

Curriculum Vitae

Daniel Evans-Yamamoto, Ph.D.

Researcher
The Systems Biology Institute

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Homepage : <https://danyamamotoevans.github.io>

Education

- March 2024 Ph.D.
Systems Biology Program, Graduate school of Media and Governance, Keio University, Tokyo, Japan
Dissertation title: Characterizing protein evolution with systematic protein-protein interaction screenings
Supervisors: Drs. Christian R. Landry (Université Laval), Yasuhiro Naito (Keio University), Akio Kanai (Keio University), Haruo Suzuki (Keio University), and Masaru Tomita (Keio University)
- March 2020 Master of Media and Governance with a certificate in Systems Biology
Systems Biology Program, Graduate school of Media and Governance, Keio University, Tokyo, Japan
Thesis title: Pooled matrix screen of protein interactomes using Barcode Fusion Genetics-Protein fragment Complementation Assay (BFG-PCA)
Supervisors: Drs. Nozomu Yachie and Masaru Tomita
- March 2018 Bachelor of Arts in Environment and Information Studies with honor
Faculty of Environment and Information Studies, Keio University, Tokyo, Japan.
Thesis title: Development of high-throughput technologies to screen protein interactomes
Supervisors: Drs. Nozomu Yachie and Masaru Tomita

Research Experiences

November 2020–September 2023

Research Intern @Landry laboratory, Université Laval, Québec, Canada

Projects:

- 1- Characterization of function and protein interaction characters of orthologous genes
- 2- Characterization of protein-protein interaction characters of orthologous subunits in a protein complex

October 2014–March 2020

Visiting student @Yachie laboratory, the University of Tokyo, Tokyo, Japan

Projects:

- 1- Development of a plasmid based DHFR-PCA system
- 2- Implementation of Barcode Fusion Genetics to DHFR-PCA

Work Experiences

April 2024– Current

Researcher @Systems Biology Institute, Tokyo, Japan

Responsibilities and Achievements:

1. Project management
2. Bioinformatic pipeline construction

October 2023– March 2024

Adjunct researcher @Systems Biology Institute, Tokyo, Japan

Responsibilities and Achievements:

1. Project management
2. Bioinformatic pipeline construction

April 2020 – October 2023

Part-time visiting researcher @Systems Biology Institute, Tokyo, Japan

Responsibilities and Achievements:

1. Analysis of biomedical data
2. Literature search of academic publication and patent applications
3. Summarizing data analysis and literature search to reports

April 2018 – May 2020

Part-time researcher @Yachie laboratory, the University of Tokyo, Tokyo, Japan

Project: Development of a novel high-throughput binary protein-protein interaction detection method

Responsibilities and Achievements:

- 1- Implementation of plasmid system for the protein-protein interaction detection method DHFR-PCA
- 2- High throughput assay of the developed DHFR-PCA with DNA barcodes (Barcode Fusion Genetics-DHFR PCA)
- 3- Development of computational pipelines to analyze massively parallel sequencing data of DNA barcodes
- 4- Mentoring interns associated in the interactome project

Teaching Experience

1. 2020 Spring Semester
Lecturer, *Keio University SFC*, B3206: Data science for Genome Dynamics

Publications

Original Research Articles

Preprints and submitted manuscripts

10. S. Jiang[¶], **D. Evans-Yamamoto**[¶], D. Bersenev, S.K. Palaniappan, A. Yachie-Kinoshita "ProtoCode: Leveraging Large Language Models for Automated Generation of Machine-Readable Protocols from Scientific Publications", 11 December 2023 *arXiv* Available from : <https://arxiv.org/abs/2312.06241> (¶ equal contribution)

Peer-reviewed articles

9. **D. Evans-Yamamoto**, A.K. Dubé[¶], G. Saha[¶], S. Plante, D. Bradley, I. Gagnon-Arsenault, C.R. Landry "Parallel nonfunctionalization of CK1δ/ε kinase ohnologs following a whole-genome duplication event", (2023) *Molecular Biology and Evolution*, **40**(12):msad246. Doi: 10.1093/molbev/msad246 (¶ equal contribution)
8. Y. Kijima, **D. Evans-Yamamoto**, H. Toyoshima, N. Yachie "A universal sequencing read interpreter", (2023) *Science Advances*, **9**(1):eadd2793. Doi: 10.1126/sciadv.add2793
7. **D. Evans-Yamamoto**, F.D. Rouleau, P. Nanda, K. Makanae, Y. Liu, P.C. Després, H. Matsuo, M. Seki, A.K. Dube, D. Ascencio, N. Yachie & C.R. Landry "BFG-PCA: tools and resources that expand the potential for binary protein interaction discovery", (2022) *Nucleic Acids Research*, **50**(9):e54. Doi: 10.1093/nar/gkac045
6. G. Suzuki, Y. Saito, M. Seki, **D. Evans-Yamamoto**, M. Negishi, K. Kakoi, H. Kawai, C. Landry, N. Yachie & T. Mitsuyama "Machine learning approach for discrimination of genotypes based on bright-field cellular images", (2021) *npj Systems Biology and Applications*, 7:31. Doi: 10.1038/s41540-021-00190-w

5. Y. Murai, T. Masuda, Y. Onuma, **D. Evans-Yamamoto**, N. Takeuchi, H. Mori, N. Masuyama, S. Ishiguro, N. Yachie, K. Arakawa “Complete Genome Sequence of Bacillus sp. Strain KH172YL63, Isolated from Deep-Sea Sediment”, (2019) *Microbiology Resource Announcements*, **9**:e00291-20. Doi: 10.1128/MRA.00291-20
4. A. Marchant, A. Cisneros, A. Dube, I. Gagnon-Arsenault, D. Ascencio, H. Jain, S. Aube, C. Eberlein, **D. Evans-Yamamoto**, N. Yachie, C. Landry., “The role of structural pleiotropy and regulatory evolution in the retention of heteromers of paralogs”, (2019) *eLife*, **8**:e46754. Doi: 10.7554/eLife.46754
3. **D. Evans-Yamamoto**¶, N. Takeuchi¶, T. Masuda, Y. Murai, Y. Onuma, H. Mori, N. Masuyama, S. Ishiguro, N. Yachie, K. Arakawa”Complete Genome Sequence of Psychrobacter sp. Strain KH172YL61, Isolated from Deep-Sea Sediments in the Nankai Trough, Japan”, (2019) *Microbiology Resource Announcements*, **8**:e00326-19. Doi: 10.1128/MRA.00326-19 (¶ equal contribution)
2. H. Mori, **D. Evans-Yamamoto**, S. Ishiguro, M. Tomita, and N. Yachie., “Fast and global detection of periodic sequence repeats in large genomic resources”, (2018) *Nucleic Acid Research*, **47**(2):e8 Doi: 10.1093/nar/gky890
1. N. Yachie, Robotic Biology Consortium (**D. Evans-Yamamoto** was involved in the IT group), and T. Natsume., “Robotic Crowd Biology: LabDroids accelerates life science experiments”, (2017) *Nature Biotechnology*, **35**(4):310-312. Doi: 10.1038/nbt.3758

Reviews and Books

English

5. Charactrizing protein evolution with systematic protein-protein interaction screenings. Ed. Yasuhiro Naito (2024) Keio SFC academic society, SFC-DT 2023-002, ISBN 978-4-87762-432-3 **D. Evans-Yamamoto**

Japanese

4. 超生物学一次のX~私たちがいま手にしている細胞工学. 編集/谷内江 望, 2021年 羊土社, ISBN 978-4-7581-2252-8 谷内江 望, 増山 七海, 関元 元昭, **山本-エヴァンス 楠**, 石黒 宗, 森 秀人, 坂田 莉奈, 今野 直輝, 松尾 仁嗣 & 木島 佑輔.
3. 実験医学 別冊あなたのラボにAI×ロボットがやってくる 124-129 2017年 ”AI・LabDroidと交わす言葉をつくりだす” **山本-エヴァンス 楠** & 谷内江 望
2. バイオサイエンスとインダストリー 2017年 VOL.75 NO.1 解説記事 ”タンパク質間相互作用ネットワークの超高速マッピング” 増山七海・**山本-エヴァンス 楠**・谷内江 望
1. 医学のあゆみ 259巻 8号 2016年 11月 p.832-838 論文詳細 ”バーコードフュージョン遺伝学” **山本-エヴァンス 楠**・増山七海・谷内江 望

Conference presentations (Poster presentation)

10. **D. Evans-Yamamoto**, F. Rouleau, P. Nanda, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, N. Yachie and C. R. Landry. “Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA): tools and resources that expands the potential for binary protein interaction discovery”, *2022 Wellcome connecting science, Evolutionary Systems Biology*. February 10th, 2022
9. **D. Evans-Yamamoto**, F. Rouleau, P. Nanda, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, N. Yachie and C. R. Landry. “Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA): tools and resources that expands the potential for binary protein interaction discovery”, *2021 IBIS student day*. August 25th, 2021
8. **D. Evans-Yamamoto**, F. Rouleau, P. Nanda, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, C. R. Landry and N. Yachie. “Pooled matrix screen of protein interactomes using Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA)”, *2021 PROTEO symposium*. May 18th, 2021
7. **D. Evans-Yamamoto**, F. Rouleau, P. Nanda, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, C. R. Landry and N. Yachie. “Pooled matrix screen of protein interactomes using Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA)”, *2021 Cold Spring Harbor meeting: Network Biology*. (Virtual). March 17th, 2021
6. **D. Evans-Yamamoto**, P. Nanda, F. Rouleau, K. Makanae, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, M. Tomita, H. Aburatani, C. R. Landry and N. Yachie. “Pooled matrix screen of protein

interactomes using Barcode Fusion Genetics-Protein-fragment Complementation Assay (BFG-PCA)", *International Conference on Systems Biology 2019 (ICSB 2019)*. Okinawa, Japan. November 4th, 2019.

5. **D. Evans-Yamamoto**, P. Nanda, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, M. Tomita, H. Aburatani, C. R. Landry and N. Yachie, "Development of Barcode Fusion Genetics-DHFR PCA", *19th Symposium on Life Sciences of the University of Tokyo*, Tokyo, Japan. April 20th, 2019.
4. **D. Evans-Yamamoto**, P. Nanda, H. Matsuo, M. Seki, A. K. Dube, D. Ascencio, M. Tomita, H. Aburatani, C. R. Landry and N. Yachie, "Development of Barcode Fusion Genetics-DHFR PCA", *13th LSBM Symposium*, Hakone, Japan. April 3rd, 2019.
3. **D. Evans-Yamamoto**, P. Nanda, H. Matsuo, M. Seki, A. K. Dube, M. Tomita, H. Aburatani, C. R. Landry and N. Yachie, "Development of Barcode Fusion Genetics-DHFR PCA", *IBIS student day 2018*, Quebec City, Canada. August 23rd, 2018
2. **D. Evans-Yamamoto**, M. Tomita and N. Yachie. "Development of high-throughput technologies to screen protein interactomes", *12th LSBM Symposium*, Fuefuku, Japan. March 8th, 2018.
1. **D. Evans-Yamamoto**, H. Matsuo, C. R. Landry, M. Yoshida, M. Tomita and N. Yachie. "Screening inter-species protein interactomes using Barcode Fusion Genetics", *From Genetic Networks to a Cellular Wiring Diagram*, Tokyo, Japan. April 27th, 2017.

Awards and Fellowships

March 2024	Outstanding doctrol dissertation awarded for the graduation thesis "Charactrizing protein evolution with systematic protein-protein interaction screenings" <i>Systems biology project, Keio University SFC</i>
April 2020–September 2023	Research Fellowship for Young Scientists, <i>Japan Society for Promotion of Science</i> 200,000 JPY / Month
April 2015–March 2024	TTCK Research Fellowship, <i>Keio University</i> (April 2023–March2024) 1,600,000 JPY (April 2022–March2023) 1,600,000 JPY (April 2021–March2022) 1,600,000 JPY (April 2020–March2021) 1,200,000 JPY (April 2019–March 2020) 800,000 JPY (April 2018–March 2019) 291,200 JPY (April 2017–March 2018) 460,000 JPY (April 2016–March 2017) 433,330 JPY (April 2015–March 2016) 454,900 JPY
June 2021–February 2023	Watanabe Foundation International Scholarship <i>The Watanabe Foundation</i> , 150,000 JPY / month
August 2021	Best Poster Award, <i>IBIS student day</i> , awarded 150 CAD as prize
July 2020	Graduate Fellowship for Young Leaders <i>Sylff organization through Keio University</i> , 1,000,000 JPY
March 2018	Graduation Thesis Award, SFC, <i>Keio University</i>

Research Funding

1. April 2020–March 2023, Grant-in-Aid for JSPS Fellows, *Japan Society for Promotion of Science*
Development of a novel analysis pipeline on protein evolution based on biophysical functionality
2,500,000 JPY
2. April 2019–March 2020, Taikichiro Mori Memorial Research Grant, *Taikichiro Mori Memorial Research Fund*
Evolution analysis on proteins from biophysical interaction properties
240,000 JPY
3. Yamagishi Student Project Support Program. (June 2017-February 2018)
Evolutionary analysis of protein complexes from an inter-species screening approach
240,000 JPY
4. Yamagishi Student Project Support Program. (June 2016-February 2017)
Expanding high-throughput protein interaction detection methods towards personal interactome technologies
270,000 JPY

Skills

1- Biological Experiment skills

a. Genetic engineering

- i. Design and construction of various plasmid DNAs for bacteria, yeast and mammalian cells
- ii. Design and construction of various gene induction circuits with DNA recombination
- iii. Design and construction of plasmid DNA libraries including ORFeome libraries and DNA barcodes
- iv. Design and construction of gRNAs for CRISPR/Cas9 genome editing

b. Yeast molecular biology and genetics

- i. Yeast cell culture and transformation
- ii. Deletion of genes in Yeast cells
- iii. In-yeast DNA assembly
- iv. Yeast two-hybrid method and DHFR-PCA to detect protein-protein interactions

c. Mammalian culture cell engineering

- i. Basic cell culture and passage of mammalian cells
- ii. Plasmid DNA transfection of mammalian cells
- iii. CRISPR/Cas9 base editing in mammalian cells

d. Operation of Next-generation sequencers

- i. Illumina MiSeq
- ii. Oxford Nanopore Technologies, MinION

2- Computational skills

a. Python

- i. Data analysis on public data
- ii. Analyzing high-throughput DNA sequencing data
- iii. Parallel computing on Sun Grid Engine servers

b. R

- i. Statistical testing
- ii. Data visualization

c. Genome editing outcome analyses

d. Single-cell transcriptome data analysis using Drop-seq tools (Moderate)

e. Single-cell transcriptome data analysis using R, Seurat package (Moderate)

f. Data processing (fastq/fast5 files to analysis outputs)

3- Other skills

- a. Project management experience
 - i. Client-based project involving domain expertise on generative AI and biomedical fields with a multi-lingual team

 - b. Written and Spoken Languages
 - i. English (Full professional proficiency)
 - ii. Japanese (Full professional proficiency)
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