

Dissecting the feedback control of gibberellin biosynthesis

using a combined wetlab *in silico* approach

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MyCIB & Rothamsted Research



Outline

Functional Structural Plant Modelling (FSPM)

Gibberellin Biosynthesis

Decoupling functional and structural

Conclusion

GroIMP — An interactive FSPM platform



- ▶ A multi-scaled ecophysiological model of barley
- ▶ Capability to represent genetic, metabolic and morphological aspects of plant development
- ▶ The model consists of a set of morphogenetic rules, combined with a metabolic regulatory network

GroIMP — An interactive FSPM platform



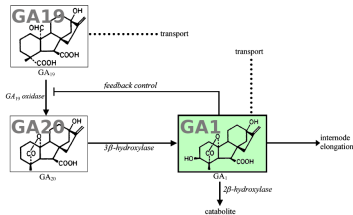
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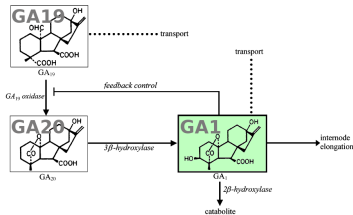
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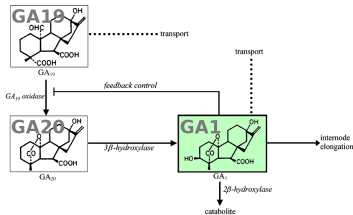
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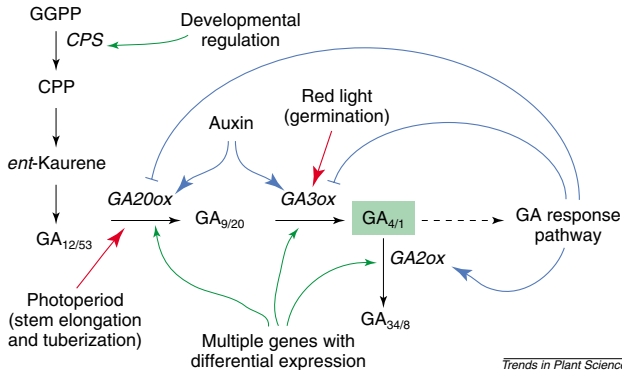
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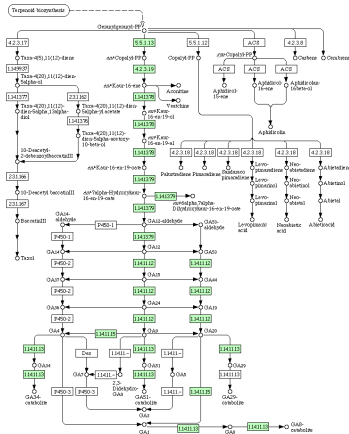
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Biologist's view

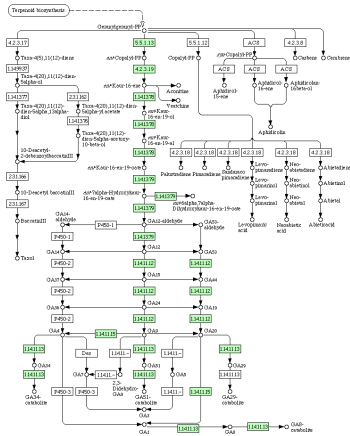


KEGG's view



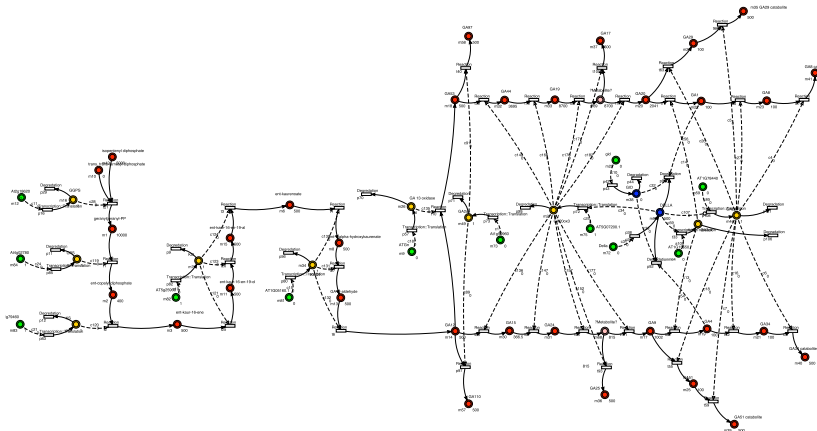
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- ▶ Unfortunately
- ▶ Not all parameters are known
- ▶ Available parameters are from different species/experiments

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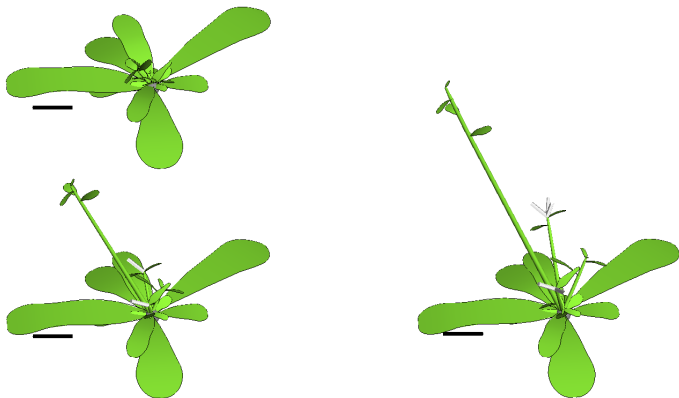


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Modeller's view

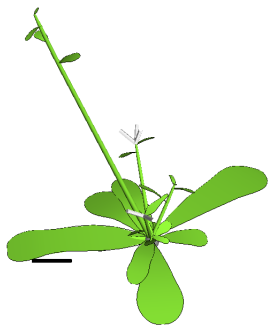


in silico Arabidopsis thaliana



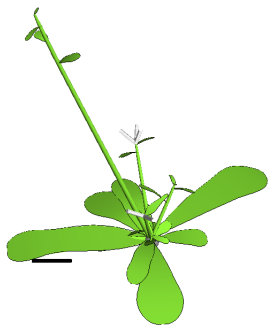
GroIMP translation of the L+C code by Mündermann, L. *et al.* Plant Physiology, 139:960 – 968, 2005

Dynamic control between functional and structural models



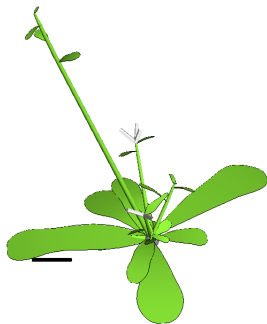
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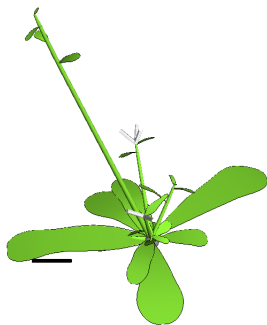
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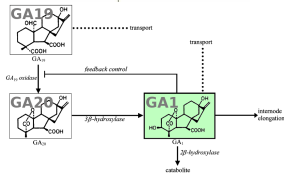
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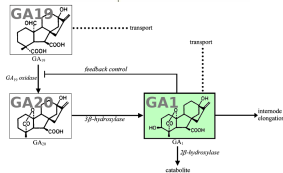
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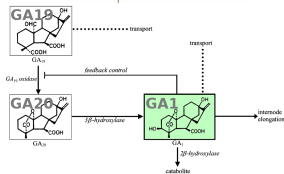
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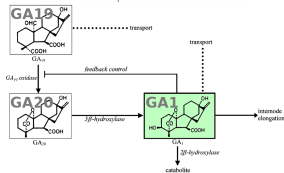
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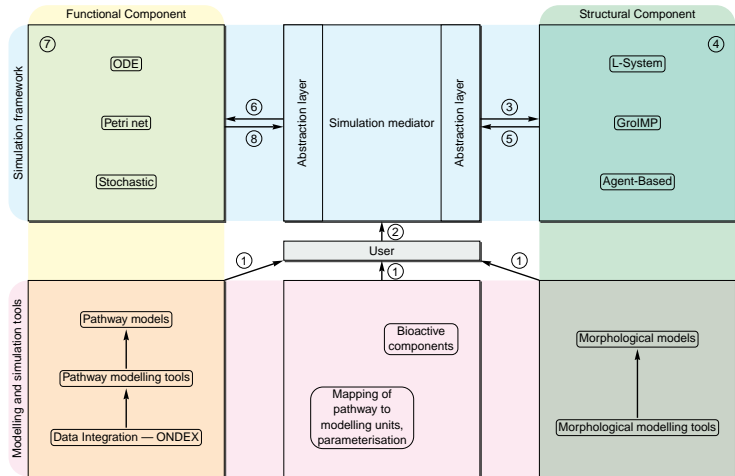
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Taking it apart and putting it back together again



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Acknowledgements



- ▶ Jacob Köhler, Andy Phillips, Peter Hedden: Rothamsted Research, UK
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- ▶ Ole Kniemeyer, Reinhard Hemmerling, Gerhard Buck-Sorlin, Winfried Kurth
- ▶ Sebastian Thiel: Uni Koblenz · Landau

Improvements

- ▶ Inclusion of monitor function
- ▶ No time standardization, only global stepping
- ▶ Current interaction with GroIMP
 - ▶ Selective copy of the underlying graph
 - ▶ Use of visitor?