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, 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 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. <u>Ericsson</u>, Gothenburg, Sweden.	
Tech/skills	C++, C, go, docker, kubernetes, helm, git, agile, CI, software-testing (UT, FT)	
2019 - *Present*	**Software developer, consultant**	
	<u>Layer10</u>, Gothenburg, Sweden	
2017 - 2019	**Postdoctoral researcher in biodiversity/phylogenetics**	
	Developed a modular pipeline for automated phylogeny generation in R. Resulted in 3 published software packages. <u>University of Gothenburg</u> & <u>Gothenburg Global Biodiversity Centre</u>, Sweden.	
Tech/skills	R, git, CI, docker, bioinformatics, phylogenetics, biodiversity, technical writing, teaching, presenting	
2017 - 2019	**Open-source code reviewer/contributor**	
	R package reviewer and contributor for/to <u>ROpenSci</u>	
2013 - 2017	**PhD** in Evolutionary Biology and Palaeobiology	
	3 published papers, 1 published software package. Thesis title: "An appraisal of the Living Fossil Concept", <u>link</u>. Imperial College London & Zoological Society of London, U.K.	
Tech/skills	Data analysis, statistics, R, C, python, git, CI, phylogenetics, technical writing, teaching, presenting	
2015 - 2017	**Online resources coordinator**	
	Quantitative Ecology Special Interest Group, British Ecological Society.	
Tech/skills	Web development, presenting	

2012 - 2013	**Masters** in Genomics and Biodiversity Informatics, Distinction
	Title: "Testing for Non-random Phylogenetic Responses to Urbanisation Using Mass Phylogeny Estimation". *Imperial College London, U.K.*
Tech/skills	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
	Nucleotide sequence discovery in scientific and legal texts. Linguamatics, Cambridge, 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*
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.

Skills

Software	R, python, golang, 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
Other	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	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.	[Palaeontologia 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](#).

References

Mark D. Sutton

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Samuel T. Turvey

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