DOMINIC JOHN BENNETT

Details: dominic.john.bennett@gmail.com   //   + 46 76 88 38 66 4   //   Irish/British

Web: dominicjbennett.com // GitHub // Google Scholar // LinkedIn

Address: Nils Dahlbecks gata 5, lgh. 1401, Göteborg, 412 49 Sweden

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

8+ years of experience in software development, statistics, data analysis, bioinformatics 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 first-/co-authored 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; proven ability to transition to new domains and learn new technologies and techniques.

Experience and Education

2020 - *Present*	**Cloud-native developer | Scrum master** *Developer with a focus on implementation in networking and security for the 5G packet cloud core. Experience includes updating network interfaces to IPv6 and; developing a new golang-based security microservice. Ericsson, Gothenburg, Sweden.*
Tech/skills	C++, C, golang, docker, kubernetes, helm, postgreSQL, git, agile, CI, testing
2019 - *Present*	**Software developer, consultant** *Layer10, Gothenburg, Sweden*
2017 - 2019	**Postdoctoral researcher in bioinformatics/biodiversity** *Bioinformatician/ developer. Developed a modular pipeline for automated phylogeny generation in R which resulted in 3 published software papers/packages. Additionally, worked alongside lab members on a range of tasks – plant genomics, environmental sequencing, biodiversity informatics – all resulting in co-authorships. University of Gothenburg & Gothenburg Global Biodiversity Centre, Sweden.*
Tech/skills	R, python, git, CI, docker, bioinformatics, genomics, metagenomics, NGS, phylogenetics, biodiversity, technical writing, teaching, presenting
2017 - 2019	**Open-source code reviewer and contributor** *R package reviewer and contributor for/ to ROpenSci*
2013 - 2017	**PhD** in Evolutionary Biology *Researcher using species-level phylogenies to infer evolutionary history, resulted in 3 published papers and 1 published software package. Thesis "An appraisal of the Living Fossil Concept", link. Additionally, collaborations in bioinformatics and data analysis led to co-authorships. Imperial College London & Zoological Society of London, U.K.*
Tech/skills	Data analysis and visualisation, statistics, simulation, bioinformatics, alignment, phylogenetics, taxonomy, R, C, python, git, CI, high-performance computing, 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*
	Thesis project on using large numbers of estimated phylogenies to determine impact of urbanisation on biodiversity across the globe. Work led to co-authorship on a Nature paper. *Imperial College London, U.K.*
Tech/skills	R, python, data analysis and visualisation, statistics, 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*
	Thesis project on metabolomics of years. *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 rainforest with Operation Wallacea. *Buton Island, Sulawesi, Indonesia.*

Skills and Knowledge

Computing	R, python, golang, C++, C, ttcn, git, Docker, kubernetes, helm, shiny, apache spark, Jenkins, Travis-CI, AppVeyor, LINUX, UNIX, HPC facility, Google Cloud, design architecture, pipeline development, unit, signal-flow and functional testing
Bioinformatics	Sequence homology and alignment, phylogenetics, GenBank, NGS, phylogenetics, taxonomy, systematics, natural language processing, fossil-calibration, genomics, metagenomics
Other	Data analysis and visualisation, statistics, simulation, macro-ecological/evolutionary analysis, R analysis, technical writing, proofreading, teaching, presenting and public speaking, agile development

First-Authored 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](#)

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 Presentations/Workshops

The Evolutionary Potential of 'Living Fossils'	2019	Royal Society, London, [link](#).
Workshop: Automated Phylogenetics Pipeline	2019	University of Gothenburg/University of Aarhus, [link](#)
A supersmartR Way to an Automated Phylogenetics Pipeline	2018	Arnold Arboretum, Harvard University
Wikithon: Quantitative Ecology Documentation (QED)	2016	British Ecological Society Annual Meeting, Liverpool
The Evolutionary Potential of 'Living Fossils'	2015	Institute of Zoology Student Conference, London
Phylogenetic non-randomness in the responses of biodiversity to human impacts: a global analysis of local responses	2013	International Ecology Conference, London

References

Mark D. Sutton

Former PhD supervisor

Senior Lecturer in Palaeontology,
Imperial College London

m.sutton@imperial.ac.uk

Samuel T. Turvey

Former PhD supervisor

Professor of Zoology,
Institute of Zoology, London

samuel.turvey@ioz.ac.uk