

Jarrett D. Phillips, Ph.D.
Adjunct Professor
School of Computer Science
Department of Integrative Biology
Department of Population Medicine
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ACADEMIC APPOINTMENTS

Adjunct Professor, School of Computer Science
University of Guelph

2023

EDUCATION

My university education has primarily focused on the use of computational statistical approaches to solve open problems in biodiversity science and conservation, with an overarching theme of aiding rapid specimen identification and species discovery in academic, applied, and regulatory settings using DNA-based techniques such as DNA barcoding.

Ph.D. in Computational Sciences, University of Guelph

2016-2022

Co-Advisors: Dr. Daniel Gillis and Dr. Robert Hanner

Advisory Committee Members: Dr. Deborah Stacey and Dr. Graham Taylor

Thesis: A Novel Statistical Framework for Assessment of Intraspecific Haplotype Sampling Completeness: Implications for DNA Barcode Gap Estimation

Master of Bioinformatics (MBinf.), University of Guelph

2013-2014

Co-Advisors: Dr. Robert Hanner and Dr. Daniel Ashlock

Thesis: Assessing DNA Barcode Haplotype Sampling Diversity in the Ray-finned Fishes (Chordata: Actinopterygii)

BSc. (Hons.) in Biological Science, University of Guelph

2009-2013

Coursework in bioinformatics, ecology, evolutionary biology, comparative physiology, mathematics, and statistics

RESEARCH EXPERIENCE

I bring extensive past research experience in the use of bioinformatics, computational, mathematical, and statistical tools for the analysis of a wide range of big data in the biological sciences.

Postdoctoral Fellow

2023-Present

University of Guelph

GBADs Informatics Team

Stacey Lab, School of Computer Science

Bernardo Lab, Department of Population Medicine

Supervisors: Drs. Deborah Stacey and Theresa Bernardo

- Development of an R package to run a compartmentalized equation-based Dynamic Population Model (DPM) for the Global Burden of Animal Diseases (GBADs) initiative to calculate the Animal Health Loss Envelope (AHLE) in livestock species

Postdoctoral Fellow

2023-Present

University of Guelph

Gillis Lab, School of Computer Science

Hanner Lab, Department of Integrative Biology

Supervisors: Drs. Daniel Gillis and Robert Hanner

- Developed a Bayesian hierarchical binary logistic time-series regression model and a R Shiny dashboard of seafood fraud in the Canadian supply chain
- Mentored and supervised an undergraduate STAT*4600/CIS*4900/CIS*4910 student and an Undergraduate Research Assistant (URA) working to develop models in R, Stan, and Shiny

Postdoctoral Fellow

2022

University of Guelph

Hanner Lab, Department of Integrative Biology

Supervisor: Dr. Robert Hanner

- Mentored and supervised a Master of Bioinformatics (MBINF.) BINF*6999 student on research project examining DNA barcoding in Canadian pests and disease vectors
- Participated in conceptualization and drafting of various manuscripts and invited book chapters

Summer Research Assistant

2016

Algoma University

Plant and Soil Ecology Lab, Department of Biology

Invasive Species Research Institute (ISRI)

Supervisor: Dr. Pedro Antunes

- Offered bioinformatics and statistical analysis support in R
- Assisted Principal Investigator and undergraduate thesis student with initial drafting of a manuscript on invasive plant root lesion staining quantification

Lab Assistant Volunteer

2014-2016

Algoma University
Plant and Soil Ecology Lab, Department of Biology
Invasive Species Research Institute (ISRI)
Supervisor: Dr. Pedro Antunes

- Offered bioinformatics and statistical analysis support in R
- Assisted with collaborative and outreach initiatives for the Terrestrial Invasive Plant Species (TIPS) Network Project through drafting communication letters to public and private conservation agencies across Canada and the USA seeking volunteers to collect invasive plant species for root lesion quantification

Undergraduate Research Assistant

2013

University of Guelph
Vaccine Discovery Research Group
Supervisor: Dr. Mario Monteiro

- Performed various experimental techniques (gas chromatography-mass spectrometry (GC-MS) and Nuclear Magnetic Resonance (NMR)) on bacterial polysaccharide samples for vaccine synthesis and development under the supervision of qualified graduate students

TEACHING EXPERIENCE

In addition to co-teaching three undergraduate courses, I was directly involved in grading assignments, creating course outlines and lab content, as well as materials for midterms and final exams.

Graduate Teaching Assistant (GTA)

2016-2020

University of Guelph

CIS*3130 – System Modelling and Simulation

2020

~ 30 students · Python

- Statistical and Monte Carlo methods

CIS*1910 – Discrete Structures in Computing I

2017

~ 300 students (~ 40 students per section)

- Deductive logic, set theory, and mathematical proof techniques

CIS*2460 – Modelling of Computer Systems

2016-2019

~ 60 students · R, Excel, Java

- Statistical and Monte Carlo methods

STUDENT SUPERVISION AND MENTORSHIP

I have either directly or indirectly supervised and mentored 16 undergraduate/graduate students in the School of Computer Science, the Department of Mathematics and Statistics, and the Department of Integrative Biology, all of whom are, or will be, coauthors on my publications. My primary role has been to guide students through the entire scientific process (*i.e.*, formulating research questions, designing, and setting up experiments to test hypotheses, collecting data and analyzing results and writing the

manuscript drafts), among other responsibilities, such as providing feedback on students' draft reports/manuscripts. Students completed research both as part of a course and as lab volunteers.

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| Nikolett Toth (with Dan Gillis) University of Guelph Summer Undergraduate Research Assistant (URA) · Mining association rules for eDNA spatiotemporal sampling | 2024 |
| Nathan Zeinstra (with Dirk Steinke) University of Guelph IBIO*6070 · Habitat occupancy modelling of sea lamprey environmental DNA | 2024 |
| Fynn De Vuono-Fraser (with Dan Gillis) University of Guelph CIS*4910 · Bayesian modelling of seafood fraud in the Canadian supply chain | 2024 |
| Fynn De Vuono-Fraser (with Dan Gillis) University of Guelph CIS*4900 · Bayesian modelling of seafood fraud in the Canadian supply chain | 2023 |
| Zaid Al-Gayyali (with Dan Gillis) University of Guelph Summer Undergraduate Research Assistant (URA) · Seafood Fraud Visualization Tool Shiny app | 2023 |
| Fynn De Vuono-Fraser (with Dan Gillis) University of Guelph STAT*4600 · Bayesian modelling of seafood fraud in the Canadian supply chain | 2023 |
| Amina Asif (with Bob Hanner) University of Guelph BINF*6999 · DNA barcode gap analysis of Canadian disease vectors and agricultural pests | 2022 |
| Navdeep Singh (with Dan Gillis) University of Guelph CIS*4900 · HACSim RShiny web application | 2021 |
| Maya Persram (with Bob Hanner) University of Guelph Hanner Lab volunteer · R reporting ecological meta-analysis | 2020-present |
| Ashley Chen (with Bob Hanner) University of Guelph Hanner Lab volunteer · R reporting ecological meta-analysis | 2020-present |
| Olivia Friesen Kroeker (with Bob Hanner) University of Guelph Hanner Lab volunteer · R reporting ecological meta-analysis | 2020-present |
| Scarlett Bootsma (with Dan Gillis) University of Guelph CIS*4900/4910 · HACSim simulation study | 2020-2021 |
| Christina Frangel (with Bob Hanner) University of Guelph BINF*6999 · DNA barcode sequence classification with machine learning | 2018-2019 |
| Jiaojia (Paula) Yu (with Bob Hanner) University of Guelph BINF*6999 · MDMAPR R Shiny app | 2018-2019 |

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| Danielle St. Jean (with Dan Gillis) University of Guelph MSc. thesis · DNA barcode sequence classification with machine learning | 2018-2019 |
| Steven French (with Dan Gillis) University of Guelph CIS*4900/4910 · HACSim R package | 2018 |
| Julia Harvie (with Bob Hanner) University of Guelph MCB*4500/4510 · Data mining GenBank and BOLD | 2018-2019 |
| Ankita Bhanderi (with Bob Hanner) University of Guelph BINF*6999 · Data mining GenBank and BOLD | 2018 |

ASSISTANTSHIPS, AWARDS, SCHOLARSHIPS AND GRANTS

Throughout my Ph.D. studies, I have been recognized and awarded numerous assistantships, awards, scholarships, and grants recognizing my research excellence and potential.

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| Food from Thought Advancing Research Impact (ARIF) Fund University of Guelph | 2022 \$30000.00 CAD |
| <ul style="list-style-type: none"> 1-year postdoctoral funding to develop a Bayesian hierarchical binary logistic time-series regression model of seafood fraud in the Canadian supply chain | |
| NSERC Postdoctoral Fellowship University of Waterloo | 2021 \$90000.00 CAD (not funded) |
| <ul style="list-style-type: none"> 2-year postdoctoral funding to develop an ensemble machine learning model for taxonomic classification of regulated species in Canada | |
| Guelph Institute for Environmental Research Small Grants Program (GIER SGP) University of Guelph | 2020 \$15000.00 CAD (not funded) |
| <ul style="list-style-type: none"> 1-year postdoctoral funding to develop a Bayesian hierarchical binary logistic time-series regression model of seafood fraud in the Canadian supply chain | |
| SoCS Travel Grant University of Guelph | 2019 \$1000.00 CAD |
| <ul style="list-style-type: none"> Supported travel to the 8th International Barcode of Life Conference in Trondheim, Norway to present doctoral research | |
| Arthur D. Latornell Graduate Travel Grant University of Guelph | 2019 \$500.00 CAD |
| <ul style="list-style-type: none"> Awarded for first-class academic standing in Ph.D. coursework Supported travel to the 8th International Barcode of Life Conference in Trondheim, Norway to present work related to resource management and conservation | |
| Graduate Teaching Assistantships University of Guelph | 2017-2020 \$34,506.00-35,148.00 CAD |
| Graduate Research Assistantships University of Guelph | 2017-2019 \$11,000.00 CAD |
| CPES Graduate Dean's Scholarship University of Guelph | 2017 \$3500.00 CAD |
| <ul style="list-style-type: none"> Awarded in recognition of achieving over 85% in Master's coursework | |

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| CPES Graduate Excellence Entrance (GEE) Scholarship | 2016 |
| University of Guelph | \$30000.00 CAD |
| <ul style="list-style-type: none"> Awarded in recognition of achieving over 85% in Master's coursework | |

ACADEMIC SERVICE

I have contributed to the growth of the SoCS through serving on two hiring panels for faculty positions in cybersecurity, specifically to support the new coursework-based Master of Cybersecurity and Threat Intelligence program. Duties included reviewing and ranking candidate applications, conducting in-person interviews, and hosting invited candidates for scheduled luncheons to meet with other faculty members.

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| School of Computer Science (SoCS) Search Committee | 2018 |
| University of Guelph | |
| <ul style="list-style-type: none"> Associate Professor position in cybersecurity | |
| School of Computer Science (SoCS) Search Committee | 2017-2018 |
| University of Guelph | |
| <ul style="list-style-type: none"> Two-year contractually-limited Assistant Professor position in cybersecurity | |

ACADEMIC PEER REVIEW SERVICE

I have served as a reviewer for numerous manuscripts in different journals, both alone or under the guidance of my Ph.D. supervisors.

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| <i>Ecology and Evolution</i> (2) | 2021-2022 |
| <i>F1000 Research</i> (1) | 2022 |
| <i>Frontiers in Ecology and Evolution</i> (2) | 2022 |
| <i>Lifestyle Genomics</i> (2) | 2022 |
| <i>Mitochondrial DNA Part A</i> (2) | 2023 |
| <i>Molecular Ecology Resources</i> (6) | 2019-2022, 2023 |
| <i>Molecular Biology Reports</i> (1) | 2020 |
| <i>Methods in Ecology and Evolution</i> (1) | 2020 |

PROCEEDINGS

I have presented or attended graduate research at national or international conferences and workshops, including both oral presentations and posters. Sessions listed here also include presentations by supervised undergraduate students.

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| GBADs Technical Workshop (oral presentation) | 2023 |
| University of Liverpool | |
| CEPS Student Research Day (student poster presentation) | 2023 |
| University of Guelph | |
| Pathway to Increase Standards and Competency of eDNA Surveys (PICSeS) | 2023 |
| International Conference (poster presentation) | |
| University of Guelph | |

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| 8th International Barcode of Life Conference (oral presentation) NTNU University Museum and Norwegian Biodiversity Information Centre | 2019 |
| Guelph BioMathematics and Statistics (BioM&S) Symposium Artificial Intelligence and Machine Learning in Biology (attended) University of Guelph | 2019 |
| CEPS Undergraduate Poster Session (student poster presentation) University of Guelph | 2018 |
| 7th International Barcode of Life Conference (oral presentation) University of Johannesburg | 2017 |
| 6th International Barcode of Life Conference (poster presentation) University of Guelph | 2015 |

SOFTWARE DEVELOPMENT

I have been directly or indirectly involved with the development and deployment of several R software package tools for molecular biodiversity analysis.

GBADs (**G**lobal **B**urden of **A**nimal **D**iseases) · R package

- A novel age- and sex-structured compartmentalized equation-based model to assess the burden of animal diseases in livestock such as cattle, small ruminants, and poultry within developing countries like Ethiopia

HACSim (**H**aplotype **A**ccumulation **C**urve **S**imulator) · R package · R Shiny web app

- A novel nonparametric stochastic (Monte Carlo) local search optimization method of iteratively generating species' haplotype accumulation curves through extrapolation to assess within-species sampling completeness
- R package and Shiny app respectively available for download through the Comprehensive R Archive Network ([CRAN](https://cran.r-project.org/)) package repository or at shinyapps.io
- Publication in *PeerJ Computer Science* was one of the top five most viewed papers in the category *Optimization Theory and Computation*
- Has been downloaded over 27000 times (c. 616 times per month) since being published in May 2019

VLF (**V**ery **L**ow **F**requency) · R package

- A tool to assess PCR errors, sequencing errors, *etc.* in the form of very low frequency variants, within DNA sequences using a sliding window approach
- R package available for download through [CRAN](https://cran.r-project.org/)
- Manuscript published in the *Biodiversity Data Journal*
- Has been downloaded over 35000 times (c. 208 times per month) since publication

REFEREED WORK

I have been directly or indirectly involved with the conceptualization, research, supervision, and eventual publication of several academic and non-academic projects.

Journal Articles

Citations: 161 · H-index: 5 (According to Google Scholar, as of January 17, 2024)

* Indicates students under my direct mentorship or supervision

** Indicates students under my indirect mentorship or supervision

Published or Accepted

7. **Phillips, J.D.** and *De Vuono-Fraser, F.A. Statistical modelling of seafood fraud in the Canadian supply chain. *bioRxiv*. <https://www.biorxiv.org/content/10.1101/2024.02.05.578947v1.abstract>.
6. **Phillips, J.D.**, Athey, T.B.T., Hanner, R.H. and McNicholas, P.D. VLF: An R package for the analysis of very low frequency variants in DNA sequences. *Biodiversity Data Journal*, e96480. DOI: [10.3897/BDJ.11.e98480](https://doi.org/10.3897/BDJ.11.e98480). Journal Impact Factor: 1.55.
5. **Phillips, J.D.**, Gillis, D.J. and Hanner, R.H. (2022). Lack of statistical rigor in DNA barcoding likely invalidates the presence of a true species' barcode gap. *Frontiers in Ecology and Evolution*, 10: 859099. DOI: [10.3389/fevo.2022.859099](https://doi.org/10.3389/fevo.2022.859099). Journal Impact Factor: 4.49. Number of article citations: 8.
4. D'Ercole, J., Dincă, V., Opler, P.A., Kondla, N.G., Schmidt, C.B., **Phillips, J.D.**, Robbins, R., Burns, J.M., Miller, S.E., Grishin, N., Zakharov, E.V., deWaard, J.R., Ratnasingham, S. and Hebert, P.D.N. (2020). A DNA barcode library for the butterflies of North America. *PeerJ*, 9: e11157. DOI: [10.7717/peerj.11157](https://doi.org/10.7717/peerj.11157). Journal Impact Factor: 3.06. Number of article citations: 13.
3. **Phillips, J.D.**, *French, S.H., Hanner, R.H. and Gillis, D.J. (2020). HACSim: An R package to estimate intraspecific sample sizes for genetic diversity assessment using haplotype accumulation curves. *PeerJ Computer Science*, 6(192): 1-37. DOI: [10.7717/peerj-cs.243](https://doi.org/10.7717/peerj-cs.243). Journal Impact Factor: 3.80. Number of article citations: 19.
2. **Phillips, J.D.**, Gillis, D.J. and Hanner, R.H. (2019). Incomplete estimates of genetic diversity within species: Implications for DNA barcoding. *Ecology and Evolution*, 9(5): 2996-3010. DOI: [10.1002/ece3.4757](https://doi.org/10.1002/ece3.4757). Journal Impact Factor: 3.17. Number of article citations: 87.
1. **Phillips, J.D.**, Gwiazdowski, R.A., Ashlock, D. and Hanner, R. (2015). An exploration of sufficient sampling effort to describe intraspecific DNA barcode haplotype diversity: examples from the ray-finned fishes (Chordata: Actinopterygii). *DNA Barcodes*, 3: 66-73. DOI: [10.1515/dna-2015-0008](https://doi.org/10.1515/dna-2015-0008). Number of article citations: 27.

Submitted or Under Revision

3. **Phillips, J.D.** and *De Vuono-Fraser, F.A. Statistical modelling of seafood fraud in the Canadian supply chain. Submitted to *Statistical Analysis and Data Mining*.
2. **Phillips, J.D.** and *De Vuono-Fraser, F.A. Swimming in uncertainty: How proper statistical modelling can help expose seafood product mislabelling. Submitted to *Significance*.
1. Raymond, K., Sobkowich, K.E., **Phillips, J.D.**, Nguyen, L., McKechnie, I., Mohideen, R.N., Fitzjohn, W., Szurkowski, M., Davidson, J., Rushton, J., Stacey, D.A. and Bernardo T.M. GBADs informatics strategy: User-centric tools, data quality, and model interoperability. Submitted to *WOAH Scientific and Technical Review*.

In Preparation or To Be Submitted

6. **Phillips, J.D.**, *Al-Gayyali, Z.B., *De Vuono-Fraser, F.A., Hanner, R.H. and Gillis, D.J. The Seafood Fraud Visualization Tool: An R Shiny web app to summarize, model, and visualize seafood mislabelling trends in the supply chain.

5. Morey, K.C., **Phillips, J.D.**, Loeza-Quintana, T. and Hanner, R.H. Haplotype diversity reveals challenges and opportunities for developing targeted detection assays for COI in Canadian freshwater fish. Targeted for *Environmental DNA*.
4. Young, R.G., **Persram, M., **Friesen, O., **Chen, A., **Yu, J., **Phillips, J.D.** and Hanner, R.H. (Under review). Incomplete and irregular reporting of the R statistical and computing environment highlights the need for citation guidelines to support scientific reproducibility. *PeerJ Computer Science*.
3. **Phillips, J.D.**, *Singh, N., Hanner, R.H. and Gillis, D.J. The HACSim R Shiny app: A web interface to estimate specimen sampling sufficiency for species genetic diversity assessment with DNA sequence data.
2. D'Ercole, J., Dapporto, L., **Phillips, J.D.**, Dincă, V.E., Vila, R., Talavera, G. and Hebert, P.D.N. Macrogenetics of North American butterflies—The impact of Quaternary climatic fluctuations. Targeted for *PNAS*.
1. **Phillips, J.D.**, *Bootsma, S.E., Hanner, R.H. and Gillis, D.J. Solving the genetic specimen sample size problem with a local search optimization algorithm. Targeted for *Methods in Ecology and Evolution*.

Book Chapters

Submitted or Under Revision

2. **Phillips, J.D.**, Griswold, C.K., Young, R.G., Hubert, N. and Hanner, R.H. A measure of the DNA barcode gap for applied and basic research. *Methods in Molecular Biology*. Springer.
1. Hubert, N., **Phillips, J.D.** and Hanner, R.H. Delimiting species with single-locus DNA sequences. *Methods in Molecular Biology*. Springer.

Conference Proceedings

4. Morey, K., Loeza-Quintana, T., **Phillips, J.** and Hanner R. (2023). Haplotype diversity reveals challenges and opportunities for developing targeted detection assays for *COI* in Canadian freshwater fish. Pathways to Increase Standards and Competency in eDNA Surveys (PISCeS) Conference. Poster.
3. **Phillips, J.D.**, Gillis, D. and Hanner, R. (2019). HACSim: Iterative extrapolation of haplotype accumulation curves for assessment of intraspecific COI DNA barcode sampling completeness Scientific abstracts from the 8th International Barcode of Life Conference, Trondheim, Norway (ed. Torbjørn Ekrem), *Genome*, 62(6): 349-453. Oral presentation.
2. **Phillips, J.D.**, Gillis, D. and Hanner, R. (2017). Intraspecific sample size estimation for DNA barcoding: Are current sampling levels enough? Scientific abstracts from the 7th International Barcode of Life Conference, Johannesburg, South Africa (ed. M. van der Bank), *Genome*, 60(11): 881-1019. Oral presentation.
1. **Phillips, J.D.**, Gwiazdowski, R.A., Ashlock, D. and Hanner, R. (2015). An exploration of sufficient sampling effort to describe intraspecific haplotype diversity in the ray-finned fishes (Chordata: Actinopterygii). Scientific abstracts from the 6th International Barcode of Life Conference, Guelph, ON., Canada (ed. S.J. Adamowicz), *Genome*, 58(5): 163-303. Poster

NON-REFEREED WORK

I have communicated aspects of my research to non-technical audiences through various online media, including blog posts and newsletters.

Blog posts

6. **Phillips, J.D.** (2022) Mind the Gap — The DNA Barcode Gap, That Is. Contributed CEPS Research Highlights article (<https://www.uoguelph.ca/ceps/news/2022/08/mind-gap—dna-barcode-gap>).
5. **Phillips, J.D.** (2020). Barcode Cracking. Contributed CEPS Research Highlights article (<https://www.uoguelph.ca/ceps/news/2020/02/barcode-cracking>).
4. **Phillips, J.D.** (2020). Protecting Biodiversity Through the Lens of Genetic Diversity. Contributed guest post to the blog of Dr. Daniel Gillis (<https://danielgillis.wordpress.com/2020/01/30/protecting-biodiversity-through-the-lens-of-genetic-diversity/>).
3. **Phillips, J.D.** (2019). IBOL8 and the Midnight Sun. Contributed guest post to the blog of Dr. Daniel Gillis (<https://danielgillis.wordpress.com/2019/07/02/reflections-ibol8-and-the-midnight-sun/>).
2. **Phillips, J.D.** (2017). The Big Five and IBOL7. Contributed guest post to the blog of Dr. Daniel Gillis (<https://danielgillis.wordpress.com/2017/12/06/reflections-the-big-five-and-ibol7/>).
1. **Phillips, J.D.** (2016). Sample size estimation for DNA barcoding: Are current sampling levels enough? Contributed guest post to the DNA Barcoding Blog of Dr. Dirk Steinke (<http://dna-barcoding.blogspot.com/2016/01/guest-post-sample-size-estimation-for.html>).

Newsletters

1. **Phillips, J.D.** (2016). Sample size estimation for DNA barcoding of ray-finned fishes: Are current sampling levels enough? Contributed newsletter article to the Barcode Bulletin, 7(1).

VOLUNTEER EXPERIENCE

I have volunteered in various capacities in the SoCS and the Department of Integrative Biology at the University of Guelph.

2. Pathways to Increase Standards and Competency in eDNA Surveys (PISCeS) Conference

University of Guelph

2023

- Participated in international eDNA conference hosted by the Hanner Lab
- Duties included registration, upload, and audiovisual support

1. Wireframing session

University of Guelph

2021

- Participated in student-led use case mobile app prototype demonstrations for CIS*3750 – System Analysis and Design in Applications
- Graded students based on several factors via Qualtrics surveys

REFERENCES

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