DOMINIC JOHN BENNETT

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

6+ years of experience in statistics, data analysis, (bio-)informatics as well as technical writing, languages and public speaking.

Experience

2017 - *Present*   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, https://ropensci.org/

2015 - 2017   Online resources coordinator
Quantitative Ecology Special Interest Group, British Ecological Society.

2012   Text-mining research intern
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 rainforest with Operation Wallacea. Buton Island, Sulawesi, Indonesia.

Education

2013 - 2017   **PhD** in Evolutionary Biology and Palaeobiology
Imperial College London & Zoological Society of London, U.K.

2012 - 2013   **MRes** in Genomics and Biodiversity Informatics, Distinction
Imperial College London, U.K.

2008 - 2012   **BSc** in Biology with French for Science, First Class Honours
Imperial College London, U.K. & Université Paris-Sud, France

Skills

Computer

Primary   R and python

Secondary   C, Java, SQL, HTML, CSS, Javascript, Perl, MatLab and Ruby

Other   LINUX, UNIX, HPC facility, docker, Git, Travis-CI, Coveralls, Jekyll, Hugo

Human

Academic articles	6 first-authorships, 8 co-authorships
Communication	Technical writing, creative writing, proofreading, teaching, presenting and public speaking
Languages	French (C2), Swedish (B1), Spanish (A2) and Japanese (A2)

Selected Software

outsider	Install and run programs, outside of R, inside of R	GitHub	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

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

References

Alexandre Antonelli	Mark D. Sutton	Samuel T. Turvey
Director of Science, Royal Botanic Gardens, Kew	Senior Lecturer in Palaeontology, Imperial College London	Professor of Zoology, Institute of Zoology, London
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