BIOGRAPHICAL SKETCH

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NAME: Jacqueline Rose Starr

eRA COMMONS USER NAME (credential, e.g., agency login): jackiestarr

POSITION TITLE: Director, Biostatistics and Epidemiology Core; Associate Member of the Staff

EDUCATION/TRAINING *(Begin with baccalaureate or other initial professional education, such as nursing, include postdoctoral training and residency training if applicable. Add/delete rows as necessary.*)

INSTITUTION AND LOCATION	DEGREE *(if applicable)*	Completion Date MM/YYYY	FIELD OF STUDY
Yale University, New Haven, CT	BS	05/1990	Biology
University of Washington, Seattle, WA	MPH	06/2000	Epidemiology
University of Washington, Seattle, WA	MS	12/2000	Biostatistics
University of Washington, Seattle, WA	PhD	06/2003	Epidemiology

A. Personal Statement

I have a unique background that combines biology, epidemiology, translational science, image analysis and quantification (due to its relevance to birth defects phenotyping), oral science, and biostatistics. I have a particular interest in epidemiologic and biostatistical methods and helped design and teach the advanced epidemiologic methods course at the University of Washington. From 2003 to 2011 my research focused primarily on the epidemiology of craniofacial birth defects (including quantitative image analysis). After moving to Forsyth in 2011, I collaborated closely with dental researchers and microbiologists and have been transitioning my research to focus on the oral microbiome. The limitations of existing statistical methods drive my methods development work. I have designed and performed extensive simulation studies to investigate methods for genetic association studies, and I have played a leadership role in several methods development projects for which manuscripts have been published or are in development.

(†denotes my senior author contribution with advisee as first author)

1. **Lee KH**†, Coull BA, Moscicki AB, Paster BJ, **Starr JR**. Bayesian variable selection for multivariate zero-inflated models: Application to microbiome count data. Biostatistics. In press.
2. Johnston CD, Cotton S, Rittling SR, **Starr JR**, Borisy GG, Dewhirst FE, and Lemon KP. SyngenicDNA: stealth-by-engineering to evade restriction-modification barriers. Proc Nat Acad Sci. In press.
3. **Starr JR**, Huang Y, Lee KH, Murphy CM, Moscicki AB, Shiboski CH, Ryder MI, Yao TJ, Faller L, Van Dyke RB, Paster BJ. Oral microbiota in youth with perinatally acquired HIV infection. Microbiome 2018;6:100.
4. Duran-Pinedo AE, Chen T, Teles R, **Starr JR**, Wang X, Krishnan K, Frias-Lopez J. Community-wide transcriptome of the oral microbiome in subjects with and without periodontitis. ISME J. 2014;8:1659-1672. PMCID: PMC4817619

B. Positions and Honors

Positions and Employment

1988 Research Fellow, National Cancer Institute-Frederick Cancer Research Facility, Frederick, MD.
1988–1989 Research Assistant, Yale/New Haven Hospital Pathology Department, New Haven, CT.
1994–1997 Research Associate, CV Therapeutics, Inc., Palo Alto, CA.

1997–2002 Predoctoral Fellowship, Dental Public Health Sciences, University of Washington, Seattle, WA.
2001–2003 Study Coordinator, Fred Hutchinson Cancer Research Center, Seattle, WA.

University of Washington, Department of Pediatrics, School of Medicine; Department of Epidemiology, School of Public Health
2003–2008 Research Assistant Professor.
2008–2010 Research Associate Professor.
2010–2011 Associate Professor.
2011–present Affiliate Associate Professor (Department of Epidemiology).

The Forsyth Institute and Harvard University
2011–2012 Associate Research Investigator, The Forsyth Institute, Cambridge, MA
2011–2020 Director, Biostatistics and Epidemiology Core, The Forsyth Institute, Cambridge, MA
2012–2020 Associate Member of the Staff, The Forsyth Institute, Cambridge, MA
2012–present Lecturer, Harvard School of Dental Medicine, Boston, MA.
2012–present Associate Director, Harvard Catalyst Biostatistics Program, Harvard University, Boston, MA.
2020–present CDNM Director of Strategic Initiatives, Channing Division of Network Medicine, Brigham and Women's Hospital, Boston, MA

Other Experience and Professional Memberships
10/2005 Invited talk, Annual Meeting of American Society for Human Genetics, "Case-control versus family-based approaches for evaluating maternal genetic associations."
10/2006 Invited talk, 6th Copenhagen Workshop on Carcinoma in situ, Testis, and Germ Cell Cancer, "Polymorphism in estrogen metabolism regulating genes and testicular germ cell cancer risk."
2006–2009 Section Editor, Cleft Palate-Craniofacial Journal, Epidemiology.
10/2006 Member, NIH/NIDCR Special Emphasis Panel (SEP) "Dental-Related SBIR/STTR."
06/2007 Member, CDC SEP "DD07-008 Optimal Resources and Care for Children with Craniofacial Malformations" and "DD07-009 Public Health Research Grants on Orofacial Clefts and Craniosynostosis."
06/2010 Member, NIH/NIDCR SEP "PAR-10-041 NIDCR Small Research Grants for Data Analysis and Statistical Methodology applied to Genome-wide Data (R03)."
10/2010 Member, NIH/NIDCR SEP "2011/01 ZDE1 JR (05) R Secondary Data Analysis R03s."
03/2011 Member, NIH/NIDCR SEP, "2011/05 Council ZDE1 MH 14 1 GWAS Statistical Methods R03."
01/2012 Member, NIH/NIDCR, "2012/05 ZDE1 RK (07) 2 Review PAR10-170 T90s & PAR10-171 T32."
03/2012 Chair, NIH/NIDCR SEP "Secondary Data Analysis R03s."
02/2013 Member, NIH/NIDCR "ZDE1 RK-(07) Review T32 (PAR10-171) and T90/R90 (PAR10-170)"
06/2013- Chair, NIH/NIDCR Clinical Study Oversight Committee, Speech Pathology
02/2015, 06/2015 Member, NIH IRAP Infectious Diseases, Reproductive Health, Asthma and Pulmonary
06/2019, 03/2020 Conditions Study Section
2016-2018 Editorial Board, Journal of Dental Research

Selected Honors
2004–2005 Young Investigator Award, Children's Hospital and Regional Medical Center.
06/2006 Invited Participant, CDC Workshop, "Prioritizing a Public Health Research Agenda for Craniosynostosis."

C. Contributions to Science (†denotes my senior author contribution with advisee as first author)

1. Through collaborations at Forsyth Institute, I have been pivoting my research focus from craniofacial birth defects to the oral microbiome. Areas of focus have included methods development and 'omics analysis related to microbiome research.
   a. Lee KH†, Coull BA, Moscicki AB, Paster BJ, **Starr JR**. Bayesian variable selection for multivariate zero-inflated models: Application to microbiome count data. Biostatistics. In press.
   b. **Starr JR**, Huang Y, Lee KH, Murphy CM, Moscicki AB, Shiboski CH, Ryder MI, Yao TJ, Faller L, Van Dyke RB, Paster BJ. Oral microbiota in youth with perinatally acquired HIV infection. Microbiome 2018;6:100.

c. Duran-Pinedo AE, Chen T, Teles R, **Starr JR**, Wang X, Krishnan K, Frias-Lopez J. Community-wide transcriptome of the oral microbiome in subjects with and without periodontitis. ISME J. 2014;8:1659-1672. PMCID: PMC4817619
d. Lee CT, Teles R, Kantarci A, Chen T, McCafferty J, **Starr JR**, Neves Brito LC, Paster B, Van Dyke TE. Resolvin E1 reverses experimental periodontitis and dysbiosis. J. Immunol.;197:2796-2806. PMCID: PMC5026932.

2. As a collaborator on oral microbiome research study teams, I help ensure that studies are designed and conducted and data analyzed in a rigorous manner, and that interpretation is consistent with the study design and questions addressed. These projects are often about how the oral microbiome might relate to development of periodontitis or early childhood caries.
   a. Johnston CD, Cotton S, Rittling SR, **Starr JR**, Borisy GG, Dewhirst FE, and Lemon KP. SyngenicDNA: stealth-by-engineering to evade restriction-modification barriers. Proc Nat Acad Sci. 2019;116:11454-11459.
   b. Teles R, Benecha HK, Preisser JS, Moss K, **Starr JR**, Corby P, Genco R, Falkner KL, Garcia N, Giannobile WV, Jared H, Cugini M. Modeling Changes in Clinical Attachment Loss to Classify Periodontal Disease Progression. J Clin Perio. 2016; 43(5):426-434. PMCID: PMC5021116
   c. Soares GM, Teles FR, **Starr JR**, Feres M, Patel M, Martin L,Teles R. Effects of azithromycin, metronidazole, amoxicillin and metronidazole plus amoxicillin on in vitro polymicrobial subgingival biofilm model. Antimicrob Agents Ch. 2015;59:2791-2798. PMCID: PMC4394767
   d. Kressirer CA, Smith DJ, King WF, Dobeck JM, **Starr JR**, Tanner ACR. Cariogenicity of Scardovia wiggsiae in an experimental rat model. J Oral Biosci. J Oral Biosci. 2017;59:135-141.

3. I collaborate broadly with dentists, oral biology researchers, and others throughout Forsyth and Harvard School of Dental Medicine and Harvard T.H. Chan School of Public Health. I have a particular interest in rigorous methods to evaluate causal hypotheses.
   a. Abreu MHNG[†], Lee KH, Luquetti DV, **Starr JR**. Temporal trend in the birth prevalence of cleft lip and/or cleft palate in Brazil, 2000-2013. Birth Defects Research Part A. 2016;106:789-792.
   b. Atia L, Bi D, Sharma Y, Mitchel JA, Gweon B, Koehler S, DeCamp SJ, Lan B, Hirsch R, Pegoraro AF, Lee KH, **Starr JR**, Weitz DA, Martin AC, Park JA, Butler JP, Fredberg JJ. Universal geometric constraints during epithelial jamming. Nat Physics. 2018;14:613-620.
   c. Abreu MHNG[†], Resende VLS, Lee KH, da Matta-Machado ATG, **Starr JR**. Regional differences in infection control conditions in a sample of primary health care services in Brazil. Cadernos de Saúde Pública/Reports in Public Health. 2017; 33:e00072416
   d. Kim JH, Pegorarob AF, Das A, Koehler S, Ujwary SA, Lan B, Mitchel JA, Atia L, He S, Wang K, Bi D, Zaman M, Park JA, Butler JP, Lee KH, **Starr JR**, Fredberg JJ. Unjamming and collective migration in MCF10A breast cancer cell lines. BBRC. 2020;521:706-715.

4. During graduate school I developed a strong interest in epidemiologic and biostatistical methods, which led to my pursuit of an additional master's degree in biostatistics. Typically, my methods development work arises to address unanswered questions in epidemiologic research. For example, while developing hypotheses about effect modification in oral cancer etiology, I wondered about the appropriate statistical scale for assessing interactions. This led to investigation of the relative performance of commonly used techniques. Similarly, one aim of my dissertation was to evaluate the operating characteristics of a then newly developed technique for estimating maternal genetic associations with offspring disease. Since joining Forsyth in 2011 I have sought closer partnership with biostatisticians who can help me pursue my methodological interests. Several of these projects have been presented at the Joint Statistical Meetings and have manuscripts in preparation or under revision. For example, we developed a double balancing score approach for estimating average treatment effects in small to moderate sample sizes. We concluded that such an approach is a useful alternative to propensity score matching or doubly robust estimation in modest sample sizes. In a second project, we are developing two-stage designs similar to those used in genomewide association studies and adapted for correlated exposures, assay platforms that differ at the two data collection stages, and modest sample sizes, work we presented at the Joint Statistical Meetings.
   a. **Starr JR**, McKnight B. Assessing interaction in case-control studies: type I errors when using both additive and multiplicative scales. Epidemiology 2004;15:422-427.

b. **Starr JR**, Hsu L, Schwartz SM. Performance of the log-linear approach to case-parent triad data for assessing maternal genetic associations with offspring disease: type I error, power, and bias. Am J Epidemiol 2005;161:196-204.
c. **Starr JR**, Hsu L, Schwartz SM. Assessing maternal genetic associations: a comparison of the log-linear approach to case-parent triad data and a case-control approach. Epidemiology 2005;16:294-303.
d. Hsu L, **Starr JR**, Zheng Y, Schwartz SM. On combining triads and unrelated subjects data in assessing genetic association with disease risk: an application to testicular cancer. Hum Heredity 2008;67:88-103.

5. After graduate school, my expertise and interest in maternal genetic and non-genetic exposures as risk factors for disease led to my taking a faculty position based at Seattle Children's Craniofacial Center. There, I collaborated closely with a highly interdisciplinary team and developed my own lines of research on the epidemiology of congenital craniofacial conditions. Among the many publications based on my work there, most pertinent to the proposed project are those that describe quantitative image analyses. Image analysis is a key part of phenotype quantification for studying congenital craniofacial anomalies. Among other things, work included 1) comparing clinicians' ratings to objective data from two- (2D) and three-dimensional (3D) images, 2) assessing the reliability of measurements made on 3D versus 2D images, and 3) developing and assessing the validity of novel mathematically based quantitative shape descriptors for measuring skull shapes.
   a. Sie KCY, **Starr JR**, Bloom DC, Davis T, MacArthur C, Milczuk HA, Perkins JA, Willging JP. Multicenter study of inter- and intrarater reliability in the evaluation of velopharyngeal insufficiency. Arch Otolaryngol Head Neck Surg 2008;134:757-763.
   b. Ruiz-Correa S, **Starr JR**, Lin HJ, Cunningham ML, Kapp-Simon KA, Sze RW, Speltz ML. New Severity Indices for Quantifying Single Suture Metopic Craniosynostosis. J Neurosurg 2008;63:318-324. PMCID: PMC3412430
   c. Atmosukarto I, Shapiro LG, **Starr JR**, Heike CL, Collett B, Cunningham ML, Speltz ML. Three-dimensional head shape quantification for infants with and without deformational plagiocephaly. Cleft Palate-Craniofac J 2010;47(4):368-377. PMCID: PMC2899494.
   d. Birgfeld C, Saltzman BS, Luquetti DV, Latham K, **Starr JR**, Heike CL. Comparison of 2D and 3D images for phenotypic assessment of craniofacial microsomia. Cleft Palate Craniofac J. 2013;50:305-14. (co-PI)

D. Additional Information: Research Support and/or Scholastic Performance

<u>Ongoing Research Support</u>

R01 DE027249 Cayabyab (PI) 07/01/17 – 06/30/22

Novel Recombinant Streptococcus mitis as an Oral Vaccine against HIV/AIDS
We will assess immunogenicity of rSmitis prime-recombinant MVA vector and Env protein boost strategy in small animals and non-human primates and fine-tune vector immunogenicity.
Role: Co-Investigator

R44 DE023714 Iftimia (PI) 04/01/2018-3/31/2020

Optical probe for real-time assessment of periodontal health status
This project proposes to develop non-invasive and practical tools with high specificity and sensitivity for the diagnosis of the periodontal conditions for high-risk populations to prevent and treat the incipient disease.
Role: Biostatistician (Subaward)

UL1 TR002541 Nadler (PI) 05/01/18 - 04/30/23

Harvard Clinical and Translational Science Center (CTSC)
At the Forsyth, Harvard CTSC funds effort for two Biostatisticians. The Biostatisticians will collaborate extensively with CT researchers on problems in biostatistics, especially in areas in which they have particular expertise.
Role: Biostatistician (Subaward)

R21 DE026874 Bidlack (PI) 08/01/18 – 07/31/20

Saliva-mediated Mechanisms of Post-Eruptive Enamel Mineralization
We will elucidate the mechanism(s) of naturally occurring post-eruptive enamel mineralization in a porcine model system by using high-resolution imaging and integrated fluorescent protein labeling.
Role: Biostatistician

R21 DE026872 Starr, Lee (PIs) 08/01/18-7/31/20

Bayesian multivariate image analysis for studying oral biogeography
The major goal of the study is to develop methods for understanding the spatial organization of microbes by using spectral imaging data using statistical point pattern analysis approaches.
Role: PI

R03 DE027486 Lee (PI) 09/01/18-08/31/20

Multivariate Bayesian variable selection for high-dimensional oral microbiome data
We will develop a multivariate regression method for joint endpoint analysis of high-dimensional zero-inflated data, including an automated variable selection method that exploits the underlying dependence among taxa.
Role: Co-investigator

Completed Research Support

R01 GM117174 Lemon (PI) 02/01/16-08/31/19

Impact of commensal Corynebacterium species on pathogen colonization and microbiota composition
We will determine how Corynebacterium species release antibacterial free fatty acids; characterize mechanisms controlling activity of extracellular lipases; and test effect of applying triolein on skin microbiota.
Role: Co-Investigator

R03 DE023608 Starr (PI) 08/01/13 - 01/31/17

NCE
Hospital Volume for Orofacial Cleft Repair and Risk of Complications
We are estimating associations between procedure volumes and outcomes following primary CL or CP repair.
Role: PI

UL1 TR001102 Nadler (PI) 09/26/13 - 04/30/18

Harvard Clinical and Translational Science Center (CTSC)
At the Forsyth, Harvard CTSC funds effort for two Biostatisticians. The Biostatisticians will collaborate extensively with CT researchers on problems in biostatistics, especially in areas in which they have particular expertise.
Role: Biostatistician (Subaward)