

University of Groningen

Inferring the drivers of species diversification

Richter Mendoza, Francisco

DOI:
[10.33612/diss.167307789](https://doi.org/10.33612/diss.167307789)

IMPORTANT NOTE: You are advised to consult the publisher's version (publisher's PDF) if you wish to cite from it. Please check the document version below.

Document Version
Publisher's PDF, also known as Version of record

Publication date:
2021

[Link to publication in University of Groningen/UMCG research database](#)

Citation for published version (APA):
Richter Mendoza, F. (2021). *Inferring the drivers of species diversification: Using statistical network science*. [Thesis fully internal (DIV), University of Groningen]. University of Groningen.
<https://doi.org/10.33612/diss.167307789>

Copyright

Other than for strictly personal use, it is not permitted to download or to forward/distribute the text or part of it without the consent of the author(s) and/or copyright holder(s), unless the work is under an open content license (like Creative Commons).

The publication may also be distributed here under the terms of Article 25fa of the Dutch Copyright Act, indicated by the "Taverne" license. More information can be found on the University of Groningen website: <https://www.rug.nl/library/open-access/self-archiving-pure/taverne-amendment>.

Take-down policy

If you believe that this document breaches copyright please contact us providing details, and we will remove access to the work immediately and investigate your claim.

Downloaded from the University of Groningen/UMCG research database (Pure): <http://www.rug.nl/research/portal>. For technical reasons the number of authors shown on this cover page is limited to 10 maximum.

Inferring the drivers of species diversification

using statistical network science

Francisco Richter

Cover design: Jorge Peña



university of
 groningen

Inferring the drivers of species diversification

using statistical network science

PhD thesis

to obtain the degree of PhD at the
 University of Groningen
 on the authority of the
 Rector Magnificus Prof. C. Wijmenga
 and in accordance with
 the decision by the College of Deans.

This thesis will be defended in public on

Friday 23 Apr 2021 at 14:30 hours

by

Francisco Javier Richter Mendoza

born on 08 August 1986
 in Las Condes, Chile

Promotors

Prof. E. C. Wit
Prof. R. S. Etienne

Assessment Committee

Prof. Alexei Drummond
Prof. Marco Grzegorzcyk
Prof. Veronica Vinciotti

To Clemente and Manu

CONTENTS

1	Introduction	1
1.1	Species diversification models	2
1.1.1	Diversity-dependent diversification models and the effect of ecological interactions on macroevolutionary processes	3
1.1.2	Example	4
1.2	The mode and tempo of diversification processes.	6
1.3	Statistical methodologies	8
1.3.1	The likelihood approach	8
1.3.2	EM algorithm	9
1.3.3	Monte-Carlo	9
1.3.4	Importance sampling and data augmentation	9
1.3.5	Stochastic gradient descent method	10
1.3.6	Generalised additive models	10
1.4	The conditioned evolutionary process	11
1.5	Model selection	11
1.6	Outline of the thesis.	13
2	Introducing a general class of species diversification models for phylogenetic trees	15
2.1	Introduction	17
2.2	A general diversification model	18
2.3	MLE inference with MCEM using importance sampling	20
2.3.1	Difficulties of MLE estimation and an MCEM algorithm	20
2.3.2	A simple importance sampler	22
2.3.3	Checking performance by comparing with direct ML	24
2.4	Diversity-dependence: diversity or phylodiversity?	26
2.5	Discussion	27
3	Detecting phylodiversity-dependent diversification with a novel phylogenetic inference framework	29
3.1	Introduction	31
3.2	Diversity-Dependent Diversification Models	32
3.3	Materials and Methods	33
3.3.1	Diversification of species as a point process	34
3.3.2	The EMPHASIS Statistical Framework	35
3.3.3	Augmentation of observed trees, a novel importance sampler for phylogenetic inference.	36
3.3.4	Model Selection	43

3.4	Application	44
3.4.1	Monte-Carlo approximation with the proposed importance sampler	44
3.4.2	Estimation and model selection	47
3.5	Discussion	48
4	Lineage-dependent phylogenetic diversity as a driver of species diversification	51
4.1	Introduction	53
4.2	Mode and tempo in evolutionary processes and real phylogenies.	54
4.3	The phylogenetic-diversity matrix in LID models	57
4.3.1	Phylogenetic diversity	57
4.3.2	The LID models	58
4.4	Parameter estimation	59
4.5	Summary	62
5	Approximating the probability of conditioning events in species diversification models using generalised additive models	63
5.1	Introduction	65
5.2	Material and methods.	65
5.2.1	Simulation	66
5.2.2	Estimation	66
5.3	Application	67
5.4	Discussion	72
6	Further considerations regarding species diversification modelling	73
6.1	Limitations in systematic biology and directions for improvement	74
6.1.1	Incomplete sampling and different levels of organisms	74
6.1.2	Extinction dynamics	75
6.1.3	Implementing the general class of models	75
6.2	Directions for statistical methods	75
6.3	Evolutionary trees applications, beyond biology	77
6.4	Network sciences applications, beyond trees	78
	References	79