

DOMINIC JOHN BENNETT

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Adept software developer/engineer, researcher and data analyst with demonstrated history in industry and academia.

7+ years of experience in software development and engineering, statistics, data analysis, (bio-)informatics as well as technical writing and public speaking; able to work independently as well as in a team; worked as professional scrum master for global software company; proven track-record in academia with multiple published scientific articles and open-source software packages; developer of own reproducible, analytical workflows; trained in the life sciences with first-hand experience with large “omic” datasets.

Experience

- 2020 - Present Cloud native software engineer | Scrum Master
A series of work packages in networking and security for the 5G packet cloud core. Experience includes updating network interfaces to IPv6 and; developing a new microservice to enable the use of Trusted Execution Environments across a network cluster. Ericsson, Gothenburg, Sweden.
- 2019 - Present Software developer, consultant
[Layer10](#), Gothenburg, Sweden
- 2017 - 2019 Postdoctoral researcher | Open-source developer
Developing a modular pipeline for automated phylogeny generation in R, University of Gothenburg & [Gothenburg Global Biodiversity Centre](#), Sweden.
- 2018 - Present Open-source code reviewer
R package reviewer for [ROpenSci](#)
- 2015 - 2017 Online resources coordinator
Quantitative Ecology Special Interest Group, British Ecological Society.
- 2012 Text-mining research intern for the pharmaceutical industry
Nucleotide sequence discovery in scientific and legal texts. Linguamatics, Cambridge, U.K.
- 2010 - 2011 Researcher in population genetics
*Population genetics of fungus, *Microbotryum*. Université Paris-Sud, Paris, France.*
- 2009 Conservation volunteer
Field experience in the rainforest with Operation Wallacea. Buton Island, Sulawesi, Indonesia.

Education

- 2013 - 2017 **PhD** in Evolutionary Biology and Palaeobiology
 Title: “An appraisal of the Living Fossil Concept”, [link](#).
Imperial College London & Zoological Society of London, U.K.
- 2012 - 2013 **MRes** in Genomics and Biodiversity Informatics, Distinction
 Title: “Testing for Non-random Phylogenetic Responses to Urbanisation Using Mass Phylogeny Estimation”.
Imperial College London, U.K.
- 2008 - 2012 **BSc** in Biology with French for Science, First Class Honours
 Final year thesis title: “Evolution of the Yeast Metabolome”.
Imperial College London, U.K. & Université Paris-Sud, France
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Skills

Computer

- Languages* R, python, go, C++, C, ttcn
- Tools/Frameworks* git, Docker, kubernetes, helm, apache spark
- Engineering* Design architecture, pipeline development, unit and functional testing
- CI/CD* Jenkins, Travis-CI, AppVeyor
- Other* LINUX, UNIX, HPC facility, Google Cloud

Human

- Management* Agile development, scrum
- Academic articles* 7 first-authorships, 9 co-authorships
- Communication* Technical writing, proofreading, teaching, presenting and public speaking
- Languages* French (C2), Swedish (B1), Spanish (A2) and Japanese (A2)
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Open-Source Software

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|----------|--|---|--------|
| outsider | Install and run programs, outside of R, inside of R | CRAN , ROpenSci | R |
| restez | Create and query a local copy of GenBank in R | CRAN , ROpenSci | R |
| phylotaR | An automated pipeline for retrieving orthologous DNA sequences from GenBank | CRAN , ROpenSci | R |
| treeman | Intuitive manipulation of phylogenetic trees in R | CRAN , GitHub | R, C |
| TNR | Resolution of taxonomic names in python | PyPi , GitHub | python |
| pG-lt | An automated pipeline for converting taxonomic names into phylogenetic trees | PyPi , GitHub | python |

Selected Publications

outsider: Install and run programs, outside of R, inside of R	2020	Bennett, D.J., Hettling, H., Silvestro, D. et al.	JOSS
How the Past Impacts the Future: Modelling the Performance of Evolutionarily Distinct Mammals through Time.	2019	Bennett, D.J., Sutton, M.D. & Turvey, S.T.	Phil. Trans. B.
Quantifying the living fossil concept	2018	Bennett, D.J., Sutton, M.D. & Turvey, S.T.	Palaeontology Electronica
phylotaR: An automated pipeline for retrieving orthologous DNA sequences from GenBank in R	2018	Bennett, D.J., Hettling, H., Silvestro, D. et al.	Life
restez: Create and Query a Local Copy of GenBank in R.	2018	Bennett, D.J., Hettling, H., Silvestro, D. et al.	JOSS
Evolutionarily distinct "living fossils" require both lower speciation and lower extinction rates	2017	Bennett, D.J., Sutton, M.D. & Turvey, S.T.	Paleobiology
treeman: an R package for efficient and intuitive manipulation of phylogenetic trees	2017	Bennett, D.J., Sutton, M.D. & Turvey, S.T.	BMC research notes

Public presentations

The evolutionary potential of 'living fossils'	2019	Royal Society, link .
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References

Mark D. Sutton

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Imperial College London

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Institute of Zoology, London

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