

Erick I. Navarro-Deltado

Profile

I am a bioinformatician passionate about working in interdisciplinary projects that improve our understanding of complex phenotypes through the analysis of high-dimensional biological and exposomic data. With a strong background in biology and data science, I am particularly interested in using machine learning and statistical methods informed by scientific knowledge to enable precision medicine and innovative healthcare strategies.

Education

2021 - TO DATE	THE UNIVERSITY OF BRITISH COLUMBIA - FACULTY OF SCIENCE	
	PhD in Bioinformatics	Grade Average: 95.9/100
2016 - 2021	UNIVERSIDAD NACIONAL AUTÓNOMA DE MÉXICO (UNAM) - FACULTY OF SCIENCE	
	B.Sc. in Biology	Grade Average: 9.85/10 (3rd highest GPA in 2021's class)
2019	KING'S COLLEGE LONDON - FACULTY OF LIFE SCIENCES & MEDICINE	
	Study Abroad (Exchange)	Grade Average: 73.5 (First-Class Honors)

Professional Development

2024-25	ROPENSCI CHAMPIONS PROGRAM. <u>ROPENSCI</u> (1 YEAR).
2024	CARPENTRIES DATA SCIENCE AND CODING INSTRUCTOR CERTIFICATION. <u>THE CARPENTRIES</u> (16 HOURS).
2021	DATA SCIENCE CERTIFICATE. <u>BEDU</u> (5 MONTHS).
2020	INTRODUCTION TO DATA ANALYSIS WITH PYTHON. <u>EMTECH TECHNOLOGIES INSTITUTE</u> (60 HOURS).

Fellowships

2023-27	4-YEAR PHD FELLOWSHIP - ~99 200 CAD, UBC'S PREMIER PHD FELLOWSHIP
2025	DR. MICHAEL SCHULZER MEMORIAL AWARD IN BIOSTATISTICS - 2 000 CAD, FACULTY OF MEDICINE GRADUATE STUDENT AWARDS - THE UNIVERSITY OF BRITISH COLUMBIA.
2021-25	INTERNATIONAL TUITION AWARD - ~12,800 CAD, THE UNIVERSITY OF BRITISH COLUMBIA.
2023	BCCHR HEALTHY STARTS MASTER'S STUDENTSHIP (ACCEPTED IN NAME) - 10 000 CAD, BCCHRI
2022	BANK OF MONTREAL GRADUATE FELLOWSHIP - 3 200 CAD, THE UNIVERSITY OF BRITISH COLUMBIA
2022	PATRICK DAVID CAMPBELL GRADUATE FELLOWSHIP - 4 325 CAD, THE UNIVERSITY OF BRITISH COLUMBIA
2022	GERTRUDE LANGRIDGE GRADUATE SCHOLARSHIP IN MEDICAL SCIENCES - 8 475 CAD, THE UNIVERSITY OF BRITISH COLUMBIA
2022	"SOCIETY TO CELL" CLYDE HERTZMAN MEMORIAL FELLOWSHIP - 13 000 CAD, SOCIAL EXPOSOME CLUSTER
2021	GRADUATE GLOBALINK FELLOWSHIP - 15 000 CAD, MITACS
2020	SANTANDER TECH FELLOWSHIP - 30 000 MXN, SANTANDER
2018-20	ACADEMIC EXCELLENCE SCHOLARSHIP - 36 000 MXN, FUNDACION TELMEX
2017-19	EXCELLENCE FELLOWSHIP FOR UNDERGRADUATE STUDENTS - 54 000 MXN, MEXICAN ACADEMY OF SCIENCES
2019	EXCELLENCE BECALOS FELLOWSHIP - 45 000 MXN, ORGANIZACIÓN BECALOS
2019	INTERNATIONAL STUDENT MOBILITY FELLOWSHIP - 95 000 MXN, UNIVERSIDAD NACIONAL AUTONOMA DE MEXICO
2019	GLOBALINK RESEARCH INTERNSHIP FELLOWSHIP - 7 500 CAD, MITACS
2018	KUPCINET-GETZ INTERNATIONAL SUMMER SCHOOL FELLOWSHIP - WEIZMANN INSTITUTE OF SCIENCE

2017 **SUMMER SCIENTIFIC RESEARCH (VIC) FELLOWSHIP** - MEXICAN ACADEMY OF SCIENCES

Awards

- 2025 **BEST POSTER AWARD** - JOINT 33RD CONFERENCE ON INTELLIGENT SYSTEMS FOR MOLECULAR BIOLOGY & 24TH EUROPEAN CONFERENCE ON COMPUTATIONAL BIOLOGY. REGULATORY AND SYSTEMS GENOMICS TRACK. LIVERPOOL, UK.
- 2025 **SOCIAL IMPACT GRANT FOR YOUTH** - 4 500 CAD, [LATINCOUVER](#)
- 2025 **STUDENT SYMPOSIUM (SECOND PLACE)** - 200 CAD, 14TH BIG RESEARCH DAY. VANCOUVER, CANADA.
- 2024 **CONFERENCE TRAVEL AWARD** - INTERNATIONAL SOCIETY FOR COMPUTATIONAL BIOLOGY
- 2024 **BEST POSTER AWARD** - 150 CAD, UBC LIFE SCIENCES SYMPOSIUM 2024. VANCOUVER, CANADA.
- 2023 **BURSARY AWARD** - EPIGENOMICS OF COMMON DISEASES 2023 CONFERENCE. HINXTON, UK.
- 2023 **SPEED TALK COMPETITION (THIRD PLACE)** - 100 CAD, 12TH BIG RESEARCH DAY. VANCOUVER, CANADA.
- 2021 **UNAM BIOLOGY EXCELLENCE AWARD** - AWARD FOR OBTAINING THE 3RD HIGHEST CLASS' GRADE AVERAGE AT UNIVERSIDAD NACIONAL AUTONOMA DE MEXICO CLASS 2021 (BIOLOGY). MEXICO CITY, MEXICO.
- 2017 **BEST POSTER AWARD (FIRST PLACE)** - UNAM BIOCHEMISTRY COLLOQUIUM. MEXICO CITY, MEXICO
- 2016 **GOLD MEDAL, X IBERO-AMERICAN BIOLOGY OLYMPIAD (OIAB)**. BRASILIA, BRAZIL.
- 2016 **UNAM HIGH SCHOOL STUDENT AWARD IN SCIENTIFIC RESEARCH**. MEXICO CITY, MEXICO.
- 2016 **THIRD PLACE, ITESM XXI INTERNATIONAL SCIENCE CONTEST (CIC)**. MONTERREY, MEXICO.
- 2016 **GOLD MEDAL, XXV NATIONAL BIOLOGY OLYMPIAD**. VERACRUZ, MEXICO.

Publications

† denotes equal contribution

JOURNAL ARTICLES

- Life B; Petkau TL; Cruz GNF; **Navarro-Delgado EI**; Shen N; Korthauer K ; Leavitt BR. (2023). FTD associated behavioural and transcriptomic abnormalities in 'humanized' progranulin-deficient mice: A novel model for progranulin-associated FTD. *Neurobiology of Disease*. 182: 1-15.
- Duncan E.M., Nowotarski S.H., Guerrero-Hernández C., Ross E.J., D'Orazio J.A., **Clubes de Ciencia México Workshop for Developmental Biology***, McKinney S., Guo L., McClain M., Alvarado A.S. (2022). Molecular characterization of a flatworm *Girardia* isolate from Guanajuato, Mexico. *Developmental Biology*; <https://doi.org/10.1016/j.ydbio.2022.06.003>.

*I was part of the Clubes de Ciencia Mexico WfDB consortium.

- Salgado-Albarrán M.†, **Navarro-Delgado EI**†, Del Moral-Morales A.†, Alcaraz N., Baumbach J., González-Barrios R., Soto-Reyes E. (2021) Comparative transcriptome analysis reveals key epigenetic targets in SARS-CoV-2 infection. *npj Systems Biology and Applications*; doi: 10.1038/s41540-021-00181-x.
- Cáceres-Gutiérrez R.E., Andonegui M.A., Oliva D.A., González-Barrios R., Luna F., Arriaga-Canon C., López A., Prada D., Castro C., Parmentier L., Díaz-Chávez J., Alfaro-Mora Y., **Navarro-Delgado EI**, Fabian-Morales E., Tran B., Shetty J., Zhao Y., Alcaraz N., De la Rosa C., Reyes J.L., Hédouin S., Hubé F., Francastel C., & Herrera L.A. (2021). Proteasome inhibition alters mitotic progression through the upregulation of a-satellite RNAs. *The FEBS Journal*; doi:10.1111/febs.16261.

BOOK CHAPTERS

- Navarro-Delgado EI**†, Salgado-Albarrán M.†, Torres-Arciga K., Alcaraz N., Soto-Reyes E., Herrera L.A. & Gonzalez-Barrios R. (2021). Bioinformatics of Transcription Factor Binding Prediction. In Diego A. Forero, *Bioinformatics and Human Genomics Research*. USA. CRC Press USA (Taylor & Francis Group); doi: 10.1201/9781003005926-10

THESIS

- **Navarro-Delgado EI.**, Gonzalez-Barrios R., Alcaraz N. (2021). Bachelors. Identificación de genes codificantes y elementos repetidos regulados por DAXX mediante RNA-SEQ. *Universidad Nacional Autónoma de México. México*. Access: <http://132.248.9.195/ptd2021/mayo/0812217/Index.html>

IN PROGRESS

- Edward, K; Merrill, SM; Konwar, C; Jude, M; Zhuang, B; Meijer, M; **Navarro-Delgado, EI**; Maclsaac, JL; Butstamante, M; Mandhane, P; Simons, E; Moraes, T; Subbarao, P; Turvey, SE; Kobor, MS. [In press] Biological sex impacts immune cell proportions and epigenetic profiles in the developing pediatric immune system. *Communications Biology*.
- **Navarro-Delgado, EI**; Czamara, D; Edwards, K; Merrill, SM; Konwar, C; Maclsaac, JL; Mandhane, P; Simons, E; Subbarao, P; Moraes, TJ; Lahti, J; Binder, EB; Raikonen, K; Turvey, SE; Korthauer, K; Kobor, MS. Multi-omics analysis with RAMEN: Untangling gene-environment contributions to DNA methylation variability in cord blood; doi: 10.1101/2025.05.08.652964. *bioRxiv* (manuscript under review).
- Life, B†; **Navarro-Delgado, EI†**; Fornes, O; Wasserman, W; Korthauer, K; Leavitt, BR. Progranulin variant rs5848 displays ancestry-specific associations with Alzheimer's Disease (manuscript under review).
- Meijer, M; Fu, M.; **Navarro-Delgado, EI**; Engelbrecht, HR; Turecki, G; Chan, MH; Kobor, MS. Leaping over the blood-brain barrier: DNA methylation as the link between peripheral and central immune systems.; doi: 10.1101/2025.08.25.672204, *bioRxiv* (manuscript under review).
- Fu, MP; Edwards K.; **Navarro-Delgado, EI**; Merrill, SM; Kitaba, NT; Konwar, C; Mandhane, P; Simons, E; Subbarao, P; Moraes, TJ; Holloway, JW; Turvey, SE; Kobor, MS. Advancing Pediatric and Longitudinal DNA Methylation Studies with CellsPickMe, an Integrated Blood Cell Deconvolution Method. doi: 10.1101/2025.04.22.649907, *bioRxiv*.
- **Navarro-Delgado, EI**; Czamara, D; Konwar, C; Merrill, SM; Maclsaac, JL; Zhao, Q; Liang, X; Mozhui, K; Lewinn, KJ; Bush, NR; Kobor, MS; Korthauer, K. (In preparation). *The same place but different: cord blood and placenta shared and unique gene-environment contributions to DNA methylome variability*.
- Chan, M. H.; Merrill, S. M.; Meijer, M.; **Navarro-Delgado, EI.**; Konwar, C., Maclsaac; J., LeWinn; K., Zhao, Q.; Mason, A.; Smith, A.; Bush, N.; Kobor, MS. (In preparation). *Converging and Diverging DNA Methylation Patterns of Childhood Internalizing and Externalizing Behaviours*.

Presentations

ORAL PRESENTATIONS

Navarro-Delgado, EI. (2025). A reproducible framework for dissecting individual, additive and interactive gene-environment contributions in genomic regions with variable DNA methylation. Presented at the joint 33rd international conference on Intelligent Systems for Molecular Biology and 24th European Conference on Computational Biology. Liverpool, UK.

Navarro-Delgado, EI. (2025). The foundation of the methylome: *dissecting the contribution of genetics and the prenatal exposome to placental and cord blood DNA methylation*. Presented at the Centre or Molecular Medicine and Therapeutics Seminar series. BC Children's Research Institute, Vancouver, Canada.

Navarro-Delgado, EI. (2025). *The foundation of the DNA methylome: dissecting gene-environment contributions in vital fetal tissues*. Presented at the 14th BIG research day. UBC Life Sciences Institute, Vancouver, Canada.

Navarro-Delgado, EI. (2024). *Análisis multi-ómico con RAMEN: identificando interacciones gen-ambiente en la metilación del ADN*. Presented at the LatinR 2024: Latin-American conference about the use of R in R&D conference. Virtual venue.

Navarro-Delgado, EI. (2024). *Multi-omic analysis with RAMEN: Untangling gene-environment contributions to DNA methylation variability in cord blood*. Presented at the ISCB-Latin America SolBio CCBCOL International Conference on Bioinformatics 2024. CES University, Medellin, Colombia.

Navarro-Delgado, EI., Shen, N (2024). *Making sense of the epigenome: Developing tools to identify DNA methylation variability*. Presented at the Centre for Molecular Medicine and Therapeutics Research Day 2024. BC Children's Research Institute, Vancouver, Canada.

Navarro-Delgado, El. (2024). *Modelling the genome-exposome contribution to newborn methylome variability with the RAMEN package*. Presented at the 13th BIG research day. UBC Life Sciences Institute, Vancouver, Canada.

Navarro-Delgado, El. (2023). *Modelling the genome and prenatal exposome contribution to newborn DNA methylome variability with the RAMEN package*. Presented at the Epigenomics of Common Diseases 2023 conference. Wellcome Genome Campus, Hinxton, UK.

Navarro-Delgado, El. (2023). *Modelling the genome and prenatal exposome contribution to newborn DNA methylome variability with the RAMEN package*. Presented at the Vancouver Bioinformatics Users Group meeting. Simon Fraser University, Burnaby, Canada.

Navarro-Delgado, El. (2023). *Genetics vs environment? Modelling their contribution to DNA methylome variability in newborns*. Presented at the Centre of Molecular Medicine and Therapeutics Seminar series. BC Children's Research Institute, Vancouver, Canada.

Navarro-Delgado, El. (2023). *Nature vs Nurture: understanding the influence of genetics and environment on DNA methylation*. Presented at the Vancouver Bioinformatics Users Group Lay-term talks competition. Langara College, Vancouver, Canada.

Navarro-Delgado, El. (2023). *Modelling the contribution of genetics and prenatal environment to DNA methylome variability with the RAMEN package*. Presented at the 12th BIG Research Day. UBC Life Sciences Institute, Vancouver, Canada.

Navarro-Delgado, El. (2020). *Identifying targetable epigenetic central players in SARS-CoV-2 infection with a systems biology approach*. Presented at the Mexican Interdisciplinary Network of Epigenomics (RIEM). Universidad Nacional Autónoma de México, Mexico..

Navarro-Delgado, El. (2019). *Identifying the main biological mechanisms in asthma and food allergy: adapting ALLIGATOR to RNA-seq data*. Presented at the Summer Student Research Day. Robson Square, Vancouver, Canada.

Navarro-Delgado, El. (2018). *Use of senolytics as a therapeutic approach to prevent cancer development*. Presented at the Kupcinet-Getz International Summer School Colloquium. Weizmann Institute of Science.

POSTER PRESENTATIONS

Navarro-Delgado, El; Konwar, C; Merrill, SM; MacIsaac, JL; Liang, X; Zhao, Q; Mozhui, K; LeWinn, KZ; Bush, NR; Kobor, MS; Korthauer K. (2025). *RAMEN: Dissecting single, additive and interactive gene-environment contributions in variably methylated regions*. Presented at the joint 33rd international conference on Intelligent Systems for Molecular Biology & 24th European Conference on Computational Biology. Liverpool, UK.

Navarro-Delgado, El; Czamara, D; Edwards, K; Merrill, SM; Konwar, C; MacIsaac, JL; the CHILD study team, the PREDO study team; Turvey, SE; Korthauer, K; Kobor, MS (2024). *RAMEN: Modelling the genome-exposome contribution to newborn methylome variability*. Presented at the 2024 Life Sciences Institute Symposium. UBC Life Sciences Institute, Vancouver, Canada.

Navarro-Delgado, El; Czamara, D; Edwards, K; Merrill, SM; Konwar, C; MacIsaac, JL; the CHILD study team, the PREDO study team; Turvey, SE; Korthauer, K; Kobor, MS (2024). *Modelling the genome-exposome contribution to newborn methylome variability with the RAMEN package*. Presented at the 13th BIG research day. UBC Life Sciences Institute, Vancouver, Canada.

Navarro-Delgado, El; Edwards, K; Merrill, SM; Konwar, C; MacIsaac, JL; the CHILD study team, Turvey, SE; Korthauer, K; Kobor, MS (2024). *Genome-exposome contribution to newborn methylome variability modelling with the RAMEN package*. Presented at the 2024 Healthy Starts Research Day. BC Children's Research Institute, Vancouver, Canada.

Navarro-Delgado, El; Konwar, C; Edwards, K; Merrill, SM; MacIsaac, JL; Liang, X; Zhao, Q; Mozhiu, K; LeWinn, KZ; Bush, NR; the CHILD study team, the CANDLE study team; Korthauer, K; Kobor, MS (2023). *Modelling the contribution of genetics and prenatal environment to cord blood and placenta DNA methylation variability*. Presented at the Centre for Molecular Medicine and Therapeutics Research Day. BC Children's Research Institute, Vancouver, Canada.

Navarro-Delgado, El; Konwar, C; Edwards, K; Merrill, SM; MacIsaac, JL; Liang, X; Zhao, Q; Mozhiu, K; LeWinn, KZ; Bush, NR; the CHILD study team, the CANDLE study team; Korthauer, K; Kobor, MS (2023). *Modelling the*

contribution of genetics and prenatal environment to cord blood and placenta DNA methylation variability. Presented at the 12th BIG research day. UBC Life Sciences Institute, Vancouver, Canada.

Navarro-Delgado, El; Edwards, K; Merrill, SM; Konwar, C; MacIsaac, JL; the CHILD study team; Korthauer, K; Kobor, MS (2023). *Modelling the contribution of genetics and prenatal environment to newborn DNA methylation variability.* Presented at the 2023 Healthy Starts Research Day. BC Children's Research Institute, Vancouver, Canada.

Invited talks

Navarro-Delgado, El. (2024). *Modelling the genome and prenatal exposome contribution to newborn DNA methylome variability with the RAMEN package.* Presented at the Genetics Seminar Series. Centre for Fertility and Health, Oslo, Norway.

Software

- **RAMEN** : Regional Association of Methylome variability with the Exposome and geNome, an R package to model the genome and exposome contribution to methylome variability (<https://ericknavarro.github.io/RAMEN>).

Research Experience

SEP 2021 - TO DATE	BC CHILDREN'S HOSPITAL RESEARCH INSTITUTE (VANCOUVER, CANADA) Supervisors: Dr. Michael Kobor & Dr. Keegan Korthauer - Developing reproducible bioinformatic frameworks to model the genome and exposome marginal, additive and interactive contribution to DNA methylome variation across early life.
NOV 2018 - JUN 2021	NATIONAL CANCER INSTITUTE (INCAN) - (MEXICO CITY) Supervisor: Dr. Rodrigo Gonzalez Barrios - Conducted a bioinformatic analysis to identify epigenetic central players in SARS-CoV-2 infection with therapeutic potential through a weighted gene co-expression network approach using RNA-seq data, leading to a first co-author publication.
JUN - SEP 2019	THE UNIVERSITY OF BRITISH COLUMBIA - (VANCOUVER, CANADA) Supervisor: Dr. Denise Daley - Adapted the GWAS permutation-based Gene Set Analysis bioinformatic tool ALLIGATOR to be used with RNA-seq data.
JUN - AUG 2018	WEIZMANN INSTITUTE OF SCIENCE - (REHOVOT) Supervisor: Dr. Valery Krizhanovsky - Tested the effect of senolytics as a therapeutic approach to prevent Pancreatic Ductal Adeno-carcinoma development in a Kras-driven transgenic mouse model and cultured human cell lines
JUN - AUG 2017	NATIONAL LABORATORY OF GENOMICS FOR BIODIVERSITY (LANGE BIO), CINVESTAV - (IRAPUATO, MEXICO) Supervisor: Dr. Alexander de Luna Fors - Analysis of epistasis among genes in the nutrient sensing regulatory pathway affecting <i>Saccharomyces cerevisiae</i> 's chronological lifespan using a high-throughput parallelizable approach
JAN - JUN 2017	FACULTY OF SCIENCE, UNAM - LABORATORY OF MOLECULAR BIOLOGY AND GENOMICS (MEXICO CITY, MEXICO) Supervisor: Dr. Claudia Segal Kischinevsky Determination of acatalacemic <i>Saccharomyces cerevisiae</i> 's chronological lifespan expressing <i>Debaryomyces hansenii</i> 's catalase in plasmids under different promoters.

SEP 2015 - MAY 2016	NATIONAL INSTITUTE OF NEUROLOGY AND NEUROSURGERY (INNN) - LABORATORY OF NEUROINFLAMMATION RESEARCH (MEXICO CITY, MEXICO) Supervisor: Dr. Agnes Fleury Evaluation of specific antibodies in patients affected with neurocysticercosis before and after regular treatment.
MAY - JUL 2015	INSTITUTE OF CHEMISTRY (IQ), UNAM - DEPARTMENT OF NATURAL PRODUCTS(MEXICO CITY) Supervisor: Dr. Ricardo Reyes Chilpa Extraction of bioactive natural products from the plant <i>Cacalia decomposita</i> with possible antiviral activity against HIV type 1.

Teaching Experience

2025	CLUBES DE CIENCIA MEXICO - GUADALAJARA, MEXICO. Developed and led a 1-week workshop about creating epigenetic clocks with Machine Learning.
2022-2024	THE UNIVERSITY OF BRITISH COLUMBIA - VANCOUVER, CANADA Teaching Assistant of STAT545 (Data Wrangling, Exploration, and Analysis with R) in the Fall terms of 2022, 2023 and 2024 (September to December). My overall student evaluation score is 4.6 out of 5 (interpolated median) and 100% Favourable Rating (the percentage of respondents who responded with a 4 or 5 on a scale of 1 to 5).
JUL 2024	TRAINEE 'OMICS GROUP, BCCHR - VANCOUVER, CANADA Led the workshop "Introduction to Functions in R"
MAR 2021	UNIVERSIDAD AUTÓNOMA METROPOLITANA - MEXICO CITY Developed and led the 20 hours-long workshop "Introduction to RNA-seq data analysis"
JAN - JUNE 2020	UNIVERSIDAD NACIONAL AUTÓNOMA DE MEXICO (UNAM) - MEXICO CITY Teaching Assistant of the Epigenetics course in the 2020-2 term.

Professional service and leadership

2024 - TO DATE	SALSEO QUEER DANCE - FOUNDER AND EXECUTIVE DIRECTOR (INSTAGRAM: @SALSEO_VAN). ACCESSIBLE QUEER SPACES FOR AFROLATINX DANCING.
2023 - 2024	TRAINEE 'OMICS GROUP SEMINAR DIRECTOR - BC CHILDREN'S RESEARCH INSTITUTE, VANCOUVER, CANADA.
2023	CLIMATE CHANGE WORKSHOP LEAD - UBC LET'S TALK SCIENCE. VANCOUVER, CANADA.
2017 - 2019	MEXICO'S NATIONAL BIOLOGY OLYMPIAD ORGANIZING COMMITTEE - MEXICO.
2015 - 2016	MEXICO CITY'S HEADQUARTER PRESIDENT - SOCIEDAD CIENTIFICA JUVENIL. MEXICO CITY, MEXICO.

Professional affiliations

- International Society for Computational Biology
- Red Mexicana de Bioinformática
- The Carpentries
- rOpenSci