The dtd data format

(descriptive tree data format)

The dtd data format of the software systems Grogra and GroIMP is only used as input for plant structures. The data which can be encoded in this format normally originate from empirical data acquisition of single branches or entire crown and root structures. A dtd file (with the file extension „.dtd“) contains merely one structure, it does not represent a temporal development.
Precondition for creating a dtd file is that all growth units of the structure are labelled with a name (a name can be a number or a combination of letters, numbers and symbols, for example 08-15a, but it is not allowed to contain a blank). These names serve as identification of the growth unit. Mandatory information, which needs to be specified for every growth unit (GU), are: the name, the length (in mm), the name of the parent GU (i.e. the supporting GU from which the considered GU originates). Additional information (like diameter, angle, ...) is optional.

Layout of the file:
Every GU is defined by a single row in the file. (Lines that start with the symbol „\“ (backslash) are an exception to this and have a special function, see below.) The order of the GUs is generally arbitrary; it is only important that the description of a GU cannot stand before the description of its parent GU (meaning that the considered row has to be further at the bottom of the file).
A line contains the following ordered entries (divided by one or several blanks):

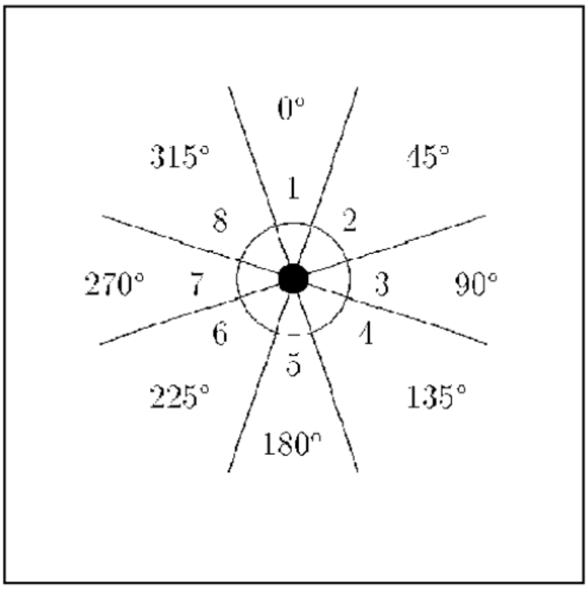
Name of the GU
L<number> (<number> denotes the length of the GU in mm, the acute brackets are not to be written!)
#<name of the parent GU> (only in case of the base GU of a branching structure, which does not have a parent-GU, the entry is ##)

Additional, optional entries can follow:

A<number>	position of the branching point (in mm distance from the base) on the parent GU (if the A-specification is missing, the position is assumed to be at the tip)
V	extension GU of the parent GU (i.e., they share the same branching order)
R<number>	specification of direction (see below)
+	right direction (equivalent to R3)
–	left direction (equivalent to R7)
W<number>	branching angle in degrees (angle between GU and parent GU)
K	marks a bud (when the option „buds are to be included“ is activated)
D<number>	diameter in mm
N<number>	needle or leaf parameter (area or dry mass)
B<number>	number of leaves (for deciduous trees)
C<number>	color index for graphic display
E<number>	number of internodes on the GU (for deciduous trees)
I<number>	index (rank) of insertion node on parent GU (counted from tip of parent GU; for deciduous trees)
*	forces interpretation of angle specification in relation to global coordinates (when working with a compass)

P<number>	dry mass of the GU without leaves (currently not interpreted by Grogra/ GroIMP)
O<number>	explicit specification of branching order
J<number>	explicit specification of age of GU (in years; important for lammas shoots)

Instead of uppercase, lowercase letters are also allowed. Convention is to use lowercase letters for estimated values and uppercase letters for measured values (Grogra and GroIMP do not differentiate between these two; the difference merely serves the purpose of transparency of the files.)
Comments, which should not be interpreted by the software, can be surrounded by acute or curly brackets (but they always should be put at the end of a line): <comment> or {comment}.
Specification of direction with R follows a 8-sector scheme, whereby R1 denotes the upward direction (when looking in direction of growth of the parent axis), or the north direction (when the parent axis has a vertical upward direction):



The precise angle in degrees can be given using S<number> instead of the R specification.

Headers in dtd files (optional; only for deciduous trees):

\phyllotaxy spiral,	produces a convoluted leaf arrangement (Alternatives: opposite, alternate)
\leaflength <number>,	specification of leaf length for all following growth units with leaves (B)
\leafbreadth <number>,	analogously: specification of leaf width
\leafarea <number>,	analogously: specification of leaf area (parameter N)
\min_intn <number>,	forces minimum number of internodes for all growth units containing leaves; leaves specified by B will be inserted at the uppermost internodes
\leafobject <file name> <symbol> <number>,	reads graphical description from L-System file, with start symbol and step count (= number) for the L-system *(Grogra only).*