

# Daniel Money

The Roslin Institute, The University of Edinburgh, Easter Bush, EH25 9RG, United Kingdom

+44 (7986) 113 958 • [daniel.money@roslin.ed.ac.uk](mailto:daniel.money@roslin.ed.ac.uk)  
[www.danielmoney.co.uk/academia](http://www.danielmoney.co.uk/academia)

## Education

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<b>University of Manchester</b> <i>PhD Bioinformatics</i> Thesis Title: Model and Algorithm Development in Computational Phylogenetics	<b>2007–2011</b> <i>Supervisor: Simon Whelan</i>
<b>University of Manchester</b> <i>MSc Bioinformatics</i>	<b>2006–2007</b>
<b>University of Wales, Swansea</b> <i>BSc Computer Science</i>	<b>1998–2001</b>

## Employment

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<b>University of Edinburgh</b> <i>Postdoctoral Fellow</i>	<b>2016–present</b> <i>Advisor: John Hickey</i>
<b>Dalhousie University</b> <i>Postdoctoral Fellow</i>	<b>2014–2015</b> <i>Advisor: Sean Myles</i>
<b>University of Kansas</b> <i>Postdoctoral Researcher</i>	<b>2011–2013</b> <i>Advisor: Mark Holder</i>
<b>Ministry of Defence (UK)</b> <i>Higher Scientific Officer</i>	<b>2001–2006</b>

## Publications

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D. MONEY, Z. MIGICOVSKY, K. GARDNER, AND S. MYLES (2017) LinkImputeR: user-guided genotype calling and imputation for non-model organisms *BMC Genomics* **18**:523

R. ANTOLIN, C. NETTELBLAD, G. GORJANC, D. MONEY, J. M. HICKEY (2017) A hybrid method for the imputation of genomic data in livestock populations *Genetics Selection Evolution* **49**:30

Z. MIGICOVSKY, J. SAWLER, D. MONEY, R. EIBACH, A. J. MILLER, J. L. LUBY, A. R. JAMIESON, D. VELASCO, S. VON KINTZEL, J. WARNER, W. WÜHRER, P. J. BROWN, S. MYLES (2016) Genomic Ancestry Estimation Quantifies Use of Wild Species in Grape Breeding *BMC Genomics* **17**:478

Z. MIGICOVSKY, K. GARDNER, D. MONEY, J. SAWLER, J. BLOOM, P. MOFFETT, C. T. CHAO, H. SCHWANINGER, G. FAZIO, G.-Y. ZHONG, AND S. MYLES (2016) Genome to phenome mapping in apple using historical data *The Plant Genome* **9**:

**D. MONEY, K. GARDNER, Z. MIGICOVSKY, H. SCHWANINGER, G-Y. ZHONG, AND S. MYLES (2015)** LinkImpute: Fast and Accurate Genotype Imputation for Non-Model Organisms *G3: Genes, Genomes, Genetics* **5**:2383-2390

**D. MONEY AND S. WHELAN (2015)** GeLL: a generalized likelihood library for phylogenetic models *Bioinformatics* **31**:2391-2393

**K. A. McCLURE, J. SAWLER, K. M. GARDNER, D. MONEY, AND S. MYLES (2015)** Genomics: A potential panacea for the perennial problem *American Journal of Botany* **101**:1780–1790

**R. M. AMES, D. MONEY, AND S. C. LOVELL (2014)** Inferring Gene Family Histories in Yeast Identifies Lineage Specific Expansions *PLoS One* **9**:e99480

**D. MONEY AND S. WHELAN (2012)** Characterizing the Phylogenetic Tree-Search Problem *Systematic Biology* **61**:228–239

**R. M. AMES, D. MONEY, V. P. GHATGE, S. WHELAN, AND S. C. LOVELL (2012)** Determining the evolutionary history of gene families *Bioinformatics* **28**:48–55

**S. WHELAN AND D. MONEY (2010)** The Prevalence of Multifurcations in Tree-space and Their Implications for Tree-search *Molecular Biology and Evolution* **27**:2674-2677

## Presentations

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### Selected Conference Talks.....

**D. MONEY AND M. T. HOLDER (2012)** Detecting and correcting alignment over compression *Society for Molecular Biology and Evolution Annual Conference* in Dublin, Ireland  
Travel reward recipient

### Selected Conference Posters.....

**D. MONEY, R. ANTOLIN, G. GORJANC, J. M. HICKEY (2017)** AlphaPhase: Enabling phasing in very large populations *Gordon Research Conference on Quantitative Genetics & Genomics* in Galveston, Texas, United States

**D. MONEY, K. M. GARDNER AND S. MYLES (2015)** LinkImpute - a new, fast and accurate imputation method for non-model organisms *Society for Molecular Biology and Evolution Annual Conference* in Vienna, Austria

**D. MONEY, K. M. GARDNER AND S. MYLES (2014)** Exploiting the full potential of next-generation DNA sequencing through genotype imputation *Evolution* in Raleigh, North Carolina, United States

**D. MONEY AND M. T. HOLDER (2013)** Using phylogenetic gap models to detect alignment over-compression *Evolution* in Snowbird, Utah, United States

**D. MONEY AND S. WHELAN (2010)** The prevalence of multifurcations in tree-space and their implications for tree-search *Society for Molecular Biology and Evolution Annual Conference* in Lyon, France

## Software

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### LinkImputeR

Money *et al.* (2017)

<http://www.cultivatingdiversity.org/software/>  
A genotype imputation tool for read count data.

### LinkImpute

Money *et al.* (2015)

<http://www.cultivatingdiversity.org/software/>  
A genotype imputation tool.

### GeLL

Money and Whelan (2015)

<http://phylo.bio.ku.edu/GeLL/>  
A Java library for general likelihood calculations.

### Dupliphly-ML

Ames *et al.* (2012)

<http://kumiho.smith.man.ac.uk/dupliphly/>  
A tool for modelling gene family size evolution.

## References

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### John Hickey

University of Edinburgh  
john.hickey@roslin.ed.ac.uk  
+44 131 651 9100  
Post-doc Advisor

### Sean Myles

Dalhousie University  
seanmichaelmyles@dal.ca  
+1-902-690-7093  
Post-doc Advisor

### Mark Holder

University of Kansas  
mtholder@ku.edu  
+1-785-864-5789  
Post-doc Advisor