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

---

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

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*

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

Title	Year	Authors	Journal
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	Samuel T. Turvey
Former PhD supervisor	*Former PhD supervisor*
Senior Lecturer in Palaeontology, Imperial College London	Professor of Zoology, Institute of Zoology, London
m.sutton@imperial.ac.uk	samuel.turvey@ioz.ac.uk