trees from plot centre (float, in metres, column E),
- DBH (float, in centimetres, column F) and
- tree height (float, in metres, column G).



The only difference to the tree data input file for rectangular sample plot is that the coordinates in columns D and E need to be provided as polar coordinates. The origin of the systems of coordinates of each circular sample plot is its centre.

For the geometry input file for circular sample plots you have to create a minimum of four columns (A-D in MS EXCEL) with the variables

- plot number (integer, column A),
- radius of the sample plot (float, in metres, column B),
- x-coordinate or easting of the sample plot centre (float, in metres, column C) and
- y-coordinate or northing of the sample plot centre (float, in metres, column D).

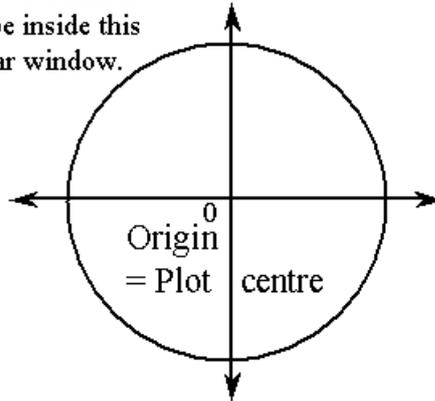


Again, the plot numbers in column A of the geometry file have to have a corresponding plot number in column A in the tree data file, otherwise the geometry information cannot be related to the tree data and the analysis will not be performed.



Do not round any numbers where floats are specified. There should be no headers in the file. No specific order of data is required and you can even mix trees of different sample plots, the program will always sort them correctly. Additional columns do not affect the computation but they must be placed after those specified above. There should be no gaps and no strings (words) in the input file. As a decimal separator you should always use a "." and never a ",".

All tree coordinates should be inside this circular window.



Radius defining the plot boundary (column B)

The program is capable of analysing whole inventories with a number of sample plots all arranged in one input file. The sample plots can be of different size, but there should be only one geometric shape (either rectangular or circular) represented in one input file. Different plots arranged in one input file will be analysed together as *one single* inventory. If you wish to obtain results for each plot separately you have to create separate input files.

Below are the first lines of the tree data sample file Graecum.dat, a rectangular sample plot

1	1	2	1.15	29.75	36.2	26.5
1	2	2	1.8	20.72	14	19.7
1	3	2	2.2	20.25	9.8	17
1	4	2	2.7	20.59	14.1	21.1
1	5	2	2.9	25.56	15.4	21.5
1	6	55	3.85	28.57	23.7	17.4
1	7	55	4.4	27.9	28.2	17.6
1	8	55	5.25	22.54	8.5	10.7
1	9	55	7.05	24.76	9.2	11
1	10	55	8.13	20.04	11.5	12.4

and the corresponding geometry file Graecum.geo:

1	40	30	0	0
---	----	----	---	---

Below is an excerpt from the tree data sample file CoedyParc.dat with circular sample plots

1	1	1	22.00	10.30	35.0	0
1	2	2	31.00	4.50	35.0	0
1	3	2	43.00	10.00	38.0	0
1	4	2	56.00	7.70	26.0	0
1	5	2	77.00	11.20	37.0	0
2	6	2	88.00	6.20	36.0	0
2	7	2	91.00	8.70	29.0	0
2	8	1	98.00	12.10	36.0	0
2	9	1	114.00	8.40	28.0	0
2	10	1	128.00	11.70	38.0	0

and the corresponding geometry file CoedyParc.geo:

1	12.6	0	0
2	12.6	0	0

Once you have finished the organisation of the input file in MS EXCEL save the file in ASCII format by selecting the option Text (Tabs delimited). Do NOT attempt to process MS EXCEL files with CRANCOD.



Note: There should be a data entry for **all** variables within the indicated column ranges. For missing/not-specified optional values enter "0" (zero). Never use "0" (zero) for species codings. Corresponding tree input data and geometry files must have exactly the same name followed by the extensions *.dat or *.geo.

4. General configuration file

CRANCOD uses a set of general parameters to steer the calculation process. Unlike other Windows based programs these settings are not entered in dialogues but in a separate configuration file. This file is another ASCII file following a specific format which usually has the extension *.cfg. An example is given in the box below. Open and edit your configuration file in the Windows Editor or Notepad programs (preferably not in MS Word). Do not modify anything in rectangular brackets [...], this is text which helps you to understand the coding of the entries which occur immediately below. Most of these entries are self-explanatory but additional comments are given here.

The entry [Main file path] has to be adjusted according to the file structure of your computer and the name of your input file. You enter only the file path including the name of the input files, but, note, do not add *.dat or *.geo. This is done automatically by the program. If you add an extension the program will not be able to find your input file. Do not use blanks in any file names.

The language options only affect the language of the program menus and the screen. It does not affect the decimal separator nor the output files. See also section 10.

With the analysis mode you determine whether you wish to obtain non-spatial results only (trees/ha, basal area, DBH distribution, stand height curve etc.) or spatial information as well. This can be handy when no spatial data were collected.

[Stand height curve model: 0: Oliveira; 1: Michailov; 2: Petterson] defines the model to be used to construct a stand height curve. Provided sufficient height data have been entered into the tree data input file (which CRANCOD checks automatically), the program will derive a model with which missing height data can be estimated. The three height models are documented in detail in section 9.

The next variable allows you to take biological variation into account by modifying the total tree heights estimated from the stand height curve with the corresponding

standard error. Only index calculations involving tree heights are affected by this setting. The procedure is explained in section 9.

```
[Main configuration file for Crancod]
[Main file path]
C:\Cyfrifiaduro\Graecum2\Graecum2
[Language: 0: English; 1: Cymraeg; 2: Deutsch]
0
[Origin of the data set: 0: rectangular sample plot(s); 1: circular sample plot(s)]
0
[Analysis mode: 0: non-spatial analysis only; 1: non-spatial + spatial analysis]
1
[Stand height curve model: 0: Oliveira; 1: Michailov; 2: Petterson]
2
[Estimated tree heights modified by standard error? 0: no, 1: yes]
1
[Number of neighbours: location, species, dimension, TD,TH,D]
4      4      4      1
[Lowest mid point & class width of DBH distribution in cm]
4      4
[Lowest mid point & class width of distance distribution in m]
0.25  0.5
[Simpson index definition: standard form[0,1], complementary[0] or reciprocal form[1]]
0      0
[Standard angle UAI in gon and tolerance in %]
80     0
[Dominance definition according to Hui et al., 1998 (0) or Aguirre et al., 2003 (1)]
1
[Species codes for special analyses (max. 3)]
2      55
[Neighbourhood definition for special analyses: 0: any species, 1: same species]
0
[Parameters for the correlation functions (number of steps, step width, kernel width, kernel type)]
30     0.5   1.9   0
[Edge correction? 0: no, 1: translation, 2: reflection, 3: buffer, 4: NN1, 5: NN2]
4
[Buffer width (3) in m]
5
Java random number? 0: false, 1: true]
0
[Write Protocol? 0: false, 1: true]
1
[Dimensions of visualisation image [pixel]: x, y]
200    200
```

[Number of neighbours: location, species, dimension, TD,TH,D] defines the number of neighbouring trees you wish to be used for the calculation of structural indices. All indices can be classified according to the three major aspects of biodiversity, diversity of tree locations, species diversity and diversity of tree dimensions (listed in section 15.1). An additional class consists of those indices which compare reference trees with only one neighbouring tree, such as diameter differentiation (TD), height differentiation (TH) and distances (D). For these indices you specify the neighbour you wish to consider with the fourth value in this data entry row. The division into these four aspects allows you to allocate different numbers of neighbours to different indices in one analysis. The numbers provided need to be delimited by tabs.

Diameter and distance distributions can be flexibly designed in CRANCOD by specifying their lowest mid points and widths. Only one uniform class width can be applied (equidistant distributions).

In the literature the Simpson index is defined in different ways (see e.g. Krebs, 1999). The settings in this line allow you to choose any of the four possible definitions. See also section 15.1.

The standard angle [in gon] is only relevant to the uniform angle index (see appendix 15.1; Hui and Gadow, 2002). An entry of "0" (zero) is automatically corrected to $400/(number\ of\ neighbours+1)$. In the same line you specify the tolerance parameter of the uniform angle index. This is the percentage tolerance allowance, which is granted to every angle between neighbouring trees when compared with the standard angle.

 **Note:** A standard angle of 100 gon (= 90°) always requires a tolerance allowance of 10% (Gadow *et al.*, 1998). For the adjusted standard angle of 80 gon (= 72°) always set the tolerance allowance to 0% (Hui and Gadow, 2002).

[Dominance definition according to Hui *et al.*, 1998 (0) or Aguirre *et al.*, 2003 (1)] refers to the two different definitions of dominance as specified in appendix 15.1.

If you wish to estimate correlation functions (most of them are second-order characteristics which are here referred to as correlation functions for convenience) or to perform sampling simulations you have to specify at least two species codes selected from your own species file. Ideally you specify the most common species in the plot. For the estimation of correlation functions you also need to provide information on number of steps, step width, kernel width and kernel type (0: Epanechnikov, 1: box kernel). For more information on these settings and the correlation functions please refer to Illian *et al.* (2008), Stoyan and Penttinen (2000) and Pommerening (2002). If the values of the latter three variables are set to 0 (zero), no calculation of correlation functions will take place.

 **Note:** Estimate second-order characteristics for single research plots only. Forest inventory sample plots are usually too small to yield reliable estimations.

The next option is for nearest neighbour summary characteristics only. Here you can choose whether the neighbours of the subject tree are only selected using distance information regardless of species (setting 0) or whether the nearest neighbours should all belong to the same species as the subject tree (setting 1). The latter is based on the philosophy that all trees of a particular species form a distinctive point pattern and population and that indices relating to the diversity of tree locations should always be calculated inside the species group. Setting 1, however, does not affect NNSS of species diversity like for example mingling. Setting 0 reflects the more traditional forestry way of NNSS calculation.

There are five options for edge corrected estimators of structural indices. These are explained in detail in Pommerening and Stoyan (2006). Option "0" does not activate any edge correction. 1, 2 and 3 use edge corrections which have a long history in spatial statistics and are well described in the literature (Radtke and Burkhart, 1998; Pretzsch, 2002). Option 4 (NN1) uses a so-called Hanisch estimator developed for nearest neighbour indices. A variation of this is option 5, NN2 (Pommerening and Stoyan, 2006). The calculation of non-spatial results is not affected by these estimators.

 The buffer width option allows you to specify the width of the buffer around the edges of the sample plot in which you believe trees are too close to the boundaries and therefore should not be utilised for the calculation of structural indices. There is no need to specify this explicitly if you have not set the edge correction to 3. However, you should NOT delete these two rows in your configuration file.

The option concerning random number generators allows you to select a random number generator for stochastic processes.

You can decide whether all settings and the calculation progress should be monitored in a protocol on screen and in a file in HTML format. This can be very useful if you wish to track down the settings which led to a specific result. However, it may also slow down the calculation process and you might like to switch this service off. If you have only just started to use CRANCOD I recommend that you always set this option to 1. The protocol also offers useful summary statistics about your input file including a stem-and-leaf-plot which offers a detailed impression of the diameter structure of the trees involved (Tukey, 1977).

You have the option of visualising the spatial data of your input/output files by specifying the dimensions of the output image. Provided the analysis mode is set to 1 and the dimension specification is > 0, this setting will create a new menu item after the data have been analysed. Visualisation of plots is only possible if tree coordinates were collected. If the dimension values are set to 0 the visualisation

module will not be created at all which saves memory. Details about the visualisation are given in section 10.

The configuration file can have any name but the file extension *.cfg is required. Once you have started CRANCOD go to File → Open File (*.cfg)... and select the configuration file. After successfully loading the configuration file your settings will be visualised in the protocol section of the program in HTML if you have set this option to 1. If your operating system is MS Windows, CRANCOD will automatically invoke your standard internet browser and display the protocol file in a much more user friendly way. If you work with a different operating system please manually open the configuration file in a browser of your choice.

You can easily develop your own independent user interface with dialogues and windows for the production of configuration files if you do not feel comfortable with the manual procedure described above.

5. Data processing

Now go to Computations and press *Computations* → *Analyse* in order to analyse your tree data. If this has been successful CRANCOD will add a couple more lines to the protocol, for example telling you where you can find the output files. Alternatively press *Computations* → *Simulate Sampling* in order to perform a sampling analysis. For the sampling analysis you need to specify parameters beforehand in another file (see section 8). If the program encountered any problems with your files it will tell you in the protocol. With your internet browser you can monitor success and failure of your computations. Any problems will be highlighted in red colour. You can use the Crancod's protocol window as an HTML editor to add personal comments and notes. Reload/refresh your browser from time to time to update the display of your protocol file.

6. Output

CRANCOD produces up to six types of output files in the folder that contains the input file, a file with individual tree results (e.g. SamplePlot_tree_org.out), summary statistics for non-spatial variables (e.g. SamplePlot_NonSpatial_org.out), summary statistics for spatial variables (e.g. SamplePlot_Spatial_org.out), two summary files for correlation functions (e.g. SamplePlot_corr_org, SamplePlot_dij_org) and a protocol file (e.g. SamplePlot_protocol.html). The protocol file also briefly summarises some of the results. If your input file contained only one rectangular or circular sample plot the summary files naturally deliver the results of this one plot. If your input file contained more than one plot the program automatically considers your analysis to be an inventory. The summary files then summarise and collate the results of all plots of the input file and do not provide an individual break down per plot.

The results of distributions such as the mingling distribution in the table below are given in hectare values (central column) and in relative terms (right column). The figures in the centre should not be mistaken as absolute numbers. The sum of all four figures of the central column of the table below exactly matches the SPH (stems per hectare) provided that no edge correction was used. For some variables such as mingling and diameter differentiation expected values are also calculated according to the method developed by Lewandowski and Pommerening (1997) and Pommerening (1997).



Because the output files are saved in the same directory as the input file, if you run a number of analyses with different settings remember that you either have to select different folders for the output or to specify different input file names. If you don't do this, your previous result files will be overwritten.

Mingling tree attribute - classes		
0	216.66667	0.18705
0.33333	491.66667	0.42446
0.66667	275	0.23741
1	175	0.15108

The result files with the extension *.out can be easily imported and processed in MS EXCEL. The protocol file is easier to read with an internet browser. All variable names and abbreviations used are explained in the appendix (15.2).

The output files of the sampling simulator are described separately in section 8.

7. Inventory aspects and representation factors

When more than one plot (regardless of shape) is specified in the input file CRANCOD assumes it is dealing with an inventory based on a systematic grid. The program is designed in a way that inventories with variable plot sizes can be processed (Šmelko and Saborowski, 1999). This can, for example, mean that you decide to sample 20 trees in each of your circular sample plots in order to avoid a situation with very few trees and a high edge bias. The radius of each plot is then dependent on the distance of the 20th tree from the plot centre.

An unbiased calculation of sample results for fixed-size sample plots is ensured by so-called representation factors or Horvitz-Thompson weights (Horvitz and Thompson, 1952; Schreuder *et al.*, 1993), i.e. how many trees per hectare tree i , of the plot, under study represents. Assuming a circular sample plot with a radius of $r = 12.62m$ (0.05 ha) each tree on this plot stands for $1/0.05 = 20$ trees per hectare. So tree representation factors (RF) can be calculated as $RF = 1/plot\ area$. The calculation of all variables in CRANCOD is based on these individual representation factors and the corresponding areas. An arithmetic mean value is thus calculated as outlined in the formula below.

$$\hat{\bar{Y}} = \frac{\sum_{i=1}^n \sum_{j=1}^{z_i} y_{ij} RF_{ij}}{\sum_{i=1}^n \sum_{j=1}^{z_i} RF_{ij}}$$

where

$\hat{\bar{Y}}$ estimator of \bar{Y} , the sample mean per tree, e.g. mean diameter, mean mingling.

n number sample plots

z_i number of trees in sample plot i .

y_{ij} individual tree target variable of sample tree j of sample plot i , e.g. frequency (=1), diameter, mingling.

RF_{ij} tree specific representation factor calculated as $RF_{ij} = 1/a_{ij}$ where a_{ij} is the tree specific sample plot size in ha.

a_{ij} is normally the same for all trees of a sample plot. However, some of the edge correction algorithms modify a_{ij} and make them tree specific. The formula above can be interpreted as a ratio of two estimators, for the total of the target variable and the total of SPH in the inventory region (Šmelko and Saborowski, 1999).

When estimating density measures such as basal area per hectare and SPH (expressed as \hat{Y}_{ha}) the formula simplifies to

$$\hat{Y}_{ha} = \frac{1}{n} \sum_{i=1}^n \sum_{j=1}^{z_i} y_{ij} RF_{ij} .$$

In the case of an inventory the program will also calculate sampling errors (SE), coefficient of variation (CV) and standard error (StE) which you can find after the estimated target variable.

The corresponding variance estimators are according to Šmelko and Saborowski (1999)

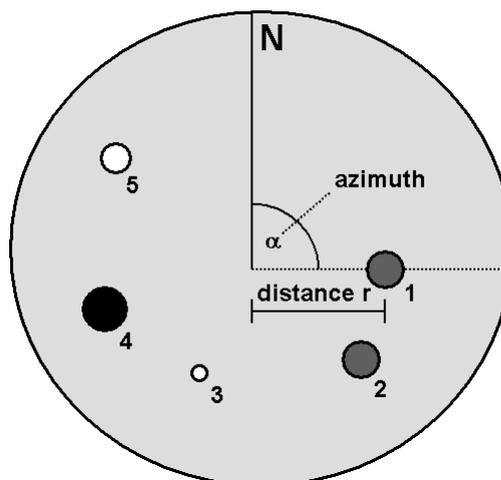
$$v(\hat{Y}_{ha}) = \frac{1}{n(n-1)} \sum_{i=1}^n (y_{i;ha} - \hat{Y}_{ha})^2 \text{ with } y_{i;ha} = \sum_{j=1}^{z_i} y_{ij} RF_{ij}$$

and

$$v(\hat{\bar{Y}}) = \frac{1}{\bar{n}_{ha}^2} \cdot \frac{1}{n(n-1)} \sum_{i=1}^n \left(y_{i;ha} - \hat{\bar{Y}} \cdot n_{i;ha} \right)^2 \text{ with}$$

$$n_{i;ha} = \sum_{j=1}^{z_i} RF_{ij}, \quad \bar{n}_{ha} = \frac{1}{n} \sum_{i=1}^n n_{i;ha} .$$

Spatial information of trees in small circular sample plots can be recorded as shown in the figure below. It is recommended that all trees are numbered in a clockwise direction before doing any measurement. The azimuth can be measured with a compass in relation to a defined reference bearing, e.g. due North. The distances should be measured from the plot centre to the tree centre.



With smaller rectangular sample plots a similar procedure can be adopted. **Note**, however, that CRANCOD expects Cartesian coordinates (x, y) with any rectangular plot. A transformation of coordinates is therefore required in this case according to

$$x_i = r_i \cdot \cos \alpha_i \text{ and } y_i = r_i \cdot \sin \alpha_i .$$

The coordinates of rectangular sample plots also need to be transformed in relation to the origin as described in section 3. For larger research plots it is recommended that computer theodolites are employed to record tree positions. These instruments normally deliver Cartesian coordinates as final output.

8. Sampling simulator Isis

CRANCOD can call an additional class called Isis to simulate systematic sampling (Motz *et al.*, 2010). Isis is based on the technology of the sampling simulator WaldSim (Pommerening and Lewandowski, 1997). This functionality is available if the user has provided not more than one sufficiently large rectangular sample plot (ideally not less than 1ha) in the tree input data file. The sampling simulator now treats this base plot as the population in terms of the sampling theory. The corresponding menu item “*Simulate Sampling*” can be found in the *Computations* base menu. The specific sampling and simulation settings are communicated to the sampling simulator Isis by means of an XML file. This file should be named *Inv.xml, e.g. SamplePlotInv.xml. The name before Inv.xml must again be identical to the file name specified in the general configuration file. A raw xml file for Isis can have the following structure:

```
<?xml version="1.0"?>
<!DOCTYPE samplingConfiguration SYSTEM "dtd/inv.dtd">
<samplingConfiguration>
  <sample>
    <method>
      <rectangularSamplePlots>
        <x>30</x>
        <y>30</y>
      </rectangularSamplePlots>
      <relascopePlots>
        <BAF>1.8784</BAF>
      </relascopePlots>
      <circularSamplePlots>
        <radius>15.00</radius>
        <numberTrees>10</numberTrees>
      </circularSamplePlots>
    </method>
    <settings>
      <minDistance>0</minDistance>
      <realNeighbours>true</realNeighbours>
      <grid>80</grid>
      <replications>10000</replications>
      <cycle>
        <on>true</on>
        <step>5</step>
      </cycle>
    </settings>
  </sample>
  <reconstruction>false</reconstruction>
</samplingConfiguration>
```

Each setting variable is wrapped by an XML tag pair, an opening and a closing tag. In the first part which is between the tags <method> and </method> the sample settings are defined. Rectangular sample plots are defined by their x and y dimensions [m], while relascope plots (angle count method; Bitterlich, 1984) are defined by the basal area factor. Circular sample plots can either be defined by a constant radius or by a constant number of trees.

In the second part the simulation settings are defined between the tags <settings> and </settings>. Between the tags <minDistance> and </minDistance> the user can determine a certain minimum distance which ensures that sample plots do not overlap. For all sampling methods with the exception of circular sample plots with fixed number of trees a minimum distance is automatically derived from the plot sample plot geometry if the minimum distance is specified as 0. In conjunction with the buffer width

specification [Buffer width (3) in m] in the general configuration file the minimum distance also ensures that sample plots are not intersected by the population boundary and that all off-plot neighbours of sample trees are within the population boundaries.

The user can choose between the tags `<realNeighbours>` and `</realNeighbours>` whether he wishes the simulator to use the real (potentially off-plot neighbours) of the sample trees (true) or whether for each tree new neighbours should be selected within the plots (false).

The variable *grid* defines the (initial) distance between sampling plot centres. Together with the geometry of the sampling plots this variable determines the sample size.

The variable *replications* defines the number of sampling replications for any sample size. A minimum number of 1000 replications is recommended for reliable results.

With the nested item *cycle* the user can determine whether he wishes to run a single or a multiple simulation. A single simulation will only simulate results for one specific sample size. A multiple simulation will simulate a whole sequence of sample sizes starting with an initial distance between sampling plot centres defined by the *grid* variable which then is subsequently decreased by the variable *step*.

In this version of CRANCOD the reconstruction option is disabled. Even when set to “true” it will not operate.

To run the simulation the XML file must be refined by deleting or disabling redundant settings. For example only one sampling method is used at a time and if this is to simulate relascope plots other methods must be deleted as below

```
<method>
  <relascopePlots>
    <BAF>1.8784</BAF>
  </relascopePlots>
</method>
```

or disabled with a specific comment syntax like this

```
<method>
  <!--rectangularSamplePlots-->
    <!--x>30</x-->
    <!--y>30</y-->
  <!--/rectangularSamplePlots-->
  <relascopePlots>
    <BAF>1.8784</BAF>
  </relascopePlots>
  <!--circularSamplePlots-->
    <!--radius>15.00</radius-->
    <!--numberTrees>10</numberTrees-->
  <!--/circularSamplePlots-->
</method>
```

Within the settings for circular sample plots a similar principle applies. When simulating circular sample plots you have to decide whether you wish to use a fixed radius or a fixed number of trees. So one of the two options either needs to be deleted or turned into a comment.

A separate file called *inv.dtd* contains a Document Type Definition (DTD) and is provided on the CRANCOD website. Copy it into a subfolder of the folder in which you keep the data you wish to analyse. Name the subfolder “*dtd*” and make sure that the file’s name is really *inv.dtd*. The DTD specified in this file validates the XML file containing the settings for the sampling simulation. If the validation fails you will be notified in the protocol and the computation process will stop.

```
<!ELEMENT samplingConfiguration (sample,reconstruction)>
<!ELEMENT reconstruction (#PCDATA)>
<!ELEMENT sample (method,settings)>
<!ELEMENT method ((circularSamplePlots|(rectangularSamplePlots|(relascopePlots))))>
<!ELEMENT circularSamplePlots ((radius|(numberTrees)))>
```

```

<!ELEMENT rectangularSamplePlots (x,y)>
<!ELEMENT relascopePlots (BAF)>
<!ELEMENT settings (minDistance?,realNeighbours,grid,replications,cycle)>
<!ELEMENT cycle (on,step)>
<!ELEMENT radius (#PCDATA)>
<!ELEMENT numberTrees (#PCDATA)>
<!ELEMENT minDistance (#PCDATA)>
<!ELEMENT realNeighbours (#PCDATA)>
<!ELEMENT grid (#PCDATA)>
<!ELEMENT replications (#PCDATA)>
<!ELEMENT on (#PCDATA)>
<!ELEMENT step (#PCDATA)>
<!ELEMENT x (#PCDATA)>
<!ELEMENT y (#PCDATA)>
<!ELEMENT BAF (#PCDATA)>
    
```

In case you cannot access the DTD file on the CRANCOD website the contents are given in the box above. Copy them into a text file and save it as inv.dtd in the dtd subfolder. Do not modify the contents of this file.

Depending on whether the user runs a single or multiple simulations 2 or more different output files are produced. In both cases at least two statistics file are created, e.g. SamplePlot_25_inv_Statistics1.out and SamplePlot_25_inv_Statistics2.out. The number in centre of the file name denotes the grid parameter. The *inv_Statistics1.out file contains the results for mean index values, the *inv_Statistics2.out file those for index distributions. The labels used in the file are explained in section 15.2. The main statistics of the *inv_Statistics1.out file are

$$Bias = \theta - \hat{\theta}$$

$$RMSE = \sqrt{\frac{1}{n-1} \sum_{i=1}^n (\hat{\theta}_i - \theta)^2}$$

where

- θ population value
- $\hat{\theta}$ sample value, estimated from the n replications
- $\hat{\theta}_i$ sample value, estimated from replication i
- n number of replications.

The r . $RMSE$ is obtained by dividing the $RMSE$ by the population value.

The main statistics of the *inv_Statistics1.out file are

$$E = \sum_{i=1}^k \left(\hat{f}(x_i) - f(x_i) \right)^2,$$

where

- E energy
- k discrete number of classes of an empirical distribution/density function
- $\hat{f}(x)$ empirical distribution/density function of the sample
- $f(x)$ empirical distribution/density function of the original

$$d_{max} = \max \left(\left| \hat{f}(x_i) - f(x_i) \right| \right),$$

where
 d_{max} maximum absolute difference

and

$$AD = \frac{1}{2} \cdot \sum_{i=1}^k \left| \hat{f}(x_i) - f(x_i) \right|$$

where
 AD absolute discrepancy

9. Stand height curve models

Three different height curve models are available in CRANCOD 1.4.

Formula	Author(s)	Code in *.cfg file
$\ln(h) = a_0 + a_1 \cdot \frac{1}{DBH}$	Oliveira cited from Gadow & Bredenkamp, 1992	0
$h = a_0 \cdot e^{\frac{a_1}{DBH}} + 1.3$	Michailoff (1943)	1
$h = 1.3 + \left(\frac{a_2}{a_0 + a_1 \cdot DBH} \right)^2$	Petterson (1955)	2

where
 h total tree height [m]
 a_0, \dots, a_2 regression coefficients
 DBH tree diameter at breast height [cm]
 e base of the natural logarithm
 \ln natural logarithm

Michailoff's function has a turning point and runs through the origin of the system of coordinates. Petterson's function has a turning point and a horizontal asymptote. It can be used for both even-aged and uneven-aged forests.

If the user has chosen this option, each individual tree height estimated from the height model will be modified according to the following principle:

$$h = h_m + SE \cdot Y$$

where
 h_m total tree height [m] estimated from the height curve model
 SE standard error [m]
 Y normally distributed random number

10. Visualisation

Details about how to enable the visualisation tool in the configuration file are given in section 4. After you have loaded the configuration file and successfully processed the data by pressing "Computations → Analyse..." the visualisation tool will be

automatically built. It will appear as a new menu item called “Visualisation”. Afterwards go to “Visualisation → Visualise *.dat file...” to receive a map which shows all the trees of the first sample plot of your data file.

The tools in the panel entitled “Map Utilities” allow you to adjust the tree map according to your preferences. With the slider you can zoom in and out. By ticking the scale checkbox you enable labels with x- and y-coordinates at the bottom and on the left hand side of the map. In the corresponding text field you can input the increment between the coordinate labels. The minimum increment is set to 10m and the maximum allowable increment is set to the maximum extension of the plot in either x or y direction. The coordinate labels are only displayed when the zoom slider is pushed towards the far left and the tree data are centred. The DBH scale checkbox allows you to enlarge the radii of the circles symbolising the trees. The radius of these circles is computed from the trees’ diameters only, when the number in the corresponding text field is set to 1. The show boundary checkbox will give you the plot boundaries as specified in your input file.

The list box in the panel “Plots” gives you the opportunity to flip through all the plots of your input file (if you have processed a forest inventory).

In the panel entitled “Plot Characteristics” you find summary statistics relating to the plot selected from the plot list box. The abbreviations and variable names follow the ones used in the output files which are explained in section 15.2.

In the panel entitled “Tree Characteristics” you can select trees you wish to obtain information about. The variable names are again the same as used in the output files and detailed in section 15.2. By ticking the checkbox “Show tree” the tree selected and its nearest *n* neighbours will be highlighted on the map.

Alternatively you can left click the map near a tree and the information about this tree will be displayed in “Tree Characteristics” and the tree will highlighted on the map. Please note that this function only works properly when the zoom slider is pushed to the far left and the tree data are centred.

You can move the tree map by right clicking it. Keep the right mouse button pressed and move the mouse to the target position. After releasing the mouse button the tree map will shift to the specified position. This allows you to “walk” through the plot when the zoom is in operation. A double click on the tree map will centre the data again.

The Save button allows you to save the map as a JPEG. You will find the file in the same folder where your input files are.



Note that all settings in text boxes need to be activated by pressing <ENTER> after inputting a new number.

11. Species settings

Species settings can be specified in a separate ASCII file with the same base name as the input file but the extension *.species (e.g. SamplePlot.species). This file should be saved in the same folder as the input file (*.dat). CRANCOD expects species files with a specific structure as outlined in section 15.3. If you provide a species file the species codes in the output files and in the visualisation module will be replaced by the species names of column CN. Also each species on the map of the visualisation module will be represented with a specific colour. The provision of a species file is optional. An example file is provided in the folder with the sample data. Do not use “0” (zero) for species codings in the input file (*.dat).



12. Language settings

With the option [Language: 0: English; 1: Cymraeg; 2: Deutsch] you can choose the language in which you wish CRANCOD to communicate with you. However, the variable names/abbreviations of the output files and the base

names of the output files always stay the same with any language option (as specified in sections 6 and 15.2) in order to avoid confusion.

Note that language settings do not affect species names (see sections 11 and 15.3) as these are edited externally. Translating species names is therefore the responsibility of the user. Also the plot and tree information in the visualisation module (see section 10) are not affected by language settings for the same reasons put forward above.

13. Feedback

The developer of the CRANCOD software is particularly interested in feedback concerning any aspect of the program to improve its functionality and usefulness in future versions. Please report your feedback to arne.pommerening@bfh.ch. The author is very open for any kind of cooperation, particularly in terms of joint publications, and it would also be possible in the future to manage CRANCOD as an open-source software with an international project team.

14. Updates

For regular updates and other support please visit the CRANCOD web site at <http://www.crancod.org>.

15. Appendix

15.1 Structural indices estimated by CRANCOD

Nº	Index (Reference)	Formula	Where	Diversity
1	Distance to 1 st , ..., n th neighbour (Pommerening, 2006)	$0.0m \leq D_j < 0.5m$ $0.5m \leq D_j < 1.0m$ $1.0m \leq D_j < 1.5m$ etc.	The distance D_j between each tree of the forest stand and its j^{th} neighbour tree is allocated to a class of the distance distribution.	Location
2	Uniform angle index (Gadow <i>et al.</i> , 1998; Hui and Gadow, 2002)	$W = \frac{1}{n} \sum_{j=1}^n w_j$	$w_j = \begin{cases} 1, & \alpha_j < \alpha_0 \\ 0, & \text{otherwise} \end{cases}$ $\alpha_0 = \frac{360^\circ}{n+1}$	Location
3	Mean directional index index (Corral-Rivas, 2006)	$R_i = \sqrt{\left(\sum_{j=1}^n \cos \alpha_{ij}\right)^2 + \left(\sum_{j=1}^n \sin \alpha_{ij}\right)^2}$	α_{ij} angle between a line pointing away from the reference tree i to neighbours j and a unique reference bearing (e.g. due North).	Location
4	Species mingling (Füldner, 1995; Aguirre <i>et al.</i> , 2003)	$M_i = \frac{1}{n} \sum_{j=1}^n m_j$	$m_j = \begin{cases} 1, & \text{species}_j \neq \text{species}_i \\ 0, & \text{otherwise} \end{cases}$	Species
5	DBH/Height differentiation (1) (Füldner, 1995; Pommerening, 1997, 2002)	$T1_i = 1 - \sum_{j=1}^n \frac{\min(Dim_i, Dim_j)}{\max(Dim_i, Dim_j)}$	j is the 1 st neighbour tree.	Dimension
6	DBH/Height differentiation (2) (Füldner, 1995; Gadow, 1999)	$T_i = 1 - \frac{1}{n} \sum_{j=1}^n \frac{\min(Dim_i, Dim_j)}{\max(Dim_i, Dim_j)}$	$j = 1..n$ neighbour trees.	Dimension
7	DBH/Height dominance (1) (Hui <i>et al.</i> , 1998)	$U_i = \frac{1}{n} \sum_{j=1}^n u_j$	$u_j = \begin{cases} 1, & Dim_j > Dim_i \\ 0, & \text{otherwise} \end{cases}$	Dimension
8	DBH/Height dominance (2) (Gadow and Hui, 2002; Aguirre <i>et al.</i> , 2003)	$U_i = \frac{1}{n} \sum_{j=1}^n u_j$	$u_j = \begin{cases} 1, & Dim_1 > Dim_j \\ 0, & \text{otherwise} \end{cases}$	Dimension

Dim can be DBH or total tree height.

Other spatial indices calculated are the aggregation index of Clark & Evans (1954), the species segregation index (Pielou, 1977) and a few simultaneous distributions of indices.

Non-spatial structural indices calculated by CRANCOD are the Shannon (Shannon and Weaver, 1949), Simpson (Simpson, 1949) and the species profile index (Pretzsch, 1998). The Shannon and Simpson indices are calculated both basal area and SPH based.

The Simpson index has two base types

$$D = \sum_{m=1}^n \frac{N_m^2}{N^2} \quad (0 \text{ in } *.cfg \text{ file}) \quad \text{and} \quad D = \sum_{m=1}^n \frac{N_m(N_m - 1)}{N(N - 1)} \quad (1 \text{ in } *.cfg \text{ file})$$

where

D Simpson-Index base
 N_m number of individuals of species m

$$N = \sum_{m=1}^n N_m$$

The final Simpson indices can be calculated as either complementary or reciprocal form:

$$1 - D \quad (0 \text{ in } *.cfg \text{ file}) \quad \text{or} \quad \frac{1}{D} \quad (1 \text{ in } *.cfg \text{ file})$$

In analogy the Simpson and Shannon index are also applied to the diameter distribution.

15.2 Variable names and abbreviations

Variable name/abbreviation	Definition/explanation	Output file
Abs. Bias	Absolute value of the bias.	*_inv_Statistics1.out
AD	Absolute discrepancy see section 8.	*_inv_Statistics2.out
Arithmetic mean DBH (dm)	Arithmetic mean diameter [cm].	*_NonSpatial_*.org.out
Basal area	See <i>Basal area per hectare</i> .	*_inv_Statistics1.out
Basal area per hectare	Basal area [m ²] per hectare.	*_NonSpatial_*.org.out
Bias	See section 8.	*_inv_Statistics1.out
Clark & Evans aggregation index	Aggregation index of Clark & Evans (1954).	*_SpatialTree_*.org.out
Coeff of variation (DBH)	Coefficient of variation of tree diameters.	*_NonSpatial_*.org.out
CV	Coefficient of variation.	*_NonSpatial_*.org.out *_SpatialTree_*.org.out
D1..n	Intertree distances between the tree of column Tree# and the <i>n</i> nearest neighbours.	*_tree_*.org.out
DBH differentiation mean of neighbours - classes	Distribution of the DBH differentiation index across all <i>n</i> neighbours (formula 6 in 15.1).	*_SpatialTree_*.org.out
DBH differentiation mean of neighbours - mean value	Arithmetic mean of the DBH differentiation index across all <i>n</i> neighbours (formula 6 in 15.1).	*_SpatialTree_*.org.out
DBH differentiation tree attribute - classes	Distribution of the DBH differentiation index separately for the <i>n</i> neighbours (formula 5 in 15.1).	*_SpatialTree_*.org.out
DBH differentiation tree attribute - mean value	Arithmetic mean of the DBH differentiation index separately for the <i>n</i> neighbours (formula 5 in 15.1).	*_SpatialTree_*.org.out
DBH distribution	Diameter distribution with user defined class width. The left column gives the mean diameter of each diameter class, the central column the trees/ha of each class and the right column the relative frequency.	*_NonSpatial_*.org.out *_inv_Statistics2.out
DBH Dominance	See <i>DBH dominance tree attribute – mean value (1) or (2)</i> .	*_inv_Statistics1.out
DBH Dominance	See <i>DBH dominance tree attribute – classes (1) or (2)</i> .	*_inv_Statistics2.out
DBH dominance tree attribute - classes (1)	Distribution of the DBH dominance index (formula 7 in 15.1).	*_SpatialTree_*.org.out
DBH dominance tree attribute - classes (2)	Distribution of the DBH dominance index (formula 8 in 15.1).	*_SpatialTree_*.org.out
DBH dominance tree attribute - mean value (1)	Arithmetic mean of the DBH dominance index (formula 7 in 15.1).	*_SpatialTree_*.org.out
DBH dominance tree attribute - mean value (2)	Arithmetic mean of the DBH dominance index (formula 8 in 15.1).	*_SpatialTree_*.org.out
DBH_Dominance1	Diameter dominance index (formula 7 in 15.1).	*_tree_*.org.out
DBH_Dominance2	Diameter dominance index (formula 8 in 15.1).	*_tree_*.org.out
DBH0	DBH [cm] of the tree of column Tree#.	*_tree_*.org.out
DBH1..n	DBHs of the <i>n</i> neighbour trees.	*_tree_*.org.out
dg	See <i>Quadratic mean DBH (dg)</i> .	*_inv_Statistics1.out
Dij(r)	Marked cumulative nearest neighbour distance distributions (1 st neighbour). <i>i</i> and <i>j</i> are species codes defined by the user. See Stoyan and Penttinen (2000).	*_dij_*.org.out
Distance distribution	See <i>Distances – classes</i> .	*_inv_Statistics2.out
Distance mean	See <i>Distances – mean value</i> .	*_inv_Statistics1.out
Distances - classes	Distribution of the intertree distances [m] separately for the <i>n</i> neighbours. Class width can be flexibly defined.	*_SpatialTree_*.org.out

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Variable name/abbreviation	Definition/explanation	Output file
Distances - mean value	Arithmetic mean of the intertree distances [m] separately for the n neighbours.	*_SpatialTree_org.out
Distribution	Name of index distribution.	*_inv_Statistics2.out
Edge_1	Boolean variable indicating whether the tree of column Tree# was used to calculate indices requiring the first neighbour only.	*_tree_org.out
Edge_Dimension	Boolean variable indicating whether the tree of column Tree# was used to calculate indices of dimension diversity.	*_tree_org.out
Edge_Position	Boolean variable indicating whether the tree of column Tree# was used to calculate indices of position diversity.	*_tree_org.out
Edge_Species	Boolean variable indicating whether the tree of column Tree# was used to calculate indices of species diversity.	*_tree_org.out
Energy	Energy see section 8.	*_inv_Statistics2.out
Est. Index	Index value estimated from the sampling simulation.	*_inv_Statistics1.out
Expectation	Expected values according to Lewandowski and Pommerening (1997) and Pommerening (1997).	*_NonSpatial_org.out
$g(r)$	Pair correlation function see Stoyan and Penttinen (2000).	*_corr_org.out
$g_a(r)$	Mark variogram (DBH as mark) see Stoyan and Penttinen (2000).	*_corr_org.out
$g_{ij}(r)$	Mark pair correlation functions. i and j are species codes defined by the user. See Stoyan and Stoyan (1994).	*_corr_org.out
Grid	Distance between sample plot centres.	*_inv_Statistics1.out *_inv_Statistics2.out
h_{100}/d_{100} ratio	H/d ratio consisting of top height (h_{100}) and top height diameter (d_{100}).	*_NonSpatial_org.out
Height differentiation mean of neighbours - classes	Distribution of the height differentiation index across all n neighbours (formula 6 in 15.1).	*_SpatialTree_org.out
Height differentiation mean of neighbours - mean value	Arithmetic mean of the height differentiation index across all n neighbours (formula 6 in 15.1).	*_SpatialTree_org.out
Height differentiation tree attribute - classes	Distribution of the height differentiation index separately for the n neighbours (formula 5 in 15.1).	*_SpatialTree_org.out
Height differentiation tree attribute - mean value	Arithmetic mean of the height differentiation index separately for the n neighbours (formula 5 in 15.1).	*_SpatialTree_org.out
Height dominance tree attribute - classes (1)	Distribution of the height dominance index (formula 7 in 15.1).	*_SpatialTree_org.out
Height dominance tree attribute - classes (2)	Distribution of the height dominance index (formula 8 in 15.1).	*_SpatialTree_org.out
Height dominance tree attribute - mean value (1)	Arithmetic mean of the height dominance index (formula 7 in 15.1).	*_SpatialTree_org.out
Height dominance tree attribute - mean value (2)	Arithmetic mean of the height dominance index (formula 8 in 15.1).	*_SpatialTree_org.out
Height_Dominance1	Height dominance index (formula 7 in 15.1).	*_tree_org.out
Height_Dominance2	Height dominance index (formula 8 in 15.1).	*_tree_org.out
Height_Est	Height [m] estimated from the stand height curve of the tree of column Tree#.	*_tree_org.out
Height_Org	Original height [m] of the tree of column Tree#.	*_tree_org.out
hg/dg ratio	H/d ratio consisting of mean height (hg) and mean DBH (dg).	*_NonSpatial_org.out
hm/dm ratio	H/d ratio consisting of mean height (hm) and mean DBH (dm).	*_NonSpatial_org.out
Index	Index name.	*_inv_Statistics1.out
$k(r)$	Mark correlation function (DBH as mark) see Stoyan and Penttinen (2000)	*_corr_org.out
$L(r)$	L function see Stoyan and Penttinen (2000)	*_corr_org.out
$L_{mm}(r)$	Marked L function see Stoyan and Stoyan (1994)	*_corr_org.out
maxAbsDiff	Maximum absolute difference see section 8.	*_inv_Statistics2.out
MDI	See <i>Mean directional index - mean value</i> .	*_inv_Statistics1.out
MDI	See <i>Mean directional index - distribution</i> .	*_inv_Statistics2.out
MDI	Mean directional index (formula 3 in 15.1).	*_tree_org.out
Mean directional index - distribution	Distribution of the mean directional index (formula 3 in 15.1).	*_SpatialTree_org.out
Mean directional index - mean value	Arithmetic mean of the mean directional index (formula 3 in 15.1).	*_SpatialTree_org.out

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Variable name/abbreviation	Definition/explanation	Output file
Mean height (hg)	Mean stand height [m] corresponding with the quadratic mean diameter usually estimated by inputting the dg in the function of the stand height curve.	*_NonSpatial_*.out
Mean height (hm)	Height [m] of the arithmetic mean DBH (dm) usually estimated by inputting the dm in the function of the stand height curve.	*_NonSpatial_*.out
Mingling	Mingling index (formula 4 in 15.1).	*_tree_*.out
Mingling	See <i>Mingling tree attribute – mean value</i> .	*_inv_Statistics1.out
Mingling	See <i>Mingling tree attribute – classes</i> .	*_inv_Statistics2.out
Mingling tree attribute - classes	Distribution of the mingling index (formula 4 in 15.1).	*_SpatialTree_*.out
Mingling tree attribute - mean value	Arithmetic mean of the mingling index (formula 4 in 15.1).	*_SpatialTree_*.out
MSE	Mean squared error see section 8.	*_inv_Statistics1.out
Neighbour	Number of neighbours involved in the index calculation.	*_inv_Statistics1.out *_inv_Statistics2.out
Neighbour1..n	Tree number of n^{th} neighbour.	*_tree_*.out
Pielou segregation index	Species segregation index (Pielou, 1977).	*_SpatialTree_*.out
pij(r)	Mark connection function. i and j are species codes defined by the user.	*_corr_*.out
Plot Numbers	Arithmetic mean of number of sample plots involved in the sampling simulation.	*_inv_Statistics1.out *_inv_Statistics2.out
Plot#	Number of sample plot as specified in the input file.	*_tree_*.out
Quadratic mean DBH (dg)	= Mean squared diameter [cm]; diameter of the mean basal area tree.	*_NonSpatial_*.out
r	Intertree distance [m].	*_corr_*.out *_dij_*.out
r. Abs. Bias	Absolute bias divided by the true population value.	*_inv_Statistics1.out
r. Bias	Bias divided by the true population value.	*_inv_Statistics1.out
r. RMSE	Root mean squared error divided by the true population value.	*_inv_Statistics1.out
R ²	Coefficient of determination.	*_NonSpatial_*.out
Relative SPH & basal area	Summary of SPH, basal area and dg with relative SPH and relative basal area.	*_NonSpatial_*.out
Rep.	Number of replications.	*_inv_Statistics1.out *_inv_Statistics2.out
Rep_Factor_1	Tree representation factor for spatial variables requiring the first neighbour only.	*_tree_*.out
Rep_Factor_Dimension	Tree representation factor for spatial variables of dimension diversity.	*_tree_*.out
Rep_Factor_NS	Tree representation factor for non-spatial variables.	*_tree_*.out
Rep_Factor_Position	Tree representation factor for spatial variables of position diversity.	*_tree_*.out
Rep_Factor_Species	Tree representation factor for spatial variables of species diversity.	*_tree_*.out
RMSE	Root mean squared error see section 8.	*_inv_Statistics1.out
SE	Sampling error.	*_NonSpatial_*.out *_SpatialTree_*.out
Shannon index (DBH, BA)	Diameter related Shannon index (Shannon and Weaver, 1949) calculated from relative basal area. See also section 15.1.	*_NonSpatial_*.out
Shannon index (DBH, SPH)	Diameter related Shannon index (Shannon and Weaver, 1949) calculated from relative SPH. See also section 15.1.	*_NonSpatial_*.out
Shannon index (species, BA)	Species related Shannon index (Shannon and Weaver, 1949) calculated from relative basal area. See also section 15.1.	*_NonSpatial_*.out
Shannon index (species, SPH)	Species related Shannon index (Shannon and Weaver, 1949) calculated from relative SPH. See also section 15.1.	*_NonSpatial_*.out
Simpson index (DBH, BA)	Diameter related Simpson index (Simpson, 1949) calculated from relative basal area. See also section 15.1.	*_NonSpatial_*.out
Simpson index (DBH, SPH)	Diameter related Simpson index (Simpson, 1949) calculated from relative SPH. See also section 15.1.	*_NonSpatial_*.out
Simpson index (species, BA)	Species related Simpson index (Simpson, 1949) calculated from relative basal area. See also section 15.1.	*_NonSpatial_*.out
Simpson index (species, SPH)	Species related Simpson index (Simpson, 1949) calculated from relative SPH. See also section 15.1.	*_NonSpatial_*.out

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Variable name/abbreviation	Definition/explanation	Output file
	1949) calculated from relative SPH. See also section 15.1.	
Simultaneous distribution Mingling (tree) - DBH dominance	Simultaneous distribution of the mingling index (formula 4 in 15.1) and the DBH dominance 1/2 index (formula 7/8 in 15.1).	*_SpatialTree_org.out
Species	Species code as specified in the input file.	*_tree_org.out *_inv_Statistics1.out *_inv_Statistics2.out
Species profile index	Variation of the Shannon index assessing species diversity in different height strata (Pretzsch, 1998).	*_NonSpatial_org.out
Species: 0 (Total stand - not species specific)	Analysis of the total stand regardless of species.	*_NonSpatial_org.out *_SpatialTree_org.out
Species: X (species specific)	Species specific analysis of the stand according to species X.	*_NonSpatial_org.out *_SpatialTree_org.out
SPH	Trees per hectare.	*_NonSpatial_org.out *_inv_Statistics1.out
Stand area(s) [ha]	Summary of areas [ha] of all plots of the input file.	*_NonSpatial_org.out
Stand height curve Regression equation 139 of 139 trees available.	Details of the stand height curve estimated from all height/diameter data of all plots of the input file. The figures explain how many height data out of the absolute number of trees were available.	*_NonSpatial_org.out
StE	Standard error.	*_NonSpatial_org.out *_SpatialTree_org.out
TD	See <i>DBH differentiation tree attribute – mean value</i> .	*_inv_Statistics1.out
TD	See <i>DBH differentiation tree attribute – classes</i> .	*_inv_Statistics2.out
TD_mean	Diameter differentiation (formula 6 in 15.1).	*_tree_org.out
TD1..n	Diameter differentiation between the tree of column Tree# and the <i>n</i> nearest neighbours (formula 5 in 15.1).	*_tree_org.out
TDmean	See <i>DBH differentiation mean of neighbours – mean value</i> .	*_inv_Statistics1.out
TDmean	See <i>DBH differentiation mean of neighbours – classes</i> .	*_inv_Statistics2.out
TH_mean	Height differentiation (formula 6 in 15.1).	*_tree_org.out
TH1..n	Height differentiation between the tree of column Tree# and the <i>n</i> nearest neighbours (formula 5 in 15.1).	*_tree_org.out
Top height (h100)	Height [m] of the top height DBH (dm) usually estimated by inputting the d100 in the function of the stand height curve.	*_NonSpatial_org.out
Top height diameter (d100)	Quadratic mean DBH (dg) of the 100 biggest (in terms of DBH) trees per hectare.	*_NonSpatial_org.out
Total number of trees	Absolute number of trees regardless of representation factors.	*_NonSpatial_org.out
Total number of trees after edge correction	Absolute number of trees after edge correction separately for indices requiring only 1 neighbour and the indices of position, species and dimension diversity.	*_SpatialTree_org.out
Total number of trees before edge correction	Absolute number of trees regardless of representation factors.	*_SpatialTree_org.out
Tree Numbers	Arithmetic mean of number of trees involved in the sampling simulation.	*_inv_Statistics1.out *_inv_Statistics2.out
Tree#	Tree number as specified in the input file.	*_tree_org.out
True Index	Index value estimated from the original tree population.	*_inv_Statistics1.out
UAI	Uniform angle index (formula 2 in 15.1).	*_tree_org.out
Uniform angle index - classes	Distribution of the uniform angle index (formula 2 in 15.1).	*_SpatialTree_org.out
Uniform angle index - mean value	Arithmetic mean of the uniform angle index (formula 2 in 15.1).	*_SpatialTree_org.out
x, y	x and y [m] Cartesian coordinates of the trees as specified in the input file or calculated from polar coordinates (circular sample plots).	*_tree_org.out

The variable names/abbreviations always stay the same with any language option.

With all height related indices and variables preference is always given to the original height values and estimated height values are only used if no original (measured) values were available. Also preference is given to species specific

stand height curves for the estimation of individual tree heights. However, where there are too few species specific height observations individual tree heights are estimated from the general stand height curve.

15.3 Species codings

Below you find the contents of a sample *.species file with species codings of the British Forestry Commission. Column LC is optional. Column C signifies the colours to be applied in the visualisation module. The significance these RGB colour codings can be explored on an HTML page provided with the program files.

NC	LC	CN	BN	C
0	All	All species	All species	255-255-255
1	SP	Scots pine	<i>Pinus sylvestris</i> L.	128-0-128
2	CP	Corsican pine	<i>Pinus nigra</i> var. <i>maritima</i> (Alton) Melville	128-0-128
3	LP	Lodgepole pine	<i>Pinus contorta</i> Douglas	128-0-128
4	AUP	Austrian pine	<i>Pinus nigra</i> var. <i>nigra</i> Harrison	128-0-128
5	MAP	Maritime pine	<i>Pinus pinaster</i> Ait.	128-0-128
6	WEP	Weymouth pine	<i>Pinus strobus</i> L.	128-0-128
7	MOP	Mountain pine	<i>Pinus uncinata</i> Miller	128-0-128
8	BIP	Bishop pine	<i>Pinus muricata</i> D. Don	128-0-128
9	RAP	Monterey pine	<i>Pinus radiata</i>	128-0-128
10	PDP	Ponderosa pine	<i>Pinus ponderosa</i> Douglas	128-0-128
11	MCP	Macedonian pine	<i>Pinus peuce</i> Griseb.	128-0-128
12	SS	Sitka spruce	<i>Picea sitchensis</i> (Bong.) Carr.	128-128-0
13	NS	Norway spruce	<i>Picea abies</i> (L.) Karst	128-128-0
14	OMS	Omorika spruce	<i>Picea omorika</i> (Pancic) Purkyne	128-128-0
15	EL	European larch	<i>Larix decidua</i> Miller	255-165-0
16	JL	Japanese larch	<i>Larix kaempferi</i> (Lambert) Carr.	255-165-0
17	HL	Hybrid larch	<i>Larix eurolepis</i> Henry	255-165-0
18	DF	Douglas fir	<i>Pseudotsuga menziesii</i> (Mirb) Franco	100-149-237
19	WH	Western hemlock	<i>Tsuga heterophylla</i> (Raf.) Sarg.	199-21-133
20	RC	Western red cedar	<i>Thuja plicata</i> D. Don	199-21-133
21	LC	Lawson's cypress	<i>Chamaecyparis lawsoniana</i> (A. Murr.) Parl	199-21-133
22	LEC	Leyland cypress	<i>Cupressocyparis leylandii</i> (Jacks. and Dallim) Dallimore	199-21-133
23	GF	Grand fir	<i>Abies grandis</i> Lindl.	199-21-133
24	NF	Noble fir	<i>Abies procera</i> Rehd.	199-21-133
25	ESF	Silver fir	<i>Abies alba</i> Mill.	199-21-133
26	JCR	Japanese cedar	<i>Cryptomeria japonica</i> (L.f.) Don	199-21-133
27	RSQ	Coast redwood	<i>Sequoia sempervirens</i> (D.Don) Endl.	199-21-133
28	WSQ	Wellingtonia	<i>Sequoiadendron giganteum</i> (Lindl.) Buchholz	199-21-133
29	POK	Pendunculate oak	<i>Quercus robur</i> L.	255-255-0
30	SOK	Sessile oak	<i>Quercus petraea</i> (Matt.) Lieblein	255-255-0
31	ROK	Red oak	<i>Quercus borealis</i> Michx. f.	255-255-0
32	BE	Beech	<i>Fagus sylvatica</i> L.	255-0-0
33	SY	Sycamore	<i>Acer pseudoplatanus</i> L.	165-42-42
34	NOM	Norway maple	<i>Acer platanoides</i> L.	100-149-237
35	AH	Ash	<i>Fraxinus excelsior</i> L.	144-238-144
36	BI	Birch	<i>Betula</i> spp.	0-100-0
37	PO	Poplar	<i>Populus</i> spp.	0-100-0
38	SC	Sweet chestnut	<i>Castanea sativa</i> Mill.	0-0-139
39	HCH	Horse chestnut	<i>Aesculus hippocastanum</i> L.	0-0-139
40	CAR	Common alder	<i>Alnus glutinosa</i> (L.) Gaertn	0-0-0

NC	LC	CN	BN	C
41	GAR	Grey alder	<i>Alnus incana</i> (L.) Moench	0-0-0
42	RAR	Red alder	<i>Alnus rubra</i> Bong.	0-0-0
43	SAR	Sitka alder	<i>Alnus sinuata</i>	0-0-0
44	VAR	Green alder	<i>Alnus viridis</i> (Chaix) DC.	0-0-0
45	CLI	Common lime	<i>Tilia europaea</i> L.	124-252-0
46	SLI	Small-leaved lime	<i>Tilia cordata</i> Miller	124-252-0
47	LLI	Large-leaved lime	<i>Tilia platyphyllos</i> Scop.	124-252-0
48	EEM	English elm	<i>Ulmus procera</i> Salisb.	144-238-144
49	WEM	Wych elm	<i>Ulmus glabra</i> Hudson	144-238-144
50	SEM	Smooth-leaved elm	<i>Ulmus carpinifolia</i> Gleditsch	144-238-144
51	WCH	Wild cherry, Gean	<i>Prunus avium</i> (L.) L.	124-252-0
52	BCH	Bird cherry	<i>Prunus padus</i> L.	124-252-0
53	HBM	Hornbeam	<i>Carpinus betulus</i> L.	0-0-139
54	OBN	Roble	<i>Nothofagus obliqua</i> (Mirb.) Blume	255-0-0
55	PRN	Rauli	<i>Nothofagus procera</i> (Peopp. and Endl.)	255-0-0
56	RAN	Raoul	<i>Nothofagus nervosa</i>	255-0-0
57	HAZ	Hazel	<i>Corylus avellana</i> L.	0-100-0
58	WIL	Willow	<i>Salix</i> spp	144-238-144
59	HOL	Holly	<i>Ilex aquifolium</i>	144-238-144
60	ROW	Rowan	<i>Sorbus aucuparia</i>	144-238-144

15.4 Disclaimer

The CRANCOD software and all its libraries and algorithms have been prepared with great care. However, neither the developer nor Bern University of Applied Sciences can be made liable in the unlikely case of damage caused to your computer while using CRANCOD or incorrect outputs.

16. References and further reading

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