Lisa M. McEwen, Ph. D.

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Victoria, British Columbia, Canada

Qualifications

- Strong research background in genomics and skilled in the analysis of RNA sequencing, microarray, and clinical electronic health record data
- Proficient in R, SQL, Bash, Cloud Computing (GCP), PowerBI, Cerner Command Language, Markdown, LaTeX, Shiny, GitHub, MS Office Suite, Adobe Illustrator
- Statistical expertise in regression, classification, clustering, unsupervised and supervised machine learning, survival analysis, risk adjustment, variance testing

Professional Affiliations

Adjunct Assistant Professor 2019 - present
School of Health Information Science, University of Victoria

Experience

Allakos Inc. Nov. 2020 - present
Consultant/Independent Contractor

- Responsibilities include consulting on study design, full processing of raw transcriptomic data, performing statistical analyses, creating publication-ready data visualizations, strategizing on scientific questions, and presenting findings to Senior Scientists and Clinical Directors.
- Managing up to five sub-contractors, financial budgeting, organizing and delegating tasks
- Set up a Google Cloud Platform virtual machine integrated with cloud storage for efficient processing of large RNA Sequencing datasets.

Clinical Analytics, Decision Support, Island Health June 2018 – present
Clinical Data Consultant

- Statistical analysis and metric development of clinical data obtained from electronic health records (Cerner) and several other data sources collected from >10 hospital facilities and numerous care settings. Develops white papers, summary reports, and presentations to engage with stakeholders (Medical Directors, Physicians, and Executives).
- Performs integration of large patient datasets, including microbiology laboratory, molecular genetics laboratory, pharmacy, and department-specific clinical data (Anesthesiology, Internal Medicine, Obstetrics, Nephrology, etc.).
- Leads team of Data Consultants in the use of the R/R Studio. Creates reproducible research practices with workflows and standards for proper organization of code and technical notes.

Dept. of Medical Genetics, University of British Columbia: Sept. 2014 – Sept. 2018
Ph.D. Candidate

- Led multiple research projects investigating population epigenetic signatures of aging across the human life course. Performed microarray experiments and analyzed high dimensional genomic data (Illumina microarrays: DNA methylation, genotyping).
- Managed several collaborations from Canada, the United States, and international based research groups.
- Awarded >$140,000 in scholarship funding and had a major role in grant writing of a successful Canadian Institute of Health Research Project Grant ($1.1 million).

University of British Columbia Sept. 2016 – Dec. 2017
Teaching Assistant (3 terms)

- Experiential Data science for Undergraduate Cross-Disciplinary Education (EDUCE): assisted with teaching R programming workshops, marking assignments, and creating teaching material for cross-disciplinary data science students.
- BIOL 200 Fundamentals of Cell Biology
- BIOL 337 Genetics Laboratory

University of British Columbia Sept. 2013 – Aug. 2014
Research Laboratory Technician

- Performed various laboratory techniques including DNA isolations from various tissues, DNA bisulfite conversions, microarray experiments, PCR, pyrosequencing, RT-qPCR, mRNA sequencing, peripheral blood mononuclear cell extractions.
- Designed experiments to reduce batch effects and ensure quality control.

Education

Doctor of Philosophy in Medical Genetics 2014 - 2018
University of British Columbia, Vancouver, BC

Bachelor of Science in Biochemistry and Microbiology with 16-month Research Internship 2008 - 2013
University of Victoria, Victoria, BC

Additional Training

Project Management Certificate 2020
Professional Development, University of Waterloo

Supervised Methods for Statistical Machine Learning 2017
Summer Institute in Statistics for Big Data - University of Washington

Instructional Skills Workshop
Centre for Teaching, Learning, and Technology - Vancouver, UBC 2017

Publications

Primary-authored Contributions

McEwen, L. M., O'Donnell, K. J., McGill, M. G., Edgar, R. D., Jones, M. J., MacIsaac, J. L., Lin, D. T. S., Ramadori, K., Morin, A., Gladish, N., Garg, E., Unternaehrer, E., Pokhvisneva, I., Karnani, N., Kee, M. Z. L., Klengel, T., Adler, N. E., Barr, R. G., Letourneau, N., et al. (2020). The PedBE clock accurately estimates DNA methylation age in pediatric buccal cells. *Proceedings of the National Academy of Sciences of the United States of America*, *117*(38), 23329–23335.

McEwen, L. M., O'Donnell, J. C., Lifoawing, L., Matias, D., & Wagar, B. (2019). Electronic Physician Profiles: Developing an Interactive Web-Based Report for Physicians at Island Health. *Studies in Health Technology and Informatics*, *257*, 310–313.

McEwen, L. M., Jones, M. J., Lin, D. T. S., Edgar, R. D., Husquin, L. T., MacIsaac, J. L., Ramadori, K. E., Morin, A. M., Rider, C. F., Carlsten, C., Quintana-Murci, L., Horvath, S., & Kobor, M. S. (2018). Systematic evaluation of DNA methylation age estimation with common preprocessing methods and the Infinium MethylationEPIC BeadChip array. *Clinical Epigenetics*, *10*(1), 123.

McEwen, L. M., Gatev, E. G., Jones, M. J., MacIsaac, J. L., McAllister, M. M., Goulding, R. E., Madden, K. M., Dawes, M. G., Kobor, M. S., & Ashe, M. C. (2018). DNA methylation signatures in peripheral blood mononuclear cells from a lifestyle intervention for women at midlife: A pilot randomized controlled trial. *Applied Physiology, Nutrition, and Metabolism = Physiologie Appliquee, Nutrition Et Metabolisme*, *43*(3), 233–239.

McEwen, L. M., Morin, A. M., Edgar, R. D., MacIsaac, J. L., Jones, M. J., Dow, W. H., Rosero-Bixby, L., Kobor, M. S., & Rehkopf, D. H. (2017). Differential DNA methylation and lymphocyte proportions in a Costa Rican high longevity region. *Epigenetics & Chromatin*, *10*, 21.

Co-authored Contributions

Cardenas, A., Ecker, S., Fadadu, R. P., Huen, K., Orozco, A**., McEwen, L. M.**, Engelbrecht, H. R., Gladish, N., Kobor, M. S., Rosero-Bixby, L., Dow, W. H., & Rehkopf, D. H. (2022). Epigenome-wide association study and epigenetic age acceleration associated with cigarette smoking among Costa Rican adults. *Scientific reports*, *12*(1), 4277. https://doi.org/10.1038/s41598-022-08160-w

McGill, M. G., Pokhvisneva, I., Clappison, A. S., **McEwen, L. M.**, Beijers, R., Tollenaar, M. S., Pham, H., Kee, M., Garg, E., de Mendonça Filho, E. J., Karnani, N., Silveira, P. P., Kobor, M. S., de Weerth, C., Meaney, M. J., & O'Donnell, K. J. (2022). Maternal Prenatal Anxiety and the Fetal Origins of Epigenetic Aging. *Biological psychiatry*, *91*(3), 303–312. https://doi.org/10.1016/j.biopsych.2021.07.025

Dill-McFarland, K. A., König, S. G., Mazel, F., Oliver, D. C., **McEwen, L. M.**, Hong, K. Y., & Hallam, S. J. (2021). An integrated, modular approach to data science education in microbiology. *PLoS Computational Biology*, *17*(2), e1008661.

Yang, C. X., Schon, E., Obeidat, M., Kobor, M. S., **McEwen, L.M.**, MacIsaac, J., Lin, D., Novak, R. M., Hudson, F., Klinker, H., Dharan, N., Horvath, S., Bourbeau, J., Tan, W., Sin, D. D., Man, S., Kunisaki, K., & Leung, J. M. (2021). Occurrence of Accelerated Epigenetic Aging and Methylation Disruptions in Human Immunodeficiency Virus Infection Before Antiretroviral Therapy. *The Journal of infectious diseases*, *223*(10), 1681–1689.

Hernandez Cordero, A. I., Yang, C. X., Obeidat, M., Yang, J., MacIsaac, J., **McEwen, L.M.**, Lin, D., Kobor, M., Novak, R., Hudson, F., Klinker, H., Dharan, N., Man, S. P., Sin, D. D., Kunisaki, K., Leung, J., & INSIGHT START Pulmonary and Genomic Substudy Groups (2021). DNA methylation is associated with airflow obstruction in patients living with HIV. *Thorax*, *76*(5), 448–455.

Clifford, R. L., Yang, C. X., Fishbane, N., Patel, J., MacIsaac, J. L., **McEwen, L. M.**, May, S. T., Castellanos-Uribe, M., Nair, P., Obeidat, M., Kobor, M. S., Knox, A. J., & Hackett, T.-L. (2020). TWIST1 DNA methylation is a cell marker of airway and parenchymal lung fibroblasts that are differentially methylated in asthma. *Clinical Epigenetics*, *12*(1), 145.

Chen, L. M., Tollenaar, M. S., Hari Dass, S. A., Bouvette-Turcot, A.-A., Pokhvisneva, I., Gaudreau, H., Parent, C., Diorio, J., **McEwen, L. M.**, MacIsaac, J. L., Kobor, M. S., Beijers, R., de Weerth, C., Silveira, P. P., Karama, S., Meaney, M. J., O'Donnell, K. J., & MAVAN Study Team. (2020). Maternal antenatal depression and child mental health: Moderation by genomic risk for attention-deficit/hyperactivity disorder. *Development and Psychopathology*, *32*(5), 1810–1821.

Hari Dass, S. A., McCracken, K., Pokhvisneva, I., Chen, L. M., Garg, E., Nguyen, T. T. T., Wang, Z., Barth, B., Yaqubi, M., **McEwen, L. M.**, MacIsaac, J. L., Diorio, J., Kobor, M. S., O'Donnell, K. J., Meaney, M. J., & Silveira, P. P. (2019). A biologically-informed polygenic score identifies endophenotypes and clinical conditions associated with the insulin receptor function on specific brain regions. *EBioMedicine*, *42*, 188–202.

Clifford, R. L., Patel, J., MacIsaac, J. L., **McEwen, L. M.**, Johnson, S. R., Shaw, D., Knox, A. J., Hackett, T.-L., & Kobor, M. S. (2019). Airway epithelial cell isolation techniques affect DNA methylation profiles with consequences for analysis of asthma related perturbations to DNA methylation. *Scientific Reports*, *9*(1), 14409.

Verschoor, C. P., **McEwen, L. M.,** Kobor, M. S., Loeb, M. B., & Bowdish, D. M. E. (2018). DNA methylation patterns are related to co-morbidity status and circulating C-reactive protein levels in the nursing home elderly. *Experimental Gerontology*, *105*, 47–52.

O'Donnell, K. J., Chen, L., MacIsaac, J. L., **McEwen, L. M.**, Nguyen, T., Beckmann, K., Zhu, Y., Chen, L. M., Brooks-Gunn, J., Goldman, D., Grigorenko, E. L., Leckman, J. F., Diorio, J., Karnani, N., Olds, D. L., Holbrook, J. D., Kobor, M. S., & Meaney, M. J. (2018). DNA methylome variation in a perinatal nurse-visitation program that reduces child maltreatment: A 27-year follow-up. *Translational Psychiatry*, *8*(1), 15.

Husquin, L. T., Rotival, M., Fagny, M., Quach, H., Zidane, N., **McEwen, L. M.**, MacIsaac, J. L., Kobor, M. S., Aschard, H., Patin, E., & Quintana-Murci, L. (2018). Exploring the genetic basis of human population differences in DNA methylation and their causal impact on immune gene regulation. *Genome Biology*, *19*(1), 222.

Garg, E., Chen, L., Nguyen, T. T. T., Pokhvisneva, I., Chen, L. M., Unternaehrer, E., MacIsaac, J. L., **McEwen, L. M.**, Mah, S. M., Gaudreau, H., Levitan, R., Moss, E., Sokolowski, M. B., Kennedy, J. L., Steiner, M. S., Meaney, M. J., Holbrook, J. D., Silveira, P. P., Karnani, N., … Mavan Study Team. (2018). The early care environment and DNA methylome variation in childhood. *Development and Psychopathology*, *30*(3), 891–903.

Forest, M., O'Donnell, K. J., Voisin, G., Gaudreau, H., MacIsaac, J. L., **McEwen, L. M.**, Silveira, P. P., Steiner, M., Kobor, M. S., Meaney, M. J., & Greenwood, C. M. T. (2018). Agreement in DNA methylation levels from the Illumina 450K array across batches, tissues, and time. *Epigenetics*, *13*(1), 19–32.

Clifford, R. L., Fishbane, N., Patel, J., MacIsaac, J. L., **McEwen, L. M.**, Fisher, A. J., Brandsma, C.-A., Nair, P., Kobor, M. S., Hackett, T.-L., & Knox, A. J. (2018). Altered DNA methylation is associated with aberrant gene expression in parenchymal but not airway fibroblasts isolated from individuals with COPD. *Clinical Epigenetics*, *10*, 32.

Chen, L. M., Yao, N., Garg, E., Zhu, Y., Nguyen, T. T. T., Pokhvisneva, I., Hari Dass, S. A., Unternaehrer, E., Gaudreau, H., Forest, M., **McEwen, L. M.**, MacIsaac, J. L., Kobor, M. S., Greenwood, C. M. T., Silveira, P. P., Meaney, M. J., & O'Donnell, K. J. (2018). PRS-on-Spark (PRSoS): A novel, efficient and flexible approach for generating polygenic risk scores. *BMC Bioinformatics*, *19*(1), 295.

Bush, N. R., Edgar, R. D., Park, M., MacIsaac, J. L., **McEwen, L. M.**, Adler, N. E., Essex, M. J., Kobor, M. S., & Boyce, W. T. (2018). The biological embedding of early-life socioeconomic status and family adversity in children's genome-wide DNA methylation. *Epigenomics*, *10*(11), 1445–1461.

Austin, M. K., Chen, E., Ross, K. M., **McEwen, L. M.**, MacIsaac, J. L., Kobor, M. S., & Miller, G. E. (2018). Early-life socioeconomic disadvantage, not current, predicts accelerated epigenetic aging of monocytes. *Psychoneuroendocrinology*, *97*, 131–134.

Mang, C. S., **McEwen, L. M.**, MacIsaac, J. L., Snow, N. J., Campbell, K. L., Kobor, M. S., Ross, C. J. D., & Boyd, L. A. (2017). Exploring genetic influences underlying acute aerobic exercise effects on motor learning. *Scientific Reports*, *7*(1), 12123.

Verschoor, C. P., **McEwen, L. M.**, Kohli, V., Wolfson, C., Bowdish, D. M., Raina, P., Kobor, M. S., & Balion, C. (2017). The relation between DNA methylation patterns and serum cytokine levels in community-dwelling adults: A preliminary study. *BMC Genetics*, *18*(1), 57.

Gopalan, S., Carja, O., Fagny, M., Patin, E., Myrick, J. W., **McEwen, L. M.**, Mah, S. M., Kobor, M. S., Froment, A., Feldman, M. W., Quintana-Murci, L., & Henn, B. M. (2017). Trends in DNA Methylation with Age Replicate Across Diverse Human Populations. *Genetics*, *206*(3), 1659–1674.

Morin, A. M., Gatev, E., **McEwen, L. M.**, MacIsaac, J. L., Lin, D. T. S., Koen, N., Czamara, D., Räikkönen, K., Zar, H. J., Koenen, K., Stein, D. J., Kobor, M. S., & Jones, M. J. (2017). Maternal blood contamination of collected cord blood can be identified using DNA methylation at three CpGs. *Clinical Epigenetics*, *9*, 75.

Moore, S. R., **McEwen, L. M.**, Quirt, J., Morin, A., Mah, S. M., Barr, R. G., Boyce, W. T., & Kobor, M. S. (2017). Epigenetic correlates of neonatal contact in humans. *Development and Psychopathology*, *29*(5), 1517–1538.

Clifford, R. L., Jones, M. J., MacIsaac, J. L., **McEwen, L. M.**, Goodman, S. J., Mostafavi, S., Kobor, M. S., & Carlsten, C. (2017). Inhalation of diesel exhaust and allergen alters human bronchial epithelium DNA methylation. *The Journal of Allergy and Clinical Immunology*, *139*(1), 112–121.

De Souza, R. A. G., Islam, S. A., **McEwen, L. M.**, Mathelier, A., Hill, A., Mah, S. M., Wasserman, W. W., Kobor, M. S., & Leavitt, B. R. (2016). DNA methylation profiling in human Huntington's disease brain. *Human Molecular Genetics*, *25*(10), 2013–2030.

Beery, A. K., **McEwen, L. M.**, MacIsaac, J. L., Francis, D. D., & Kobor, M. S. (2016). Natural variation in maternal care and cross-tissue patterns of oxytocin receptor gene methylation in rats. *Hormones and Behavior*, *77*, 42–52.

Kaplow, I. M., MacIsaac, J. L., Mah, S. M., **McEwen, L. M.**, Kobor, M. S., & Fraser, H. B. (2015). A pooling-based approach to mapping genetic variants associated with DNA methylation. *Genome Research*, *25*(6), 907–917.

Fagny, M., Patin, E., MacIsaac, J. L., Rotival, M., Flutre, T., Jones, M. J., Siddle, K. J., Quach, H., Harmant, C., **McEwen, L. M.**, Froment, A., Heyer, E., Gessain, A., Betsem, E., Mouguiama-Daouda, P., Hombert, J.-M., Perry, G. H., Barreiro, L. B., Kobor, M. S., & Quintana-Murci, L. (2015). The epigenomic landscape of African rainforest hunter-gatherers and farmers. *Nature Communications*, *6*, 10047.

Chen, L., Pan, H., Tuan, T. A., Teh, A. L., MacIsaac, J. L., Mah, S. M., **McEwen, L. M.**, Li, Y., Chen, H., Broekman, B. F. P., Buschdorf, J. P., Chong, Y. S., Kwek, K., Saw, S. M., Gluckman, P. D., Fortier, M. V., Rifkin-Graboi, A., Kobor, M. S., Qiu, A., … Gusto Study Group. (2015). Brain-derived neurotrophic factor (BDNF) Val66Met polymorphism influences the association of the methylome with maternal anxiety and neonatal brain volumes. *Development and Psychopathology*, *27*(1), 137–150.

Teh, A. L., Pan, H., Chen, L., Ong, M.-L., Dogra, S., Wong, J., MacIsaac, J. L., Mah, S. M., **McEwen, L. M.**, , … Holbrook, J. D. (2014). The effect of genotype and in utero environment on interindividual variation in neonate DNA methylomes. *Genome Research*, *24*(7), 1064–1074.

Jones, M. J., Farré, P., **McEwen, L. M.**, Macisaac, J. L., Watt, K., Neumann, S. M., Emberly, E., Cynader, M. S., Virji-Babul, N., & Kobor, M. S. (2013). Distinct DNA methylation patterns of cognitive impairment and trisomy 21 in Down syndrome. *BMC Medical Genomics*, *6*, 58.

Book Chapters

McEwen L.M., Goodman S., Kobor M.S., Jones M.J.. (2017). The DNA methylome: an interface between the environment, immunity, and aging. Valquiria Bueno, Thomas Jackson and Janet M. Lord. Ageing Immune System and Health.

Awards/Funding

Agency	Award Name	Comp	Total Value (CAD$)	Eligible Years of Funding
CIHR	Project Grant (Co-Investigator)	C	1,095,000	2016 - 2020
CIHR	Frederick Banting and Charles Best Canada Graduate Doctoral Scholarship (ranked 12/723)	C	105,000	2016 - 2019
UBC	Medical Genetics 4-Yeard Fellowship and Tuition Award	C	72,800* + Tuition	2016 - 2020
BCCHR	Healthy Starts Graduate Studentship	C	20,000*	2016 – 2017
CIHR	Research Centre of Aging and CIHR Institute of Aging (IA) Travel Award	C	800	2017
UBC	James Miller Award – Top Medical Genetics Graduate Student	C	500	2017
CEEHRC	Travel Award – 4th Canadian Conference on Epigenetics (Whistler, BC)	C	1,100	2017

*Accepted in name only, conflict in funding with CIHR; Comp: Competitive (C) or Non-Competitive (NC); CIHR: Canadian Institute of Health Research; BCCHR: British Columbia Children's Hospital Research Institute UBC: University of British Columbia; CEEHR: Canadian Epigenetics, Environment and Health Research Consortium

Service to the Community

Guest Lecturer – UVic HINF 573	2020, 2022
Peer Reviewer: Bioinformatics	2019-present
Peer Reviewer: Scientific Reports	2018-present
Peer Reviewer: BMC Medical Genomics	2017-present
Peer Reviewer: Epigenetics	2017-present
Ladies Learning Code Vancouver - Python Workshop Volunteer	2016-2018
UBC-ECOSCOPE R Programming Workshop Beginner & Advanced Series	2016-2018
UBC Medical Genetics - New Graduate Student Mentor	2015-2018
Let's Talk Science (Knowledge Translation Program) - Facilitator	2014-2018