

# DOMINIC JOHN BENNETT

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Adept data scientist, software developer and researcher with a demonstrated history in industry and academia.

7+ years of experience in software development, 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.

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## Experience and Education

2020 - Present Cloud native software engineer | Scrum master

*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.*

*Tech/skills* C++, C, go, docker, kubernetes, helm, git, agile, CI, software-testing (UT, FT)

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2019 - Present Software developer, consultant

*[Layer10](#), Gothenburg, Sweden*

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2017 - 2019 Postdoctoral researcher in biodiversity/phylogenetics

*Developed a modular pipeline for automated phylogeny generation in R. Resulted in 3 published software packages. [University of Gothenburg](#) & [Gothenburg Global Biodiversity Centre](#), Sweden.*

*Tech/skills* R, git, CI, docker, bioinformatics, phylogenetics, biodiversity, technical writing, teaching, presenting

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2017 - 2019 Open-source code reviewer/contributor

*R package reviewer and contributor for/to [ROpenSci](#)*

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2013 - 2017 **PhD** in Evolutionary Biology and Palaeobiology

*3 published papers, 1 published software package. Thesis title: “An appraisal of the Living Fossil Concept”, [link](#). [Imperial College London](#) & [Zoological Society of London](#), U.K.*

*Tech/skills* Data analysis, statistics, R, C, python, git, CI, phylogenetics, technical writing, teaching, presenting

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2015 - 2017 Online resources coordinator

*Quantitative Ecology Special Interest Group, [British Ecological Society](#).*

*Tech/skills* Web development, presenting

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2012 - 2013	<b>Masters</b> in Genomics and Biodiversity Informatics, Distinction Title: "Testing for Non-random Phylogenetic Responses to Urbanisation Using Mass Phylogeny Estimation". <i>Imperial College London, U.K.</i>
<i>Tech/skills</i>	R, python, data analysis, statistics, HPC, ecology, conservation biology, genomics, bioinformatics, phylogenetics, technical writing, teaching, presenting
2012	Text-mining research intern for the pharmaceutical industry <i>Nucleotide sequence discovery in scientific and legal texts. Linguamatics, Cambridge, U.K.</i>
2008 - 2012	<b>BSc</b> in Biology with French for Science, First Class Honours Final year thesis title: "Evolution of the Yeast Metabolome". <i>Imperial College London, U.K. &amp; Université Paris-Sud, France</i>
2010 - 2011	Researcher in population genetics <i>Population genetics of fungus, Microbotryum. Université Paris-Sud, Paris, France.</i>
2009	Conservation volunteer <i>Field experience in the rainforest with Operation Wallacea. Buton Island, Sulawesi, Indonesia.</i>

## Skills

<i>Software</i>	R, python, go, C++, C, ttcn, git, Docker, kubernetes, helm, apache spark, Jenkins, Travis-CI, AppVeyor, LINUX, UNIX, HPC facility, Google Cloud, design architecture, pipeline development, unit and functional testing
<i>Other</i>	Statistics, data analysis, technical writing, proofreading, teaching, presenting and public speaking, agile development

## Open-Source Software

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

## Selected Publications

outsider: Install and run programs, outside of R, inside of R	2020	Bennett, D.J., Hettling, H., Silvestro, D. et al.	<a href="#">JOSS</a>
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.	<a href="#">Phil. Trans. B.</a>

Quantifying the living fossil concept	2018	Bennett, D.J., Sutton, M.D. & Turvey, S.T.	<a href="#">Palaeontologia Electronica</a>
phylotaR: An automated pipeline for retrieving orthologous DNA sequences from GenBank in R	2018	Bennett, D.J., Hettling, H., Silvestro, D. et al.	<a href="#">Life</a>
restez: Create and Query a Local Copy of GenBank in R.	2018	Bennett, D.J., Hettling, H., Silvestro, D. et al.	<a href="#">JOSS</a>
Evolutionarily distinct "living fossils" require both lower speciation and lower extinction rates	2017	Bennett, D.J., Sutton, M.D. & Turvey, S.T.	<a href="#">Paleobiology</a>
treeman: an R package for efficient and intuitive manipulation of phylogenetic trees	2017	Bennett, D.J., Sutton, M.D. & Turvey, S.T.	<a href="#">BMC research notes</a>

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## Public presentations

The evolutionary potential of 'living fossils'	2019	Royal Society, <a href="#">link</a> .
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## References

Mark D. Sutton

*Former PhD supervisor*

Senior Lecturer in Palaeontology,  
Imperial College London

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Samuel T. Turvey

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Institute of Zoology, London

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