

**BIOGRAPHICAL SKETCH**

Provide the following information for the key personnel and other significant contributors in the order listed on Form Page 2. Follow this format for each person. **DO NOT EXCEED FOUR PAGES.**

NAME Meaghan Jones		POSITION TITLE Assistant Professor	
eRA COMMONS USER NAME (credential, e.g., agency login)			
EDUCATION/TRAINING (Begin with baccalaureate or other initial professional education, such as nursing, and include postdoctoral training.)			
INSTITUTION AND LOCATION	DEGREE (if applicable)	YEAR(s)	FIELD OF STUDY
Mount Allison University, Sackville, New Brunswick, Canada	B.Sc. H	05/04	Biology
University of British Columbia, Vancouver, British Columbia, Canada	Ph.D.	05/10	Medical Genetics
Centre for Molecular Medicine and Therapeutics, Vancouver, British Columbia, Canada	Postdoctoral	Present	Medical Genetics

**A. Personal Statement**

My research career has been focused on genetic regulation and has progressed from single cell organisms to animal and in vitro models, and finally to human populations. In my earliest research training, I studied simple environmentally regulated gene expression in aquatic bacteria. From this initial exposure to genetic regulation, I became interested in epigenetics as a potentially important mechanism of environmental regulation in mammals. I believed that epigenetics had great potential for human health research, though the field was still in its infancy. Thus for my PhD I moved to UBC and the Molecular Epigenetics Research Group to study the role of DNA methylation in regulating genomic imprinting during development. My work there combined cell culture work with mouse models to identify long-range epigenetic interactions.

The fundamental epigenetic work of my PhD was an excellent base from which to transition into my postdoctoral research examining how epigenetic regulation influences human health in a population context. Since beginning my post-doctoral fellowship, I have focused on two main areas: DNA methylation as a signature of biological embedding, and improving methods in population epigenetic studies. My work on human populations has been centered on discovering DNA methylation signatures associated with prenatal and early life exposures, human disease, and aging. I have used birth cohorts to examine short term embedding of prenatal exposures, and adolescent or adult cohorts to identify signatures associated with age and disease. I have also been productive in creating tools and resources for the epigenetic community. In particular, I am interested in understanding and being able to control for the large epigenetic differences between cell types. This is a vital but often-neglected part of population epigenetic studies as most common tissues contain a mixture of cell types, each with its own unique epigenetic pattern, which have a strong influence on epigenetic profiles. Together, this has resulted in a total of 30 peer-reviewed publications, and creates a strong foundation on which to build my research program.

## B. Positions and Honors

### Positions and Employment

- September 2018 Assistant Professor, Department of Biochemistry and Medical Genetics, University of Manitoba
- 2012-2018 Post-doctoral Fellow, BC Children's Hospital, University of British Columbia, Vancouver, BC  
Supervisor: Dr. Michael Kobor
- 2010-2011 Post-doctoral Fellow, University of British Columbia, Vancouver, BC  
Supervisor: Dr. Louis Lefebvre

### Honors

- 2009 *Lalor travel award*  
Mammalian Gametogenesis and Embryogenesis Gordon Conference, Waterville Valley, NH, USA.
- 2008 *UBC Department of Medical Genetics James Miller Memorial Award*  
Awarded to a PhD student showing creative leadership, originality and independence.
- 2008 *EMBO World Workshop travel award*  
Workshop on Genomic Imprinting in Singapore, Singapore.
- 2006 *Junior poster prize*
- 2004 *UBC Medical Genetics Research Day.*
- 2004 *Fensom Prize*  
Biology/Biochemistry final Honours Presentations at Mount Allison University.
- 2004 *Second Place in Oral Presentations*  
Atlantic Undergraduate Universities Biology Conference, Sydney, Nova Scotia.
- 2003 *Mount Allison Biology Department Steeves Prize*  
Awarded to an Honours student with high academic standing and research potential.

## C. Selected Peer-reviewed Publications

1. **Jones, MJ**, Moore, SR, and Kobor, MS. (2018) Principles, Methodologies and Challenges of applying Epigenetic Epidemiology to Psychology. *Annual Reviews of Psychology*, 69:14.1–14.27. Role: FA
2. North, ML, **Jones, MJ**, Maclsaac, JL, Morin, AM, Steacy, LM, Gregor, A, Kobor, MS, Ellis, AK. (2018) Blood and Nasal Epigenetic Changes Correlate to Symptoms in Environmental Exposure Unit Allergen Challenges. *Allergy* 73(1):196-205. Role: CA
3. McDade, TW, **Jones, MJ**, Miller, G, Borja, J, Kobor, MS, Kuzawa, CW. (2017) Birth weight and postnatal microbial exposures predict the distribution of peripheral blood leukocyte subsets in young adults in the Philippines. *JDOHaD* 9(2):198-207. Role: CA
4. Morin, AM, Gatev, E, McEwen, LM, Maclsaac, JL, Lin, DTS, Koen, N, Czamara, D, Raikonen, K, Zar, HJ, Koenen, K, Stein, DJ, Kobor, MS, and **Jones, MJ**. (2017) Maternal blood contamination of collected cord blood can be identified using DNA methylation at three CpGs. *Clinical Epigenetics*, 9:75. Role: SA
5. Edgar, RD, **Jones, MJ**, Meaney, MJ, Turecki, G, Kobor, MS. (2017) BECon: A tool for interpreting DNA methylation findings from blood in the context of brain. *Translational Psychiatry*, 7, e1187. Role: CA
6. McDade, TW, Ryan, C, **Jones, MJ**, Maclsaac, JL, Morin, AM, Meyer, J, Borja, JB, Miller, GE, Kobor, MS, Kuzawa, CW. (2017) Social and physical environments during early development predict DNA methylation of inflammatory genes in young adulthood. *Proceedings of the National Academy of Science*, 114(29):7611-7616. Role: CA
7. McEwen, LM, **Jones, MJ**, Maclsaac, JL, Verschoor, C, Dow, WH, Rosero-Bixby, L, Horvath, S, Kobor, MS, Rehkopf, DH. (2017) Differential DNA methylation and lymphocyte proportions in a Costa Rican high longevity region. *Epigenetics and Chromatin*, 10:21. Role: CA
8. Edgar, RD, **Jones, MJ**, Robinson, WP, Kobor, MS. (2017) An empirically driven data reduction method on the human 450K methylation array to remove tissue specific non-variable CpGs. *Clinical Epigenetics*, 2:9. Role: CA

9. Portales-Casamar, E\*, Lussier, AA\*, **Jones, MJ**, Maclsaac, JL, Edgar, RD, Mah, SM, Barhdadi, A, Provost, S, Lemieux-Perreault, L-P, Cynader, MS, Chudley, AE, Dubé, M-P, Reynolds, JN, Pavlidis, P, and Kobor, MSK. (2016). DNA methylation signature of human fetal alcohol spectrum disorder. *Epigenetics Chromatin*, 9:25. Role: CA
10. Clifford, RL, **Jones, MJ**, Maclsaac, JL, McEwen, LM, Goodman, SJ, Mostafavi, S, Kobor, MSK, and Carlsten, C. (2016) Inhalation of diesel exhaust and allergen alters human bronchial epithelium DNA methylation. *Journal of Allergy and Clinical Immunology*, 139(1):112-121. Role: CA
11. Esposito, E\*, **Jones, MJ\***, Doom, J, Maclsaac, JL, Kobor, MS, Gunnar, M. (2016) Differential DNA Methylation of Peripheral Blood Mononuclear Cells in Adolescents Adopted as Young Children from Orphanages in Russia and Eastern Europe. *Development and Psychopathology*, 28:1385-1399. Role: FA
12. Farré, P, **Jones, MJ**, Meaney, MJ, Emberly, E, Turecki, G, Kobor, MS. (2015) Concordant and Discordant DNA Methylation Signatures of Aging in Human Blood and Brain. *Epigenetics and Chromatin*, 8:19. Role: CA
13. **Jones, MJ**, Goodman, SG, Kobor, MS. (2015) DNA methylation and healthy human aging. *Aging Cell*, 14(6):924-932. Role: FA
14. Jiang, R\*, **Jones, MJ\***, Chen, E, Neumann, SM, Fraser, HB, Miller, GE, & Kobor, MS. (2015) Discordance of DNA Methylation Variance Between two Accessible Human Tissues. *Scientific Reports*, 5:8257. Role: FA
15. **Jones, MJ**, Farré, P, McEwen, LM, Maclsaac, JL, Watt, K, Neumann, SM, Emberly, E, Cynader, MS, Virji-Babul, N, and Kobor, MS. (2013) Distinct DNA methylation patterns of cognitive impairment and trisomy 21 in down syndrome. *BMC Medical Genomics*, 6:58. Role: FA

#### D. Research Support

Key

COMP: Competitive (C) or Non-competitive (NC)

Role: Principal investigator (PI), Co-Principal Investigator (Co-PI), Co-Investigator (Co-I)

#### Research Grants Awarded

Granting Agency	Award Name	COMP	\$ Per Year	Years	Role	Principal Investigator
NIH	R21	C	\$105,416	2016-2018	Co-I	Sheila Crowell
CIHR	CIHR Team Grant: Developmental Origins of Health and Disease	C	300,000	2016-2021	Co-I	Michael Kobor
CIHR	CIHR Team Grant: Environments, Genes and Chronic Disease	C	400,000	2016-2021	Co-I	Stuart Turvey
CFRI	CFRI Clinical Translational Seed Grant	C	5,000	2016	Co-PI	Meaghan Jones

#### Salary Support Awards

Granting Agency	Award Name	COMP	\$ Per Year	Years
CFRI	Mining for Miracles Post-doctoral Fellowship	C	37,000	2013-2015
MSFHR	Senior Graduate Scholarship	C	20,000	2008-2010
CIHR	Post Graduate Scholarship - Doctoral	C	21,000	2006-2008
MSFHR	Junior Graduate Scholarship	C	7,000*	2006-2008
NSERC	Canada Graduate Scholarship	C	17,500	2004-2006
NSERC	Undergraduate Student Research Award	C	6,000	2003

\* Actual value \$20,000 per year, accepted at top-up rate of \$7,000 as addition to concurrent CIHR PGS-D.