Descriptive tree data format and analysis functions in GroIMP

Contribution on

"Modelling and visualisation of biological and chemical systems"

- Jan-Anton Dérer -

Overview

- Descriptive tree data (short DTD)
- Analysis functions

What is DTD?

- Plain text file
- Every line represents a shoot
- Whole file represents a plant or a part of a plant
  - Used primary for trees
  - General: All branching structures
- Import interface in GroIMP and Grogra
- Developed by W. Kurth

Why another format?

- Simple usage
- Easy to learn
- Fast way to describe a complex structure
- Writing in any text editor

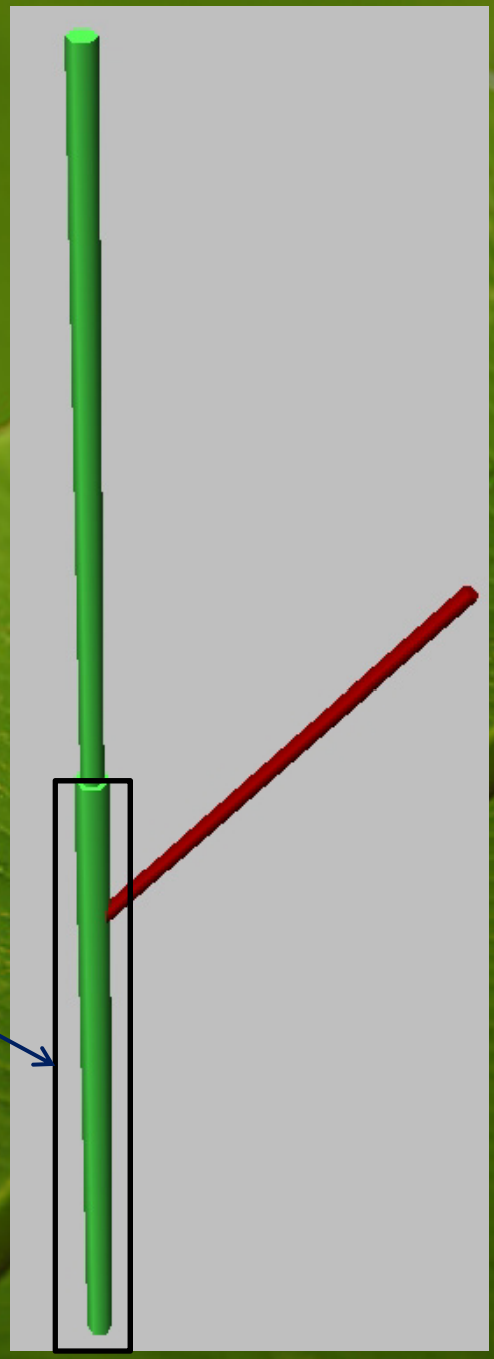
→Efficient working

DTD

- Minimum description for a shoot
  - **<Name> [L<length> | Q<short shoot series>] [## | #<Mothername>]**
- Sample
  - **1 L100 ##**
  - A single shoot with the length 100 (mm)
- Sample
  - **S1 L100 ##**
  - **S2 Q5 #S1**
  - S1 is the root with the length 100
  - Followed by a short shoot series of five shoots (described by S2)

Sample 1

```
1 L100 ## D3
2 L65   #1 V D2
3 L50   #1 A80 W35 C4 D1.5
```



Sample 1

```
1 L100 ## D3
2 L65   #1 V D2
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```
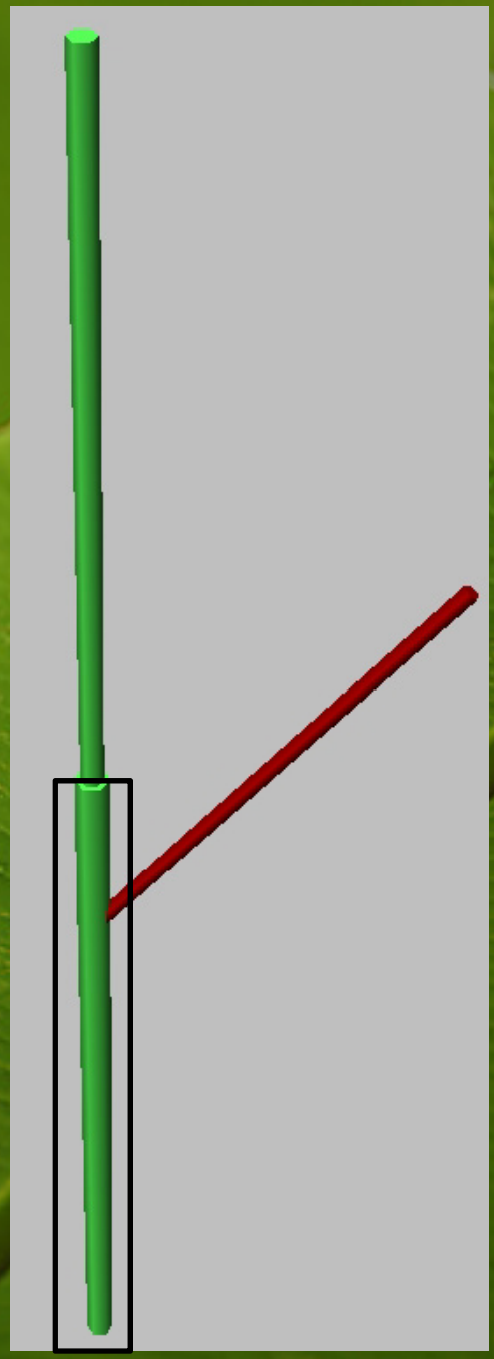

Diameter in mm



Sample 1

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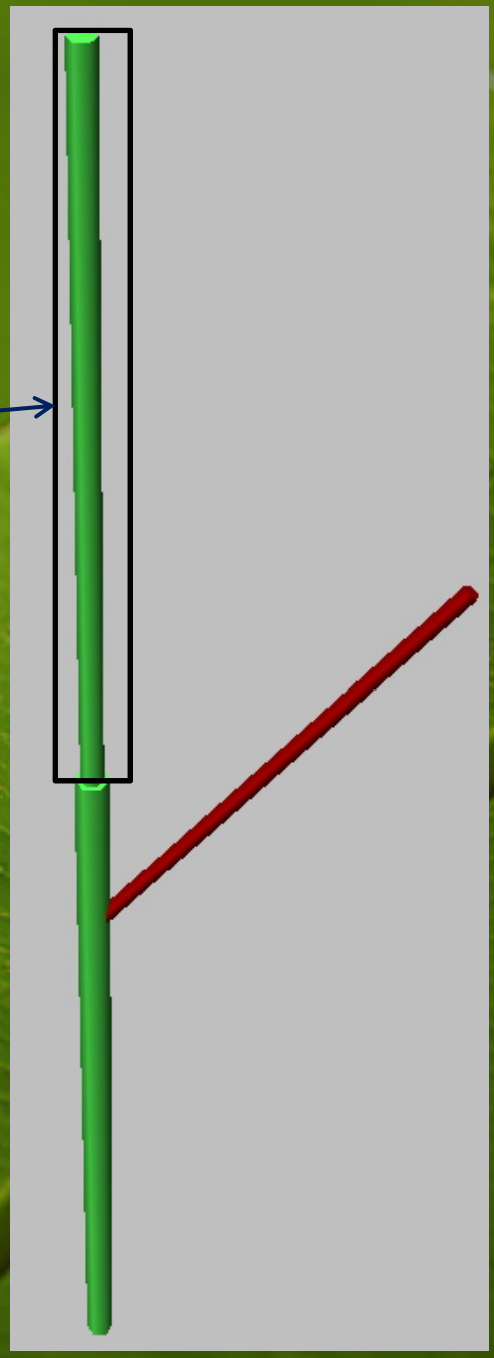
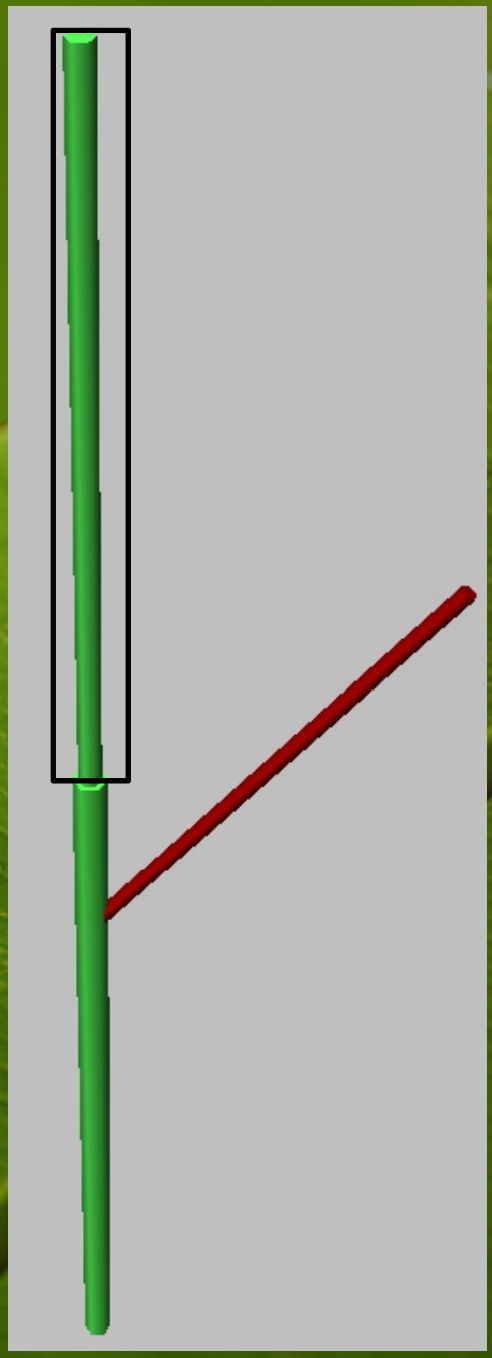


Sample 1

```
1 L100 ## D3
2 L65  #1 V D2
3 L50  #1 A80 W35 C4 D1.5
```

Extension of mothershoot (same order)



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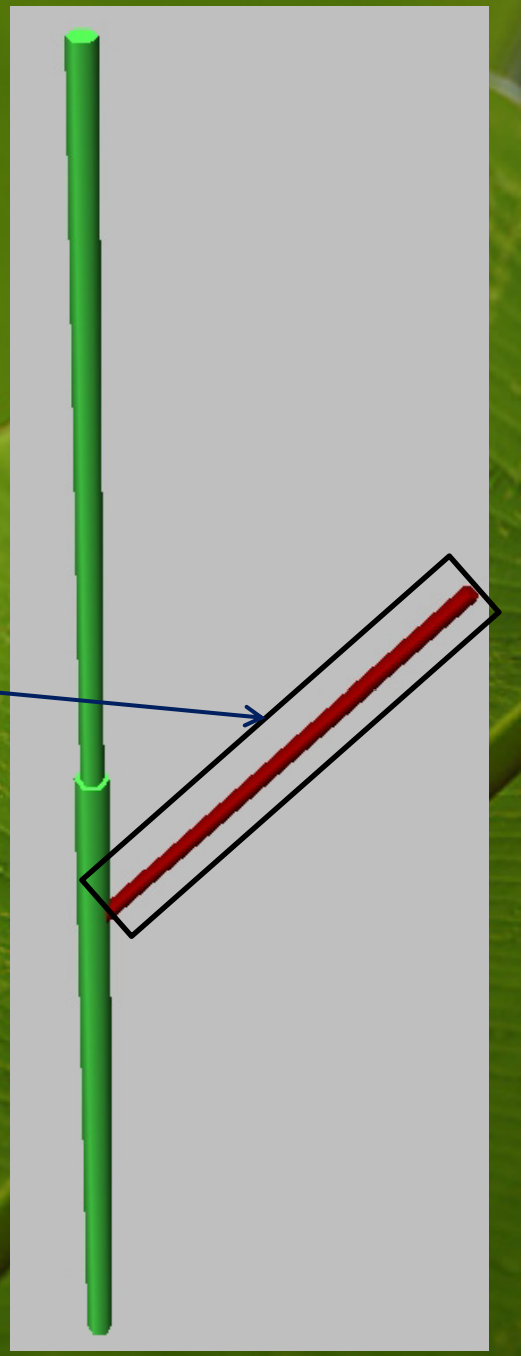
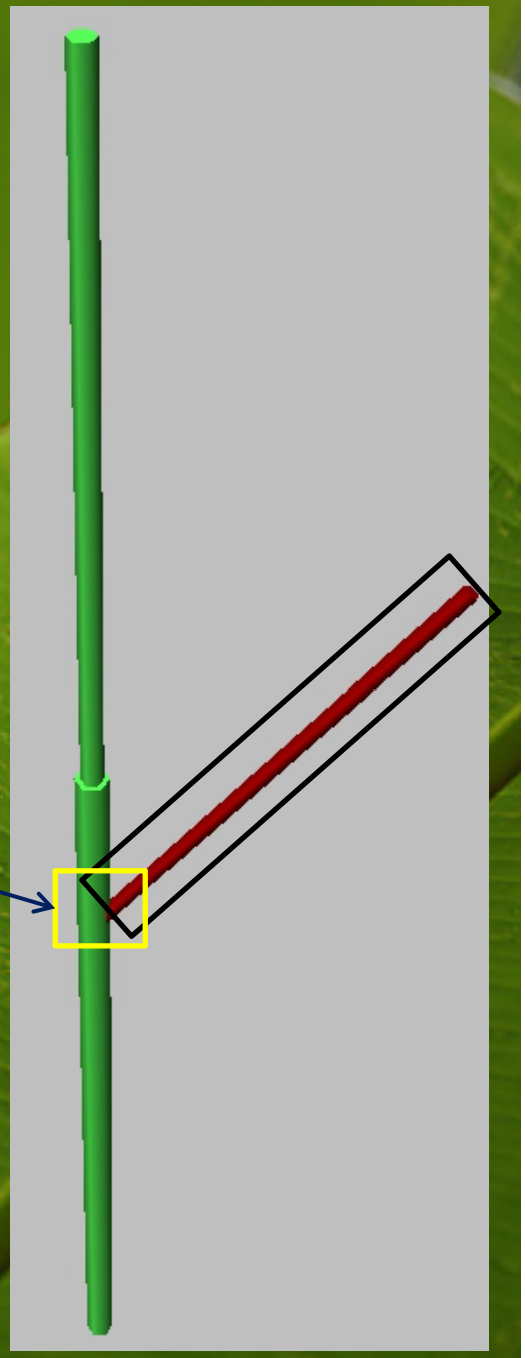


Sample 1

```
1 L100 ## D3
2 L65  #1 V D2
3 L50  #1 A80 W35 C4 D1.5
```

Insertion point at mothershoot in mm



Sample 1

```
1 L100 ## D3
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```
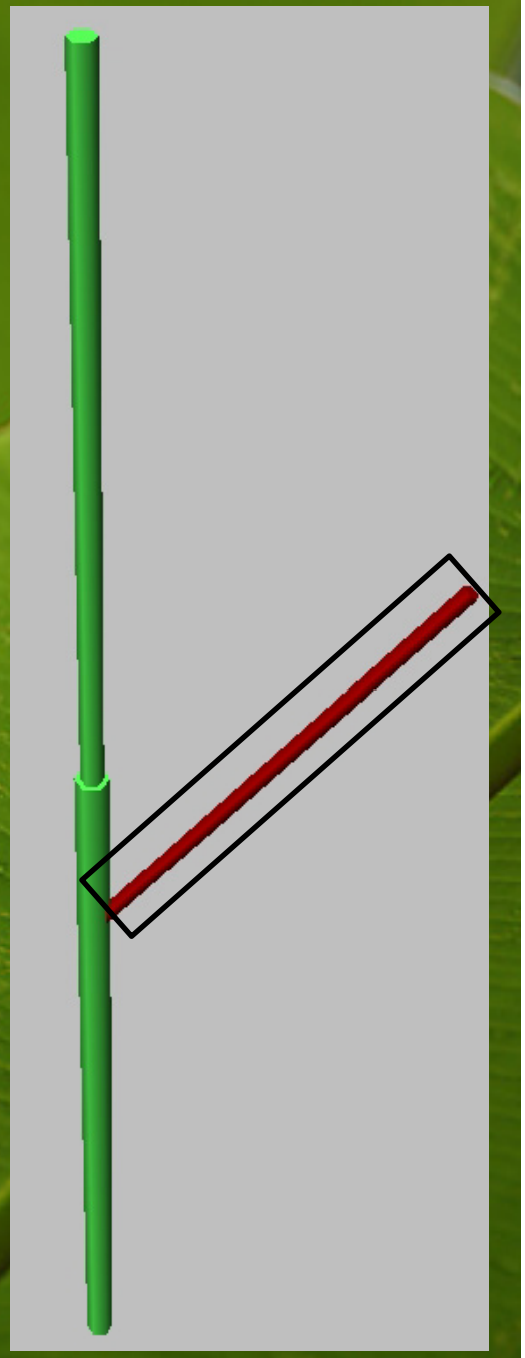

Angle in degree



Sample 1

```
1 L100 ## D3
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```
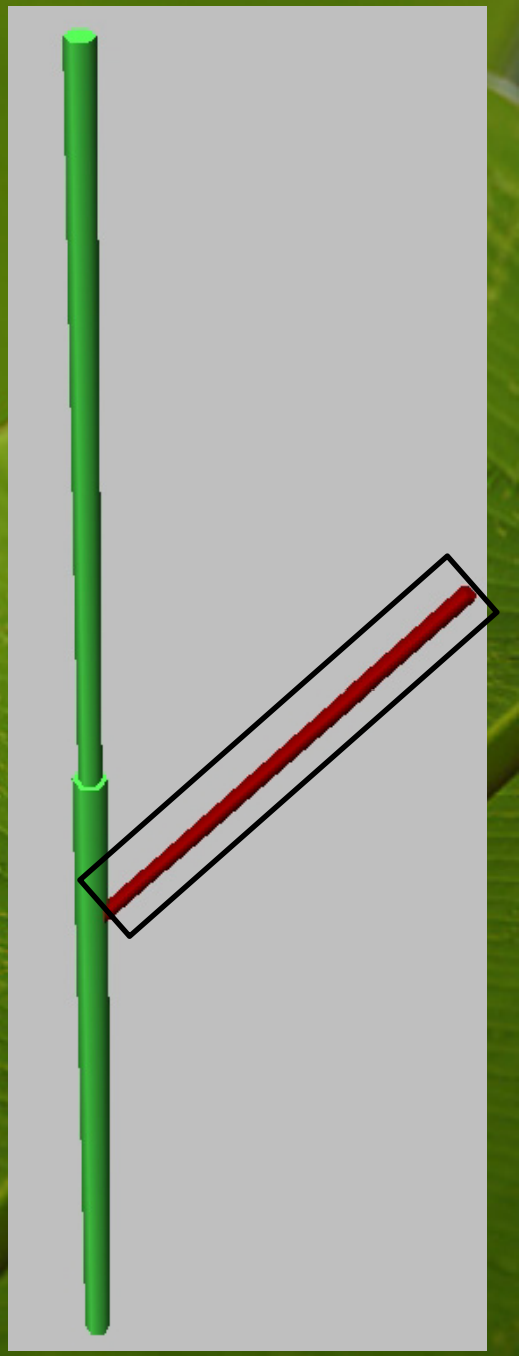
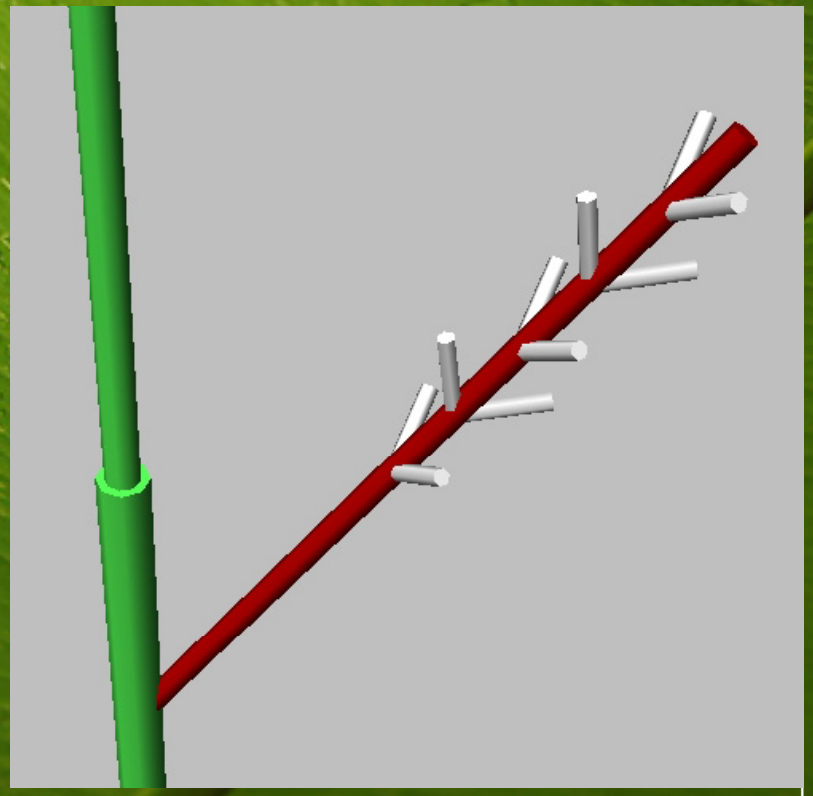

Color



Sample 2

```
\phyllotaxy opposite,
1 L100 ## D3
2 L65  #1 V D2
3 L50  #1 A80 W35 C4 D1.5 E10 B10
```

Alternatives: spiral, alternate



Sample 2

```
\phyllotaxy opposite,
1 L100 ## D3
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3 L50  #1 A80 W35 C4 D1.5 E10 B10
```
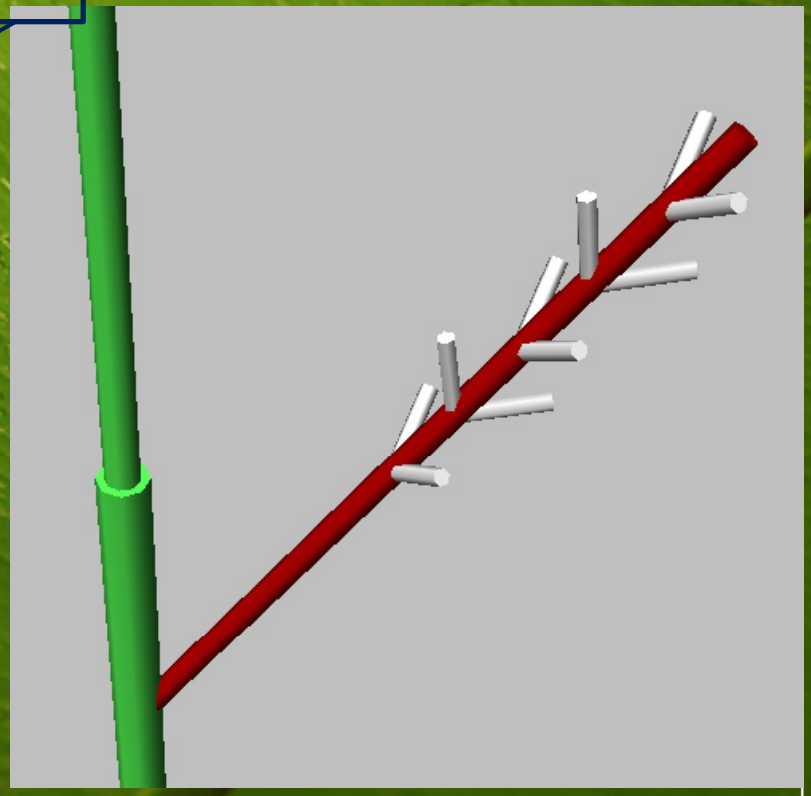

Number of internodes



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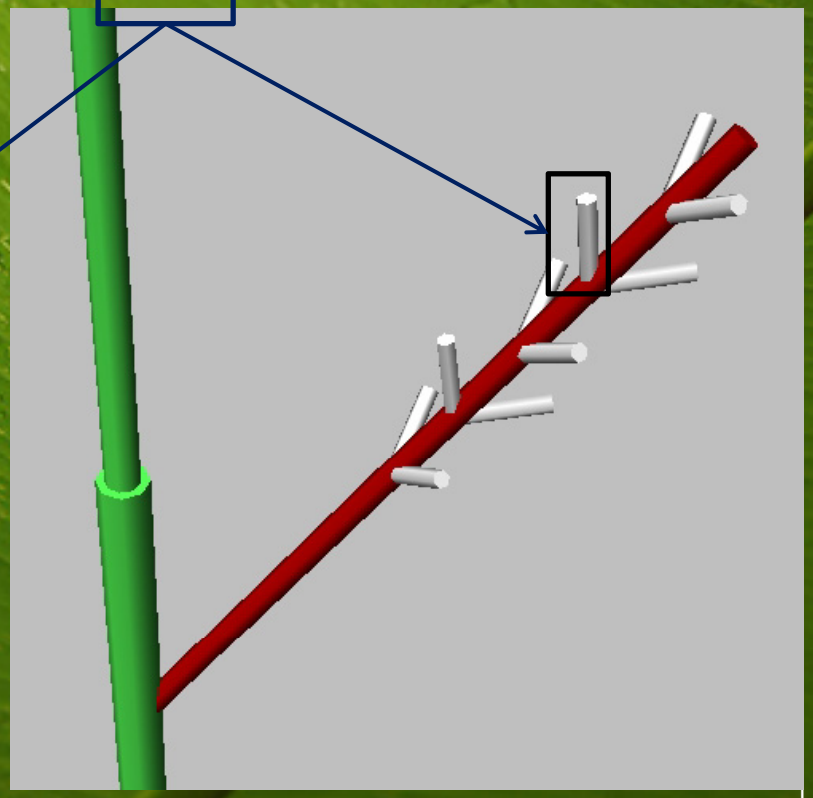


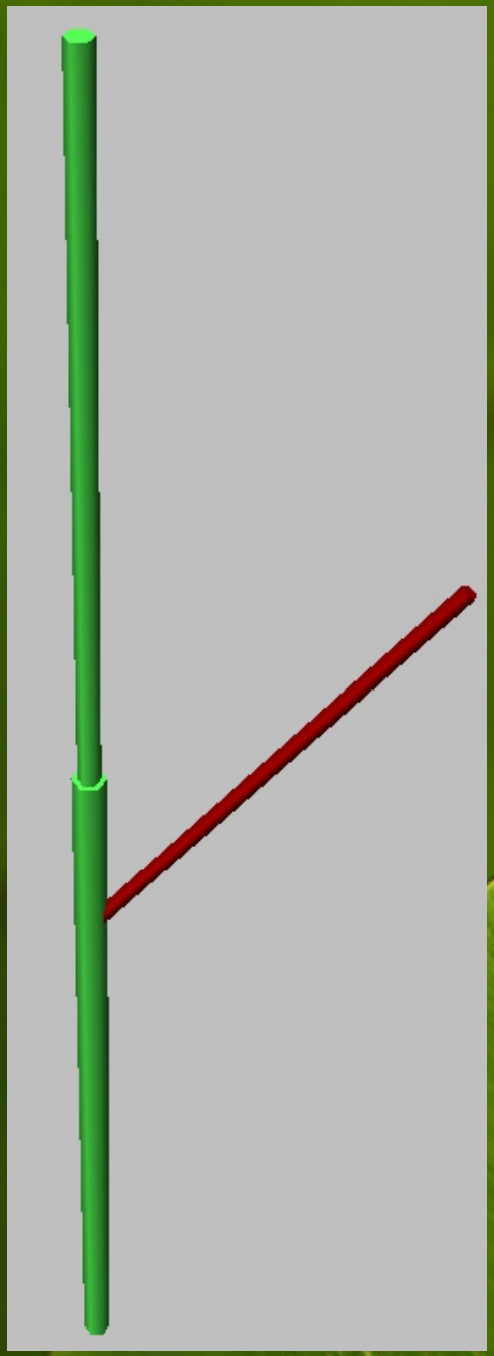
Number of leaves

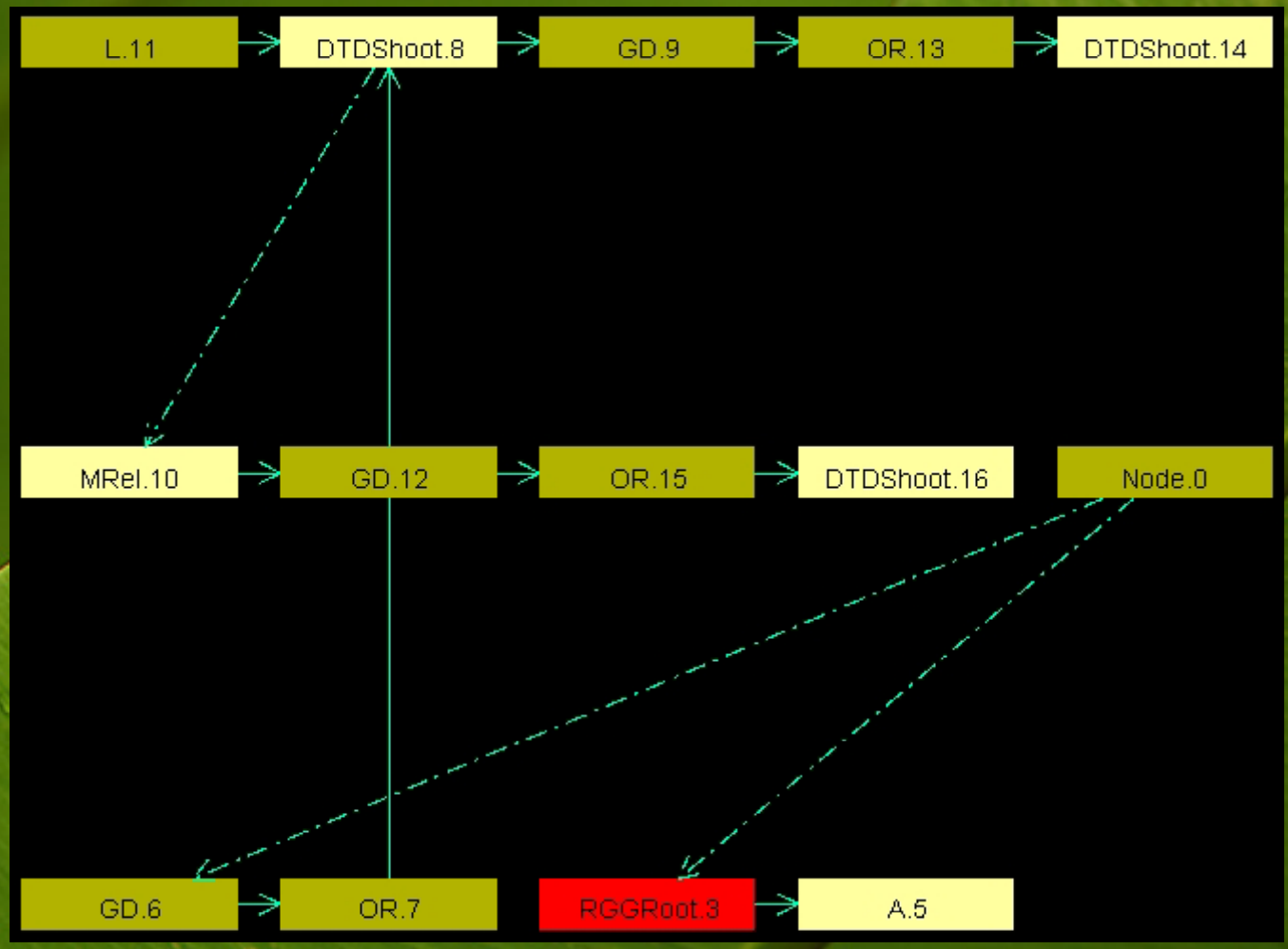
Sample 3

Graph

- Mapping information from dtd-file to RGG/XL
- Using turtle-commands (like F or DTDShoot) to visualize the structure
- Saving information like needle surface or no. of internodes with turtle-commands

Graph





Open issues

- No optimized usage of turtle-commands
- Actually not completely compatible with the interpretation of Grogra
  - But mostly
  - Missing: K, \leafobject, \fruitobject
  - Multiple roots like
    - `1 L100 ##`
      `2 L100 ## W20`

Upcoming

- Including buds
  - sleeping buds, dead buds
- \leafobject and \fruitobject
  - Cylinder will be replaced by complex models e. g. RGG-models
  - More realistic representation

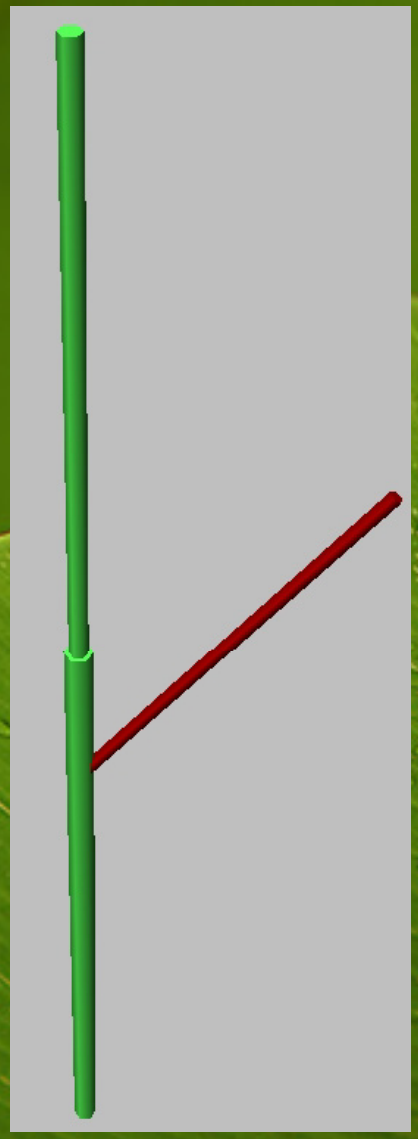
Upcoming

- New phyllotaxy to realize:

Analysis functions - general

- Usable for all on XL-based structures, e. g. RGG-models, models from DTD/LSY/SSY-files
- Export interfaces
  - *.txt, *.html, *.xml, *.csv, *.xls, *.pdf
- Functions based on the Grogra analysis functions

Basis for samples



Analysis functions

- List of all shoots
  - HTML sample
  - Excel sample
  - XML sample
- Elementary
  - HTML sample
- Basic tree parameters
  - HTML sample
- Number of daughter shoots
  - HTML Sample
  - PDF Sample

Analysis functions

- Some analysis functions give a list for further processing e. g. statistic software like SAS
  - e. g. number of daughter shoots, branching positions, length and angles, …
- It‘s a small overview of the analysis functions
  - Current 16 analysis functions
  - Topological & distribution analysis, …

Problems in realization

- Some analysis functions in Grogra act on copied structures or manipulate the original structure to e. g. fuse axes
  - Creating an emulation of the Grogra structure
  - Manipulated the emulated structure
  - Used in the axes analysis and topological analysis

Problems in realization

- Realizing vector-computation with available classes and methods
  - Writing only new vector-computations
  - Using object-oriented paradigms

Open issues

- Not all analysis functions are completely tested
  - Current task
- Grid with cubic cells for fractal analysis
- The fractal analysis