

3D Reconstructions of Grape Bunch Architecture Based on Optimisation Theory

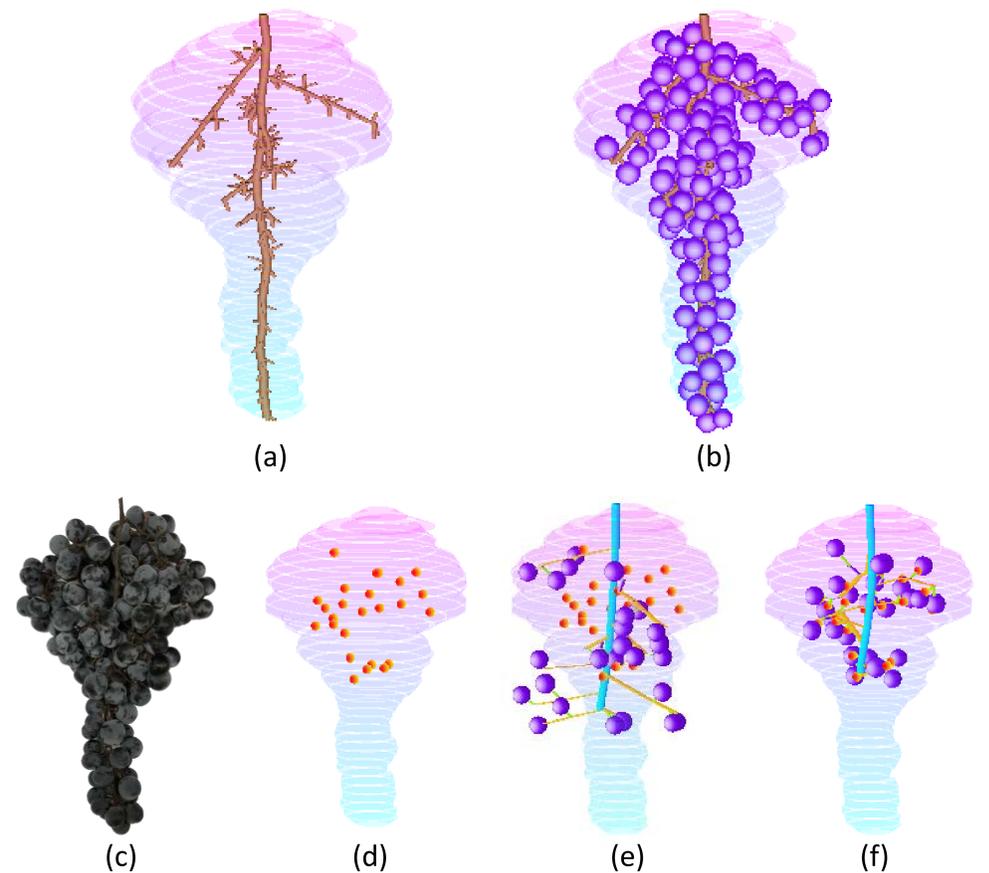
Bolai Xin & Mark Whitty, School of Mechanical & Manufacturing Engineering, UNSW

MOTIVATION

Phenotypic traits of grape bunches are known to have a close relationship with productive indices [1-2], from which guides further studies on phenotype improvement. Since current phenotyping methods are facing a bottleneck of labour intensity [3], 3D reconstruction provides a feasible solution towards a fast phenotypic traits extraction.

Since existing works on 3D bunch modelling reveal limitations on either function or accuracy, a new reconstruction method is proposed with following contributions:

- A better correlation of reconstructed element positions to the real bunch;
- An improved accuracy of element properties.



(a) Internode framework reconstruction. (b) Overall bunch reconstruction. (c) The original image of a bunch. (d) Detected berry positions. (e) Initial guess of bunch architecture. (f) Optimum result of bunch architecture.

Table: Evaluation on the reconstruction performance

	Error of Overall Number (%)	Error of Internode Length (%)
Rachis	28.3	2.8
Secondary	13.3	2.4
Tertiary	35.7	24.3
Pedicel	26.4	3.8

METHODS & RESULTS

Visible berries are detected and positioned from a 2D image through image processing. Giving visible berry positions, an objective function is specified as the sum of distances between reconstructed berries and real ones. Statistical analysis is conducted with respect to element properties before general topological and geometrical rules are concluded. By serving these rules as constraints, optimisation algorithms were employed to figure out the optimum solution including individual internode length and orientation. The final reconstructed model is then completed through the execution of a reconstruction grammar.

CONCLUSIONS

According to the preliminary test, the average percentage error of internode number and internode length are 25% and 8% respectively. The coincidence of visible berry position indicates an improvement comparing with traditional bunch reconstruction methods. The proposed work provides a feasible solution towards phenotyping bottleneck, which will in turn guide studies on improvements to viticultural products through breeding programs and vineyard management.

References

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3. Furbank, R. T., Tester, M., (2011) Phenomics – technologies to relieve the phenotyping bottleneck. Trends Plant Sci. 16 (2), 635–644.