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Bruce Spencer Weir

1 Contact Information

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2 Education

B.Sc.(HONS)	with First Class Honors in Mathematics, 1965 University of Canterbury, New Zealand
Ph.D.	in Statistics, with minor in Genetics, 1968 North Carolina State University, Raleigh, NC
Postdoctoral	Postgraduate Research Geneticist, 1969 University of California, Davis, CA

3 Professional Positions

1970–76	Massey University, Palmerston North, New Zealand
	Senior Lecturer 1970–75, Reader 1976, Department of Mathematics
1976–05	North Carolina State University, Raleigh, NC
	Associate Professor 1976–81, Professor 1981–92, Department of Statistics
	William Neal Reynolds Distinguished Professor of Statistics and Genetics 1992–2005
	Coordinator, Bioinformatics Graduate Program, 1999–2005
	Director, Bioinformatics Research Center, 2000–2005
2005–	University of Auckland, New Zealand
	Adjunct Professor of Bioinformatics, 2005–2008
	Adjunct Professor of Statistics, 2008–2015
	Honorary Professor of Statistics, 2016–
2006–	University of Washington, Seattle, WA
	Professor, Department of Biostatistics, 2006–
	Chair, Department of Biostatistics, 2006-2014
	Adjunct Professor, Department of Genome Sciences, 2006–
	Director, Genetics Analysis Center, 2015–
	Director, Institute of Public Health Genetics,
	Director of Graduate Program in Public Health Genetics, 2015–
2006–	Fred Hutchinson Cancer Research Center, Seattle, WA
	Joint Member, Division of Public Health Sciences

4 Honors and Awards

1961	New Zealand University Entrance Scholarship
1965	Cook Memorial Prize for Mathematics, University of Canterbury
1965	Fulbright Travel Grant
1968	Sigma Xi membership
1981	Alumni Association Award for Outstanding Research, NC State University
1983	Guggenheim Fellowship (at Department of Genetics, University of Edinburgh)
1990	United States Department of Agriculture Superior Service Award for Scientific Research (Group Award)
1992	William Neal Reynolds Distinguished Professor, North Carolina State University
1994	D.D. Mason Award, NC State University Statistics Department
1996	Osborne Memorial Lecture, University of Edinburgh
1996	Samuels Memorial Lecture, Purdue University
1998	Fellow of the American Association for the Advancement of Science
1998	Honorary Fellow of the Royal Society of New Zealand
1999	Fellow of the American Statistical Association
1999	Snedecor Lecture, Iowa State University
2001	Fisher Lecture, University of Adelaide
2003	O. Max Gardner Award, University of North Carolina System
2005	Holladay Medal for Excellence, North Carolina State University
2008	Fellow of the American Academy of Forensic Sciences
2014	Fulbright - Science Without Borders Distinguished Chair (at University of Sao Paulo, Brazil).
2016	Award for Contributions to Teaching and Research in Quantitative Genetics, 5th International Conference on Quantitative Genetics
2016	Cockerham Lecture, North Carolina State University
2019	Genetics Society of America: Elizabeth W. Jones Award for Excellence in Education.

5 Professional Activities

5.1 Editorial Positions

1977–97	Associate Editor of *Genetics*
1979–87	Associate Editor of *Theoretical Population Biology*
1979–94	Contributing Editor of *Current Index to Statistics*
1984–89	Associate Editor of *Biometrics*
1990–05	Associate Editor of *Journal of Heredity*
1993–95	Associate Editor of *American Journal of Human Genetics*
1993–05	Editor of *Theoretical Population Biology*
1997–12	Associate Editor of *Genetics Research*
2000–10	Associate Editor of *Genetic Epidemiology*
2005–08	Associate Editor of *Journal of the American Statistical Association*
2012–22	Editorial Board of *Journal of Forensic Sciences*

5.2 Professional Society Memberships

American Academy of Forensic Sciences (Fellow)
American Society of Human Genetics
American Statistical Association (Fellow)
Biometric Society
Genetics Society of America
International Society for Forensic Genetics
New Zealand Statistics Association
Society for the Study of Evolution

5.3 Professional Service

1979–83	Member of Genetics Study Section, NIH
1984–86	Member Regional Advisory Board, Biometric Society, ENAR
1987	Secretary, 2nd International Conference on Quantitative Genetics, Raleigh, NC
1991–95	Member Genetic Basis of Disease Review Committee (Training Grant Reviews), NIGMS
1993	Vice Chair, Gordon Conference on Quantitative Genetics and Biotechnology
1995	Chair, Gordon Conference on Quantitative Genetics and Biotechnology
1994–95	Defense Science Board Task Force on Use of DNA for Ancient Remains
1996-98	Council member, American Genetic Association
1998–00	Research and Development Working Group, Natl. Commission on the Future of DNA Evidence
1999	Chair, 4th International Conference on Forensic Statistics, Raleigh, NC
2000–04	Scientific Advisory Board, Wellcome Trust Center for Human Genetics, Oxford
2000–02	Scientific Advisory Board, Paradigm Genetics
2000–04	Member of Genome Study Section, NIH
2002–05	Board of Scientific Counselors, National Toxicology Program
2002–05	Treasurer, Genetics Society of America
2003–08	External Advisory Board, New Zealand Institute of Mathematics and its Applications
2007	Program Co-Chair, 3rd International Conference on Quantitative Genetics, Hangzhou, China
2008	Program Cttee, 7th International Conf. on Forensic Inference and Statistics, Lausanne
2008–	External Advisory Committee, Virtual Institute on Statistical Genetics, New Zealand
2008–	Technical Advisory Committee, Western Alaskan Salmon Stock Identification Program
2011	Chair, 8th International Conference on Forensic Inference and Statistics, Seattle, WA
2011–	Bioinformatics Research Advisory Group, National Marrow Donor Program
2011–	Strategic Science Advisory Panel, Environmental and Scientific Research, New Zealand
2012	Program Cttee, 4th International Conference on Quantitative Genetics, Edinburgh, UK
2012–	Y-chromosome Working Group, Scientific Working Group on DNA Analysis Methods
2012–	American Statistical Association Advisory Committee on Forensic Science
2013	Organizing Committee: "Impact of Large-Scale Genomic Data on Statistical and Quantitative Genetics" Conference, University of Washington.
2014–	Member, Biology/DNA Scientific Area Committee within the Organization of Scientific Area Committees, NIJ/NIST.
2016,2018	Grant Review Panel, National Institute of Justice.

6 Bibliography

6.1 Refereed Research Publications

1. Weir BS. 1965. Mixed self and sib mating. New Zealand Mathematics Magazine 2:78–89.
2. Cockerham CC, Weir BS. 1968. Sib mating with two linked loci. Genetics 60:629–640. [PMCID: PMC1212066]
3. Weir BS, Cockerham CC. 1969a. Pedigree mating with two linked loci. Genetics 61:923–940. [PMCID: PMC1212252]
4. Weir BS, Cockerham CC. 1969b. Group inbreeding with two linked loci. Genetics 63:711–742. [PMCID: PMC1212379]
5. Brown AHD, Weir BS, Marshall DR. 1970. Optimum family size for the estimation of heterozygosity in plant populations. Heredity 25:233–239.
6. Weir BS. 1970. Equilibria under inbreeding and selection. Genetics 65:371–378. [PMCID: PMC1212451]
7. Weir BS. 1971. Two locus inbreeding functions. Journal of Theoretical Biology 30:423–425.
8. Allard RW, Kahler AL, Weir BS. 1972. The effect of selection on esterase allozymes in a barley population. Genetics 72:489–503. [PMCID: PMC1212847]
9. Weir BS, Allard RW, Kahler AL. 1972. Analysis of complex allozyme polymorphisms in a barley population. Genetics 72:505–523. [PMCID: PMC1212848]
10. Weir BS. 1972. An undergraduate programme in biomathematics. New Zealand Mathematics Magazine 9:152–167.
11. Cockerham CC, Weir BS. 1973. Descent measures for two loci with some applications. Theoretical Population Biology 4:300–330.
12. Weir BS, Cockerham CC. 1973. Mixed self and random mating at two loci. Genetical Research 21:247–262.
13. Weir BS, Cockerham CC. 1974. Behavior of pairs of loci in finite monoecious populations. Theoretical Population Biology 6:323–354.
14. Weir BS, Allard RW, Kahler AL. 1974. Further analysis of complex allozyme polymorphisms in a barley population. Genetics 78:911–919. [PMCID: PMC1224564]
15. Weir BS. 1974. Linkage in population genetics. New Zealand Statistician 9:35–40.
16. Ross MD, Weir BS. 1975. Maintenance of male sterility in plant populations. III. Mixed selfing and random mating. Heredity 35:21–29.
17. Brown AHD, Marshall DR, Weir BS. 1975. Population differentiation under the charge state model. Genetics 81:739–748. [PMCID: PMC1213431]
18. Ross MD, Weir BS. 1976. Maintenance of males and females in hermaphrodite populations and the evolution of dioecy. Evolution 30:425–441.

19. Weir BS, Brown AHD, Marshall DR. 1976. Testing for selective neutrality of electrophoretically detectable protein polymorphisms. Genetics 84:639–659. [PMCID: PMC1213600]

20. Cockerham CC, Weir BS. 1977. Quadratic analyses of reciprocal crosses. Biometrics 33:187–203.

21. Choy SC, Weir BS. 1977. Two-locus inbreeding measures for recurrent selection. Theoretical and Applied Genetics 49:63–77.

22. Cockerham CC, Weir BS. 1977. Digenic descent measures for finite populations. Genetical Research 30:121–147.

23. Weir BS, Brook RJ. 1977. PSI for a large service course. New Zealand Journal of Educational Studies 12:176–181.

24. Weir BS, Cockerham CC. 1978. Testing hypotheses about linkage disequilibrium with multiple alleles. Genetics 88:633–642. [PMCID: PMC1224605

25. Choy SC, Weir BS. 1978. Exact inbreeding coefficients in populations with overlapping generations. Genetics 89:591–614. [PMCID: PMC1213856]

26. Weir BS. 1979. Inferences about linkage disequilibrium. Biometrics 35:235–254.

27. Weir BS, Cockerham CC. 1979. Estimation of linkage disequilibrium in randomly mating populations. Heredity 42:105–111.

28. Marshall R, Weir BS. 1979. Maintenance of genetic variation in apomictic plant populations. I. Single locus models. Heredity 42:159–172.

29. Laurie-Ahlberg CC, Weir BS. 1979. Allozymic variation and linkage disequilibrium in some laboratory populations of Drosophila melanogaster. Genetics 92:1295–1314. [PMCID: PMC1214072]

30. Laurie-Ahlberg CC, Maroni G, Bewley GC, Lucchesi JC, Weir BS. 1980. Quantitative genetic variation of enzyme activities in natural populations of *Drosophila melanogaster*. Proceedings of the National Academy of Sciences USA 77:1073–1077. [PMCID: PMC348426]

31. Stuber CW, Moll RH, Goodman MM, Schaffer HE, Weir BS. 1980. Allozyme frequency changes associated with selection for increased grain yield in maize (*Zea mays L.*). Genetics 95:225–236. [PMCID: PMC1214218]

32. Weir BS, Hill WG. 1980. Effect of mating structure on variation in linkage disequilibrium. Genetics 95:477–488. [PMCID: PMC1214241]

33. Weir BS, Avery PJ, Hill WG. 1980. Effect of mating structure on variation in inbreeding. Theoretical Population Biology 18:396–429.

34. Weir BS, Cockerham CC, Reynolds J. 1980. The effects of linkage and linkage disequilibrium on the covariances of noninbred relatives. Heredity 45:351–359.

35. Cockerham CC, Weir BS. 1983. Variance of actual inbreeding. Theoretical Population Biology 23:85–109.

36. Reynolds J, Weir BS, Cockerham CC. 1983. Estimation of the coancestry coefficient: basis for a short-term genetic distance. Genetics 105:767–779. [PMCID: PMC1202185]

37. Cockerham CC, Weir BS. 1983. Linkage between a marker locus and a quantitative trait of sibs. American Journal of Human Genetics 35:263–273. [PMCID: PMC1685528]

38. Cockerham CC, Weir BS. 1984. Covariances of relatives stemming from a population undergoing mixed self and random mating. Biometrics 40:157–164.

39. Weir BS, Cockerham CC. 1984. Estimating F-statistics for the analysis of population structure. Evolution 38:1358–1370.

40. Marshall DR, Weir BS. 1985. Multiline varieties and disease control. V. The "dirty crop" approach with complex mixtures of genotypes based on overlapping gene sets. Theoretical and Applied Genetics 69:463–474.

41. Weir BS. 1985. Statistical analysis of molecular genetic data. Journal of Mathematics Applied in Medicine and Biology 2:1–39.

42. Weir BS, Ohta T, Tachida H. 1985. Gene conversion models. Journal of Theoretical Biology 116:1–8.

43. Barker JSF, East PD, Weir BS. 1986. Temporal and microgeographic variation in allozyme frequencies in a natural population of *Drosophila buzzatii*. Genetics 112:577–611. [PMCID: PMC1202765]

44. Weir BS, Hill WG. 1986. Nonuniform recombination within the human beta-globin gene cluster. American Journal of Human Genetics 38:776–778. [PMCID: PMC1684823]

45. Cockerham CC, Weir BS. 1986. Estimation of inbreeding parameters in stratified populations. Annals of Human Genetics 50:271–281.

46. Weir BS, Wilson SR. 1986. Log-linear models for linked loci. Biometrics 42:665–670.

47. Weir BS, Brooks LD. 1986. Disequilibrium on human chromosome 11p. Genetic Epidemiology Supplement 1:177–183.

48. Cockerham CC, Weir BS. 1987. Correlations, descent measures: Drift with migration and mutation. Proceedings of the National Academy of Sciences USA 84:8512–8514. [PMCID: PMC299574]

49. Hill WG, Weir BS. 1988. Variances and covariances of squared linkage disequilibria in finite populations. Theoretical Population Biology 33:54–78.

50. Weir BS. 1988. Statistical analysis of DNA sequences. Journal of the National Cancer Institute 80:395–406.

51. Brooks LD, Weir BS, Schaffer H. 1988. Probabilities of similarities in DNA sequence comparisons. Genomics 3:207–216.

52. Hernandez JL, Weir BS. 1989. A disequilibrium coefficient approach to Hardy-Weinberg testing. Biometrics 45:53–70.

53. Weir BS, Reynolds J, Dodds KG. 1990. The variance of sample heterozygosity. Theoretical Population Biology 37:235–353.

54. Macpherson JN, Weir BS, Leigh Brown AJ. 1990. Extensive linkage disequilibrium in the achaete-scute complex of *Drosophila melanogaster*. Genetics 126:121–129. [PMCID: PMC1204116]

55. Dean M, Amos JA, Lynch J, Romeo G, Devoto M, Ward K, Halley D, Oostra B, Ferrari M, Russo S, Weir BS, Finn PB, Collins FS, Iannuzzi MC. 1990. Prenatal diagnosis and linkage disequilibrium with cystic fibrosis for markers surrounding D7S8. Human Genetics 85:275–278.

56. Weir BS, Basten CJ. 1990. Sampling strategies for distances between DNA sequences. Biometrics 46:551–582.

57. Basten CJ, Weir BS. 1990. Effect of gene conversion on variances of digenic identity measures. Theoretical Population Biology 38:125–148.

58. Weir BS. 1992. Independence of VNTR alleles defined as fixed bins. Genetics 130:873–887. [PMCID: PMC1204936]

59. Berkman N. Weir BS, Pressman-Schwartz S, Reshef A, Leitersdorf E. 1992. Haplotype analysis at the low density lipoprotein receptor locus: application to the study of familial hypercholesterolemia in Israel. Human Genetics 88:405–410.

60. Maiste PJ, Weir BS. 1992. Estimating linkage disequilibrium from conditional data. American Journal of Human Genetics 50:1139–1140. [PMCID: PMC1682602]

61. Muse SV, Weir BS. 1992. Testing for equality of evolutionary rates. Genetics 132:269–276. [PMCID: PMC1205125]

62. Kaplan N, Weir BS. 1992. Expected behavior of conditional linkage disequilibrium. American Journal of Human Genetics 51:333–343. [PMCID: PMC1682675]

63. Weir BS. 1992. Independence of VNTR alleles defined as floating bins. American Journal of Human Genetics 51:992–997. [PMCID: PMC1682849]

64. Evett IW, Weir BS. 1992. Flawed reasoning in court. Chance 4:19–21.

65. Cockerham CC, Weir BS. 1993. Estimation of gene flow from F-statistics. Evolution 47:855–863.

66. Weir BS, Gaut BS. 1993. Matching and binning DNA fragments in forensic science. Jurimetrics Journal 34:9–19.

67. Weir BS, Gaut, BS 1993. Variances for distances between plant sequences. New Zealand Journal of Botany 31:317–321.

68. Weir BS. 1993. Tests for independence of VNTR alleles defined as quantile bins. American Journal of Human Genetics 53:1107–1113. [PMCID: PMC1682316]

69. Weir BS. 1993. Analysis of DNA sequences. Statistical Methods in Medical Research 2:225–239.

70. Weir BS, Hill WG. 1993. Population genetics of DNA profiles. Journal of Forensic Science Society 33:219–226.

71. Hill WG, Weir BS. 1994. Maximum likelihood estimation of gene location by linkage disequilibrium. American Journal of Human Genetics 54:705–714. [PMCID: PMC1918089]

72. Gaut BS, Weir BS. 1994. Detecting substitution rate heterogeneity among regions of a nucleotide sequence. Molecular Biology and Evolution 11:620–629.

73. Weir BS. 1994. Effects of inbreeding on forensic calculations. Annual Review of Genetics 28:597–621

74. Zhu J, Weir BS. 1994. Analysis of cytoplasmic and maternal effects. I. A genetic model for diploid plant seeds and animals. Theoretical and Applied Genetics 89:153–159.

75. Zhu J, Weir BS. 1994. Analysis of cytoplasmic and maternal effects. II. Genetic models for triploid endosperms. Theoretical and Applied Genetics 89:160–166.

76. Kaplan NL, Lewis PO, Weir BS. 1994. Age of the Delta F508 cystic fibrosis mutation. Nature Genetics 8:216

77. Zhu J, Weir BS. 1994. Clustering populations by mixed linear models. Journal of Biomathematics 9:1–14.

78. Kaplan NL, Hill WG, Weir BS. 1995. Likelihood methods for locating disease genes in non-equilibrium populations. American Journal of Human Genetics 56:18–32. [PMCID: PMC1801340]

79. Zaykin D, Zhivotovsky L, Weir BS. 1995. Exact tests for disequilibria with arbitrary numbers of loci and alleles. Genetica 96:169–178.

80. Maiste PJ, Weir BS. 1995. Comparison of tests for independence in the FBI RFLP databases. Genetica 96:125–138.

81. Kaplan NL, Weir BS. 1995. Are moment bounds on the recombination fraction between a marker and a disease locus too good to be true? Allelic association mapping revisited for simple genetic diseases in the Finnish population. American Journal of Human Genetics 57:1486–1498. [PMCID: PMC1801420]

82. Evett IW, Gill PD, Scranage JK, Weir BS. 1996. Establishing the robustness of STR statistics for forensic applications. American Journal of Human Genetics 58:398–407. [PMCID: PMC1914534]

83. Zhu J, Weir BS. 1996. Diallel analysis for sex-linked and maternal effects. Theoretical and Applied Genetics 92:1–9.

84. Hamilton JF, Starling L, Cordiner SJ, Monahan DL, Buckleton JS, Chambers GK, Weir BS. 1996. New Zealand population data at five VNTR loci: validation as databases for forensic identity testing. Science and Justice 36:109–117.

85. True JR, Weir BS, Laurie CC. 1996. A genome-wide survey of hybrid incompatibility factors by the introgression of P-element marked segments of *Drosophila mauritiana* chromosomes into Drosophila simulans. Genetics 142:819–837. [PMCID: PMC1207021]

86. Weir BS, Buckleton JS. 1996. Statistical issues in DNA profiling. Proceedings of the 16th International Congress on Forensic Haemogenetics 6:457–464.

87. Zeng ZB, Weir BS. 1996. Statistical methods for mapping quantitative trait loci. Acta Agronomica Sinica 22:535–549.

88. Evett IW, Lambert JA, Buckleton JS, Weir BS. 1996. Statistical analysis of a large file of data from STR profiles of British Caucasians to support forensic casework. International Journal of Legal Medicine 109:173–177.

89. Zhu J, Weir BS. 1996. Mixed model approaches for diallel analysis based on a biomodel. Genetical Research 68:233–240.

90. Weir BS, Triggs CM, Starling L, Stowell LI, Walsh KAJ, Buckleton JS. 1997. Interpreting DNA mixtures. Journal of Forensic Science 42:213–222.

91. Zhu J, Weir BS. 1997. Mixed model approaches for diallel analysis based on a biomodel. Genetical Research 68: 233-240.

92. Shaw AJ, Weir BS, Shaw FH. 1997. The occurrence and significance of epistatic variance for quantitative characters and its measurement in haploids. Evolution 51:348-353.

93. Kaplan NL, Martin ER, Weir BS. 1997. Power studies for transmission/disequilibrium tests with multiple alleles. American Journal of Human Genetics 60:691-702. [PMCID: PMC1712498]

94. Martin ER, Kaplan NL, Weir BS. 1997. Tests for linkage and association in nuclear families. American Journal of Human Genetics 61:439-448. [PMCID: PMC1715892]

95. Doerge RW, Zeng ZB, Weir BS. 1997. Statistical issues in the search for genes affecting quantitative traits in experimental populations. Statistical Science 12:195-219.

96. McIntyre LM, Weir BS. 1997. Hardy-Weinberg testing for continuous data. Genetics 147:1965–1975. [PMCID: PMC1208361]

97. Buckleton JS, Evett IW, Weir BS. 1998. Setting bounds for the likelihood ratio when multiple hypotheses are postulated. Science and Justice 38:23–26.

98. Kaplan NL, Martin ER, Morris RW, Weir BS. 1998. Marker selection for the transmission/disequilibrium test in recently admixed populations. American Journal of Human Genetics 62:703–712. [PMCID: PMC1376954]

99. Shoemaker J, Painter I, Weir BS. 1998. A Bayesian characterization of Hardy-Weinberg disequilibrium. Genetics 149:2079–2088. [PMCID: PMC1460273]

100. Monks SA, Kaplan NL, Weir BS. 1998. A comparative study of sibship tests of linkage and/or association. American Journal of Human Genetics 63:1517–1530. [PMCID: PMC1377561]

101. Nielsen DM, Ehm MG, Weir BS. 1998. Detecting marker-disease association by testing for Hardy-Weinberg disequilibrium at a marker locus. American Journal of Human Genetics 63:1531–1540. [PMCID: PMC1377570]

102. Curran J, Triggs CM, Buckleton J, Weir BS. 1999. Interpreting DNA mixtures in structured populations. Journal of Forensic Sciences 44:987–995.

103. Weir BS. 1999. Are DNA profiles unique? Pp. 114–117, in Proceedings of the 9th International Symposium on Human Identification (http://www.promega.com/geneticidentity/proceed.html)

104. Nielsen DM, Weir BS. 1999. A classical setting for associations between markers and loci affecting quantitative traits. Genetical Research 74:271–277.

105. Weir BS. 2000. What is the structure of human populations? Evolutionary Biology 32: 195–202.

106. Graham J, Curran J, Weir BS. 2000. Conditional genotypic probabilities for microsatellite loci. Genetics 155:1973–1980. [PMCID: PMC1461189]

107. Rahman Z, Afroze T, Weir BS. 2001. DNA typing results from two urban sub-populations of Pakistan. Journal of Forensic Sciences 46:111–115.

108. Hardy SW, Weir BS, Kaplan NL, Martin ER. 2001. Analysis of SNPs in candidate genes using the pedigree disequilibrium test. Genetic Epidemiology 21:S441–S446.

109. Czika WA, Weir BS, Edwards SR, Thompson RW, Nielsen DM, Brocklebank JC, Zinkus C, Martin ER, Hobler KE. 2001. Applying data mining techniques to the mapping of complex disease genes. Genetic Epidemiology 21:S435–S440.

110. Huang SP, Weir BS. 2001. Estimating the total number of alleles using a sample coverage method. Genetics 159:1365–1373. [PMCID: PMC1461871]

111. De Luca M, Rose G, Bonafé M, Garasto S, Greco V, Weir BS, Franceschi C, De Benedictis G. 2001. Sex-specific longevity associations defined by Tyrosine Hydoxylase-Insulin-Insulin growth factor 2 on the 11p15.5 chromosomal region. Experimental Gerontology 36:1663–1671.

112. Nielsen DM, Weir BS. 2001. Association studies for general disease models. Theoretical Population Biology 60:253–263.

113. Zaykin D, Zhivotovsky LA, Westfall PH, Weir BS. 2002. Truncated product method for combining p-values. Genetic Epidemiology 22:170–185.

114. Chu TM, Weir BS, Wolfinger R. 2002. A systematic statistical linear modeling approach to oligonucleotide array experiments. Mathematical Biosciences 176:35–51.

115. Curran JM, Buckleton JS, Triggs CM, Weir BS. 2002. Assessing uncertainty in DNA evidence caused by sampling effects. Science and Justice 42:29–37.

116. Weir BS, Hill WG. 2002. Estimating F-statistics. Annual Review of Genetics 36:721–750.

117. Spruill S, Hardy S, Weir BS, Lu J. 2002. Assessing sources of variability in microarray gene expression data. BioTechniques 33:916–923.

118. Weir BS. 2002. Genetic distances and population histories: traps and bootstraps. Proceedings of the 7th World Congress on Genetics Applied to Livestock Production. Communication 26-01.

119. Weir BS 2002. Bioinformatics and approaches for identifying polygenic susceptibility traits. Annals of Periodontology 7:1–7.

120. Law B, Buckleton JS, Triggs CM, Weir BS. 2003. Effects of population structure and admixture on exact tests for association between loci. Genetics 164:381–387. [PMCID: PMC1462537]

121. Brenner CH, Weir BS. 2003. Issues and strategies in the DNA identification of World Trade Center victims. Theoretical Population Biology 63:173–178.

122. Laurie C, Weir BS. 2003. Dependency effects in multi-locus match probabilities. Theoretical Population Biology 63:207–219.

123. Chu TM, Weir BS, Wolfinger R. 2004. Comparison of Li-Wong and loglinear mixed models for the statistical analysis of oligonucleotide arrays. Bioinformatics 20:500-506.

124. Hill WG, Weir BS. 2004. Moment estimation of population diversity and genetic distance from data on recessive markers. Molecular Ecology 13:895–908.

125. Czika WA, Weir BS. 2004. The multiallelic trend test. Biometrics 60:69-74.

126. Weir BS. 2004. Matching and partially-matching DNA profiles. Journal of Forensic Sciences 49:1009–1014.

127. Weir BS, Bagdonavicius A, Blair B, Eckhoff C, Pearman C, Stringer P, Sutton J, West J, Wynen D. 2004. Allele frequency data for Profiler Plus loci in Australia. Journal of Forensic Sciences 49:1121–1123.

128. Maiste PJ, Weir BS. 2004. Optimal testing strategies for large, sparse multinomial tables. Computational Statistics and Data Analysis 46:605–620.

129. Weir BS, Hill WG, Cardon LR. 2004. Allelic association patterns for a dense SNP map. Genetic Epidemiology 24:442–450.

130. Nielsen, D.M., M.G. Ehm, D. Zaykin and B.S. Weir. 2004. Effect of two- and three-locus linkage disequilibrium on the power to detect marker/phenotype associations. Genetics 168:1029-1040. [PMCID: PMC1448814]

131. Liu, W. and B.S. Weir. 2004. Affected sib-pair tests in inbred populations. Annals of Human Genetics 68:606–619.

132. Liu W, Weir BS. 2005. Genotypic probabilities for pairs of inbred relatives. Philosophical Transactions of the Royal Society: Biological Sciences 360:1379-1385. [PMCID: PMC1855075]

133. Weir BS, Cardon LR, Anderson AD, Nielsen DM, Hill WG. 2005. Measures of human population structure show heterogeneity among genomic regions. Genome Research 15:1468-1476. [PMCID: PMC1310634]

134. The International HapMap Consortium (B.S. Weir is one of many authors). 2005. A haplotype map of the human genome. Nature 437:1299-1320.

135. Anderson AD, Weir BS. 2005. It was one of my brothers. International Journal of Legal Medicine 120:95–104. [PMID 16133567: PubMed Indexed for Medline]

136. Anderson AD, Weir BS. 2006. An assessment of the behavior of the population structure parameter θ at the CODIS loci. Progress in Forensic Genetics 11:495-497.

137. Wang T, Weir BS, Zeng ZB. 2006. A population-based latent variable approach for association mapping of quantitative trait loci. Annals of Human Genetics 70:506–523.

138. Skalski GT, Crouch CR, Garber AF, Weir BS, Sullivan CV. 2006. Evaluation of DNA pooling for the estimation of microsatellite allele frequencies: A case study using striped bass (*Morone saxtilis*). Genetics 173:863-875. [PMCID: PMC1526518]

139. Diatchenko L, Anderson AD, Slade GD Fillingham RB, Shabalina SA, Higgins TJ, Sama S, Inna B, Goldman D, Max MB, Weir BS, Maixner WJ. 2006. Three major haplotypes of the beta 2 adrenergic receptor define psychological profile, blood pressure, and the risk for development of a common muscoskeletal pain disorder. American Journal of Medical Genetics Part B - Neuropsychiatric Genetics 141B: 449–462. [PMCID: PMC2570772]

140. Weir BS, Anderson AD, Hepler AB. 2006. Genetic relatedness analysis: modern data and new challenges. Nature Reviews Genetics 7:771–780. [PMID 16983373, PubMed - indexed for MEDLINE]

141. Yoo YR, Ke X, Hong S, Jang HY, Park L, Kim S, Ahn TJ, Lee YD, Song O, Rho NY, Lee MS, Lee YS, Kim J, Kim YJ, Yang JM, Song K, Kim K, Weir B, Cardon LR, Lee JE, Hwang JJ. 2006. Fine-scale map of encyclopedia of DNA elements regions in the Korean population. Genetics 174:491–497.

142. Gill P, Brenner CH, Buckleton JS, Carracedo A, Krawczak M, Mayr WR, Morling N, Prinz M, Schneider PM, Weir BS. 2006. DNA Commission of the International Society of Forensic Genetics (ISFG): Recommendations on the interpretation of mixtures. International Journal of Legal Medicine 160:90–101. [PMID 16750605]

143. Weir BS. 2007. Impact of dense genetic marker maps on plant population genetic studies. Euphytica 154: 355–364.

144. Anderson AD, Weir BS. 2007. A maximum likelihood method for the estimation of pairwise relatedness in structured populations. Genetics 176: 421–440. [PMCID: PMC1893072]

145. Sabeti PC, Varilly P, Fry B, Lohmueller J, Hostetter E, Cotsapas C, Xie X, Byrne EH, McCarroll SA, Gaudet R, Schaffner SF, Lander ES; International HapMap Consortium, Frazer KA, Ballinger DG, Cox DR, Hinds DA, Stuve LL, Gibbs RA, Belmont JW, Boudreau A, Hardenbol P, Leal SM, Pasternak S, Wheeler DA, Willis TD, Yu F, Yang H, Zeng C, Gao Y, Hu H, Hu W, Li C, Lin W, Liu S, Pan H, Tang X, Wang J, Wang W, Yu J, Zhang B, Zhang Q, Zhao H, Zhao H, Zhou J, Gabriel SB, Barry R, Blumenstiel B, Camargo A, Defelice M, Faggart M, Goyette M, Gupta S, Moore J, Nguyen H, Onofrio RC, Parkin M, Roy J, Stahl E, Winchester E, Ziaugra L, Altshuler D, Shen Y, Yao Z, Huang W, Chu X, He Y, Jin L, Liu Y, Shen Y, Sun W, Wang H, Wang Y, Wang Y, Xiong X, Xu L, Waye MM, Tsui SK, Xue H, Wong JT, Galver LM, Fan JB, Gunderson K, Murray SS, Oliphant AR, Chee MS, Montpetit A, Chagnon F, Ferretti V, Leboeuf M, Olivier JF, Phillips MS, Roumy S, Salle C, Verner A, Hudson TJ, Kwok PY, Cai D, Koboldt DC, Miller RD, Pawlikowska L, Taillon-Miller P, Xiao M, Tsui LC, Mak W, Song YQ, Tam PK, Nakamura Y, Kawaguchi T, Kitamoto T, Morizono T, Nagashima A, Ohnishi Y, Sekine A, Tanaka T, Tsunoda T, Deloukas P, Bird CP, Delgado M, Dermitzakis ET, Gwilliam R, Hunt S, Morrison J, Powell D, Stranger BE, Whittaker P, Bentley DR, Daly MJ, de Bakker PI, Barrett J, Chretien YR, Maller J, McCarroll S, Patterson N, Pe'er I, Price A, Purcell S, Richter DJ, Sabeti P, Saxena R, Schaffner SF, Sham PC, Varilly P, Altshuler D, Stein LD, Krishnan L, Smith AV, Tello-Ruiz MK, Thorisson GA, Chakravarti A, Chen PE, Cutler DJ, Kashuk CS, Lin S, Abecasis GR, Guan W, Li Y, Munro HM, Qin ZS, Thomas DJ, McVean G, Auton A, Bottolo L, Cardin N, Eyheramendy S,

Freeman C, Marchini J, Myers S, Spencer C, Stephens M, Donnelly P, Cardon LR, Clarke G, Evans DM, Morris AP, Weir BS, Tsunoda T, Johnson TA, Mullikin JC, Sherry ST, Feolo M, Skol A, Zhang H, Zeng C, Zhao H, Matsuda I, Fukushima Y, Macer DR, Suda E, Rotimi CN, Adebamowo CA, Ajayi I, Aniagwu T, Marshall PA, Nkwodimmah C, Royal CD, Leppert MF, Dixon M, Peiffer A, Qiu R, Kent A, Kato K, Niikawa N, Adewole IF, Knoppers BM, Foster MW, Clayton EW, Watkin J, Gibbs RA, Belmont JW, Muzny D, Nazareth L, Sodergren E, Weinstock GM, Wheeler DA, Yakub I, Gabriel SB, Onofrio RC, Richter DJ, Ziaugra L, Birren BW, Daly MJ, Altshuler D, Wilson RK, Fulton LL, Rogers J, Burton J, Carter NP, Clee CM, Griffiths M, Jones MC, McLay K, Plumb RW, Ross MT, Sims SK, Willey DL, Chen Z, Han H, Kang L, Godbout M, Wallenburg JC, L'Archevque P, Bellemare G, Saeki K, Wang H, An D, Fu H, Li Q, Wang Z, Wang R, Holden AL, Brooks LD, McEwen JE, Guyer MS, Wang VO, Peterson JL, Shi M, Spiegel J, Sung LM, Zacharia LF, Collins FS, Kennedy K, Jamieson R, Stewart J. 2007. Genome-wide detection and characterization of positive selection in human populations. Nature 449:913–918. [PMID 1793131: PubMed Indexed for Medline]

146. International HapMap Consortium, Frazer KA, Ballinger DG, Cox DR, Hinds DA, Stuve LL, Gibbs RA, Belmont JW, Boudreau A, Hardenbol P, Leal SM, Pasternak S, Wheeler DA, Willis TD, Yu F, Yang H, Zeng C, Gao Y, Hu H, Hu W, Li C, Lin W, Liu S, Pan H, Tang X, Wang J, Wang W, Yu J, Zhang B, Zhang Q, Zhao H, Zhao H, Zhou J, Gabriel SB, Barry R, Blumenstiel B, Camargo A, Defelice M, Faggart M, Goyette M, Gupta S, Moore J, Nguyen H, Onofrio RC, Parkin M, Roy J, Stahl E, Winchester E, Ziaugra L, Altshuler D, Shen Y, Yao Z, Huang W, Chu X, He Y, Jin L, Liu Y, Shen Y, Sun W, Wang H, Wang Y, Wang Y, Xiong X, Xu L, Waye MM, Tsui SK, Xue H, Wong JT, Galver LM, Fan JB, Gunderson K, Murray SS, Oliphant AR, Chee MS, Montpetit A, Chagnon F, Ferretti V, Leboeuf M, Olivier JF, Phillips MS, Roumy S, Salle C, Verner A, Hudson TJ, Kwok PY, Cai D, Koboldt DC, Miller RD, Pawlikowska L, Taillon-Miller P, Xiao M, Tsui LC, Mak W, Song YQ, Tam PK, Nakamura Y, Kawaguchi T, Kitamoto T, Morizono T, Nagashima A, Ohnishi Y, Sekine A, Tanaka T, Tsunoda T, Deloukas P, Bird CP, Delgado M, Dermitzakis ET, Gwilliam R, Hunt S, Morrison J, Powell D, Stranger BE, Whittaker P, Bentley DR, Daly MJ, de Bakker PI, Barrett J, Chretien YR, Maller J, McCarroll S, Patterson N, Pe'er I, Price A, Purcell S, Richter DJ, Sabeti P, Saxena R, Schaffner SF, Sham PC, Varilly P, Altshuler D, Stein LD, Krishnan L, Smith AV, Tello-Ruiz MK, Thorisson GA, Chakravarti A, Chen PE, Cutler DJ, Kashuk CS, Lin S, Abecasis GR, Guan W, Li Y, Munro HM, Qin ZS, Thomas DJ, McVean G, Auton A, Bottolo L, Cardin N, Eyheramendy S, Freeman C, Marchini J, Myers S, Spencer C, Stephens M, Donnelly P, Cardon LR, Clarke G, Evans DM, Morris AP, Weir BS, Tsunoda T, Mullikin JC, Sherry ST, Feolo M, Skol A, Zhang H, Zeng C, Zhao H, Matsuda I, Fukushima Y, Macer DR, Suda E, Rotimi CN, Adebamowo CA, Ajayi I, Aniagwu T, Marshall PA, Nkwodimmah C, Royal CD, Leppert MF, Dixon M, Peiffer A, Qiu R, Kent A, Kato K, Niikawa N, Adewole IF, Knoppers BM, Foster MW, Clayton EW, Watkin J, Gibbs RA, Belmont JW, Muzny D, Nazareth L, Sodergren E, Weinstock GM, Wheeler DA, Yakub I, Gabriel SB, Onofrio RC, Richter DJ, Ziaugra L, Birren BW, Daly MJ, Altshuler D, Wilson RK, Fulton LL, Rogers J, Burton J, Carter NP, Clee CM, Griffiths M, Jones MC, McLay K, Plumb RW, Ross MT, Sims SK, Willey DL, Chen Z, Han H, Kang L, Godbout M, Wallenburg JC, L'Archevque P, Bellemare G, Saeki K, Wang H, An D, Fu H, Li Q, Wang Z, Wang R, Holden AL, Brooks LD, McEwen JE, Guyer MS, Wang VO, Peterson JL, Shi M, Spiegel J, Sung LM, Zacharia LF, Collins FS, Kennedy K, Jamieson R, Stewart J. 2007. A second generation human haplotype map of over 3.1 million SNPs. Nature 449:851–861. [PMID 17943122: PubMed Indexed for Medline]

147. Hill W, Weir BS. 2007. Prediction of multi-locus inbreeding coefficients and relation to linkage disequilibrium in random mating populations. Theoretical Population Biology 72:179–185. [PMCID: PMC2729754]

148. Laurie CC, Nickerson DA, Anderson AD, Weir BS, Livingston RJ, Dean MD, Smith KL, Schadt EE, Nachman MW. 2007. Linkage disequilibrium in wild mice. PLoS Genetics 3:1487–1495. [PMCID: PMC1950958]

149. Weir BS. 2007. The rarity of DNA profiles. Annals of Applied Statistics 1:358-370. [PMCID: PMC2585748]

150. Hepler AB, Weir BS. 2008. Object-oriented Bayesian networks for paternity cases with allelic dependencies. Forensic Science International: Genetics 2:166-175. [PMCID: PMC2600569]

151. Weir BS. 2008. Linkage disequilibrium and association tests. Annual Reviews of Genomics and Human Genetics 9:129–142. [PMID18505378, PubMed - indexed for MEDLINE]

152. Zaykin DV, Pudovkin A, Weir BS. 2008. Correlation based inference for linkage disequilibrium with multiple alleles. Genetics 180:533–545. [PMCID: PMC2535703]

153. Rohlfs R, Weir BS. 2008. Distributions of Hardy-Weinberg equilibrium test statistics. Genetics 180:1609–1616. [PMCID: PMC2581961]

154. Samanta S, Li YJ, Weir BS. 2009. Drawing inferences about the coancestry coefficient. Theoretical Population Biology 75:312–319. [PMCID: PMC2722911]

155. Holsinger KE, Weir BS. 2009. Genetics in geographically structured populations: defining, estimating, and interpreting F_{ST}. Nature Reviews Genetics 10:639–650. [PMCID: PMC4687486]

156. Choi Y, Wisjman EM, Weir BS. 2009. Case-control association testing in the presence of unknown relationships. Genetic Epidemiology 33:668–678. [PMCID: PMC2790016]

157. P^3G Consortium, Church G, Heeney C, Hawkins N, de Vrie J, Boddington P, Kaye J, Weir B. 2009. Public access to genome-wide data: five views on balancing research with privacy and protection. PLoS Genetics 5: e1000665. [PMCID: PMC2749921]

158. Rohlfs RV, Swanson WJ, Weir BS. 2010. Detecting coevolution through allelic association between physically unlinked loci. American Journal of Human Genetics 86:674-685. [PMCID: PMC2869012]

159. Laurie CC, Doheny KF, Mirel DB, Pugh EW, Bierut LJ, Bhangale T, Boehm F, Caporaso NE, Cornelis MC, Edenberg, HJ, Gabriel SB, Harris EL, Hu F, Jacobs K, Kraft P, Landi MT, Lumley T, Manolio TA, McHugh C, Painter I, Paschall J, Rice JP, Rice KM, Zheng X, Weir BS for the GENEVA Investigators. 2010. Quality control and quality assurance in genotypic data for genome-wide association studies. Genetic Epidemiology 34:591–602. [PMCID: PMC3061487]

160. Browning SR, Weir BS. 2010. Population structure with localized haplotype clusters. Genetics 185:1337–1344. [PMCID: PMC2927760]

161. Weir BS. 2010. Statistical genetic issues for genome-wide association studies. Genome 53:869–875. [PMCID: PMC4686343]

162. Beecham GW, Weir BS. 2011. Confidence intervals for DNA evidence likelihood ratios. Journal of Forensic Sciences 56 Supplement 1:S166–S171. [PMCID: PMC4574915]

163. Buckleton JS, Krawczak M, Weir BS. 2011. The interpretation of lineage markers in forensic DNA testing. Forensic Science International: Genetics 5:78–83. [PMCID: PMC 3058155]

164. Weir BS, Laurie CC. 2011. Characterizing allelic association in the genome era. Genetics Research 92:461–470. [PMCID: PMC4688043]

165. Hill WG, Weir BS. 2011. Variation in actual relationship as a consequence of Mendelian sampling and linkage. Genetics Research 93:47–74. [PMCID: PMC3070763]

166. Yang J, Manolio TA, Pasquale LR, Boerwinkle E, Caporaso N, Cunningham JM, de Andrade M, Feenstra B, Feingold E, Hayes MG, Hill WG, Landi MT, Lettre G, Lin P, Ling H, Lowe W, Mathias RA, Melby M, Pugh E, Cornelis MC, Weir BS, Goddard ME, Visscher PM. 2011. Genome partitioning of genetic variation for complex traits using common SNPs. Nature Genetics 43:519–525. [PMCID: PMC4295936]

167. Laurie CC, Laurie CA, Rice K, Doheny KF, Zelnick LR, McHugh CP, Ling H, Hetrick KN, Pugh EW, Amos C, Wei Q, Wang L, Lee JE, Barnes KC. Hansel NN, Mathias R, Daley D, Beaty TH, Scott AF, Ruczinski I, Scharpf RB,, Bierut LJ, Hartz SM, Landi MT, Freedman ND, Goldin LR, Ginsburg D, Li J, Desch RC, Strom SS, Blot WJ, Signorello LB, Ingles SA, Chanock SJ, Berndt SI, Le Marchand L, Henderson BE, Monroe KR, Heit JA, de Andrade M, Armasu SM, Regnier C, Lowe WL, Hayes MG, Marazita ML, Feingold E, Murray JC, Melbye M, Feenstra B, Kang JH, Wiggs JL, Jarvik G, McDavid AN, Seshan VE, Mirel DB, Crenshaw A, Sharopova N, Wise A, Shen J, Crosslin DR, Levine DM, Zheng X, Udren JI, Bennett S, Nelson SC, Gogarten SM, Conomos MP, Heagerty P, Manolio T, Pasquale LR, Haiman CA, Caporaso N, Weir BS. 2012. Detectable clonal mosaicism from birth to old age and its relationship to cancer. Nature Genetics 44:642–650.[PMCID: PMC3366033]

168. Rohlfs R, Fullerton SM, Weir BS. 2012. Familial identification: population structure and relative distinguishability. PLoS Genetics e:1002469. [PMCID: PMC 3276546]

169. Smith SR, Maixner WB, Greenspan DW, Dubner JD, Fillingim, RB, Ohrbach R, Knott C, Slade GD, Bair E, Gibson DG, Zaykin DV, Weir BS, Maixner W, Diatchenko L. 2011. Potential genetic risk factors for chronic TMD: Genetic associations from the OPPERA case control study. Journal of Pain 12, Suppl. 3: T92–T101. [PMCID: PMC3268684]

170. Menotti-Raymond M, David V, Weir BS, O'Brien S. 2012. A population genetic database of cat breeds developed in coordination with a domestic cat STR multiplex. Journal of Forensic Sciences 57:596–601. [PMCID: PMC4688040]

171. Hill WG, Weir BS. 2012. Variation in actual relationship among descendants of inbred individuals. Genetics Research 94:267–274. [PMCID: PMC4694724]

172. Gill P, Gusmao L, Haned H, Mayr WR, Morling N, Parson W, Prieto L, Prinz M, Schneider H, Schneider PM, Weir BS. 2012. DNA commission of the International Society of Forensic Genetics: Recommendations on the evaluation of STR typing results that may include drop-out and/or drop-in using probabilistic methods. Forensic Science International: Genetics 6:679–688. [PMCID: PMC4689582]

173. Zheng X, Levine D, Shen J, Gogarten SM, Laurie C, Weir BS. 2012. A high-performance computing toolset for relatedness and principal component analysis of SNP data. Bioinformatics 28:3326–3328. [PMCID: PMC 3519454]

174. Gogarten SM, Bhangale T, Conomos MP, Laurie CA, McHugh CP, Painter I, Zheng X, Crosslin DR, Levine D, Lumley T, Nelson DC, Rice K, Shen J, Swankar R, Weir BS, Laurie CC. 2012. GWASTools: an R/Bioconductor package for quality control and analysis of Genome-Wide Association Studies. Bioinformatics 28:3329–3331. [PMCID: PMC 3519456]

175. Weir BS. 2012. Estimating F-statistics: A historical view. Philosophy of Science 79:637–643. [PMCID: PMC4578636]

176. Nelson SC, Doheny KF, Pugh EW, Romm JM, Laurie CA, Browning SR, Weir BS, Laurie CC. 2013. Imputation-based genome coverage: Assessment of current human genotyping arrays. G3 3:1795-1807. (Featured in “2013 Spotlight: A showcase of research and scholarship in selected articles from 2013” for the journal G3:Genes/Genomes/Genetics.) [PMCID: PMC 3789804]

177. Weir BS. 2013. Interpreting whole-genome marker data. Statistics in Biosciences 5:316–329. [PMCID: PMC 3836609]

178. Smith SB, Mir E, Bair E, Slade GD, Dubner R, Fillingim RB, Greenspan JD, Ohrbach R, Knott C, Weir B, Maixner W, Diatchenko L. 2013. Genetic variants associated with development of TMD and its intermediate phenotypes: The genetic architecture of TMD in the OPPERA prospective cohort study. Journal of Pain 14:T91-T101. [PNCID: PMC 3855664]

179. Zheng X, Shen J, Cox CJ, Wakefield JC, Ehm MG, Nelson MR, Weir BS. 2014. HIBAG – HLA genotype imputation with attribute bagging. The Pharmacogenomics Journal 14:192-202. [PMCID: PMC 3772955]

180. Zhu ZH, Bakshi1 A, Vinkhuyzen AAE, Hemani G, Lee SH, Nolte IM, van Vliet-Ostaptchouk JV, Snieder H, The LifeLines Cohort Study, Esko T, Milani L, Mgi R, Metspalu A, Hill WG, Weir BS, Goddard ME, Visscher PM, Yang J. 2015. Dominance genetic variation contributes little to the missing heritability for human complex traits. American Journal of Human Genetics 96:377–385. [PMCID: PMC4375616]

181. Wasser SK, Brown L, Mailand C, Mondol S, Clark W, Laurie C, Weir BS. 2015. Genetic assignment of large seizures of elephant ivory reveals Africa’s major poaching hotspots. Science 349:84–87.

182. Graffelman J, Nelson S, Gogarten SM, Weir BS. 2015. Exact Inference for Hardy-Weinberg proportions with missing genotypes: Single and multiple imputation. G3 (Genes, Genomes, Genetics) 5:2365–2373. [PMCID: PMC4632056]

183. Weir BS, Zheng X. 2015. SNPs and SNVs in Forensic Science. Forensic Science International: Genetics Supplement Series 5:e267–e268. [PMCID: PMC5545933]

184. Zheng X, Weir BS. 2015. Eigenanalysis of SNP data with an interpretation of identity by descent. Theoretical Population Biology 107:65–76. [PMCID: PMC4716003]

185. Conomos MP, Reiner AP, Weir BS, Thornton TA. 2016. Model-free estimation of recent genetic relatedness. American Journal of Human Genetics 98:127–148. [PMCID: PMC4716688]

186. Conomos MP, Laurie CA, Stilp AM, Gogarten SM, McHugh CP, Nelson SC, Sofer T, Fernández-Rhodes L, Justice E, Graff M, Young KL, Seyerle AA, Avery CL, Taylor KD, Rotter JT, Talavera GA, Daviglus ML Wassertheil-Smoller S, Schneiderman N, Heiss G, Kaplan RC, Franceschini N, Reiner AP, Shaffer JR, Barr RG, Kerr KF, Browning SR, Browning BL, Weir BS, Avilés-Santa ML, Papanicolaou GJ, Lumley T, Szpiro AA, North KE, Rice K, Thornton TA, Laurie CC. 2016. Genetic diversity and association studies in U.S. Hispanic/Latino populations: Applications in the Hispanic Community Health Study/Study of Latinos. American Journal of Human Genetics 98:165–184. [PMCID: PMC4716704]

187. Schick UM, Jan D, Hodonsky CJ, Morrison JV, Dvis JP, Brown L, Sofer T, Conomos MP, Schumann C, McHugh CP, Nelson SC, Vadiamudi S, Stilp A, Plantinga A, Baier L, Bien SA, Gogarten SM, Laurie CA, Taylor KD, Liu Y, Auer PL, Franceschini N, Szpiro A, Rice K, Kerr KF, Roter JI, Hanson RL, Papanicolaou, Rich SS, Loos RJF, Browning BL, Browning SR, Weir BS, Laurie CC, Mohike KL, North KE, Thornton TA, Reiner AP. 2016. Genome-wide association study of platelet count identifies ancestry-specific loci in Hispanic/Latino Americans. American Journal of Human Genetics 98:229–242. [PMCID: PMC4746331]

188. Buckleton JS, Curran JM, Goudet J, Taylor D, Thiery A, Weir BS. 2016. Population-specific F_{ST} values: A worldwide survey. Forensic Science International: Genetics 23:91-100. [PMCID: PMC4899164]

189. Graffelman J, Weir BS. 2016. Testing for Hardy-Weinberg equilibrium at bi-allelic genetic markers on the X chromosome. 2016. Heredity 116:558–568. [PMCID: PMC4868269]

190. Curran JM, Weir BS. 2016. Modern methods of DNA interpretation. Chance 29:17-26.

191. Weir BS, Goudet J. 2017. A unified characterization for population structure and relatedness. Genetics 206:2085-2103. [PMCID: PMC5560808]

192. Gittelson S, Moretti TR, Onorato AJ, Budowle B, Weir BS, Buckleton J. 2017. The factor of 10 in forensic DNA match probabilities. Forensic Science International: Genetics 28:178-187. [PMID 28273509]

193. Graffelman J, Jain D, Weir BS. 2017. A genome-wide study of Hardy-Weinberg equilibrium with next generation sequence data. Human Genetics 136:727-741. [PMID 29071737]

194. Yengo L, Zhu Z, Wray NR, Weir BS, Yang J, Robinson MR, Visscher PM. 2017. Detection and quantification of inbreeding depression for complex traits from SNP data. Proceedings of the National Academy of Sciences USA 114:8602-8607 [PNCID PMC5550994]

195. Zheng XW, Gogarten SM, Lawrence M, Stilp A, Conomos MP, Weir BS, Laurie C, Levine D. 2017. SeqArray – a storage-efficient high-performance data format for WGS variant calls. Bioinformatics 33:2251-2257. [PMID 38334390]

196. Bodah ET, Weir BS. 2017. New method application for marker-trait association studies in plants: Partial least square regression aids detection of simultaneous correlations. Agricultural Research and Technology: Open Access Journal 12(5). DOI: 10.19080/ARTOAJ2017.12.555864.

197. Graffelman J, Weir BS. 2018. On the testing of Hardy-Weinberg proportions and equality of allele frequencies in males and females at bi-allelic genetic markers. Genetic Epidemiology 42:34-48.

198. Gittelson S, Evett IW, Berger CEH, Jackson G, Robertson B, Curran JM, Taylor D, Weir BS, Coble MD, Champod C, Buckleton JS. 2018. A response to “Likelihood ratio as weight of evidence: A closer look” by Lund and Iyer. Forensic Science International 288:E15-E19.

199. Graffelman J, Weir BS. 2018. Multi-allelic exact tests for Hardy-Weinberg equilibrium that account for gender. Molecular Ecology Resources 18: 461-473.

200. Yengo L, Zhu Z, Wray NR, Weir BS, Yang J, Robinson MR, Visscher PM. 2018. Estimation of inbreeding depression from SNP data REPLY. Proceedings of the National Academy of Sciences USA 115:E2494-E2495.

201. Goudet J, Kay T, Weir BS. 2018. How to estimate kinship. Molecular Ecology 27:4121-4135.

202. Wasser SK, Torkelson A, Winters M, Horeaux Y, Tucker S, Otiende MY, Sitam FAT, Buckleton J, Weir BS. 2018. Combating transnational organized crime by linking multiple large ivory seizures to the same dealer. Science Advances 4:eaat0625.

203. Kraja AT, Liu C, Fetterman JL, Graff M, Have CT, et al. 2019. Associations of mitochondrial and nuclear mitochondrial variants with seven metabolic traits. American Journal of Human Genetics 104:112-138.

6.2 Books

1. Weir BS. 1968. *The Two Locus Inbreeding Function.* Ph.D. Thesis, North Carolina State University. Dissertation Abstracts 29:2235B, University Microfilms, Ann Arbor, MI.

2. Weir BS. 1983. (Editor) *Statistical Analysis of DNA Sequence Data.* Dekker, New York

3. Weir BS, Eisen EJ, Goodman MM, Namkoong G. (Editors) 1988. *Proceedings of the Second International Conference on Quantitative Genetics.* Sinauer, Sunderland, MA.

4. Brown AHD, Clegg MT, Kahler AL, Weir BS. (Editors) 1989. *Plant Population Genetics, Breeding and Genetic Resources.* Sinauer, Sunderland, MA

5. Weir BS. 1990. *Genetic Data Analysis.* Sinauer, Sunderland, MA. (Russian edition published by Mir, Moscow, 1995; Chinese edition published by Publishing House of Agricultural Science, Beijing, 1996).

6. Weir BS. (Editor) 1995. *Human Identification: The Use of DNA Markers.* Kluwer, Amsterdam.

7. Weir BS. 1996. *Genetic Data Analysis II.* Sinauer, Sunderland, MA.

8. Evett IW, Weir BS. 1998. *Interpreting DNA Evidence.* Sinauer, Sunderland, MA.

9. Fleming TR, Weir BS. (Editors) 2012. *Proceedings of the Fourth Seattle Symposium in Biostatistics: Clinical Trials.* Lecture Notes in Statistics 1205. Springer, New York.

6.3 Book Chapters

1. Allard RW, Kahler AL, Weir BS. 1971. Isozyme polymorphisms in barley populations. In: Barley Genetics 2. Washington State University Press, Pullman, Washington. pp 1–13.
2. Weir BS, Cockerham CC. 1977. Two-locus theory in quantitative genetics. In: Proceedings of the International Conference on Quantitative Genetics, (Eds.) E. Pollak, O. Kempthorne and T.B. Bailey. Iowa State University Press, Ames, IA. pp 247–269.
3. Brown AHD, Marshall DR, Weir BS. 1981. Current status of the charge state model for protein polymorphisms. In: Genetic Studies of Drosophila Populations. Proceedings of the Kioloa Conference.(Eds.) J.B. Gibson and J.G. Oakeshott. Australian National University Press, Canberra, Australia. pp 15–43.
4. Brown AHD, Weir BS. 1983. Measuring genetic variability in plant populations. In: Isozymes in Plant Breeding and Genetics, Part A. (Eds.) S.D. Tanksley and T.J. Orton. Elsevier, Amsterdam. pp 219–239.
5. Weir BS. 1986. Unraveling DNA information. In: The Fascination of Statistics, (Eds.) R.J. Brook, G.C. Arnold, T.H. Hassard and R.M. Pringle. Dekker, New York. pp 183–191.
6. Weir BS. 1988. The contributions of C. C. Cockerham. In Proceedings of the Second International Conference on Quantitative Genetics. (Editors) B.S. Weir, E.J. Eisen, M.M. Goodman and G. Namkoong. Sinauer, Sunderland, MA.
7. Weir BS, Cockerham CC. 1989. Complete characterization of disequilibrium at two loci. In: Mathematical Evolutionary Theory, (Ed.) M.W. Feldman, Princeton Univ. Press. pp 86–110.
8. Weir BS. 1989. Locating the cystic fibrosis gene on the basis of linkage disequilibrium with markers? In: Multipoint Mapping and Linkage Based Upon Affected Pedigree Members: Genetic Analysis Workshop 6, (Eds.) R.C. Elston, M.A. Spence, S.E. Hodge, and J.W. MacCluer. A.R. Liss, New York. pp 81–86.
9. Weir BS. 1989. Sampling properties of gene diversity. In:Plant Population Genetics, Breeding and Genetic Resources, (Eds.) A.H.D. Brown, M.T. Clegg, A.L. Kahler and B.S. Weir. Sinauer, Sunderland, MA. pp 23–42.
10. Weir BS. 1990. Looking for the cystic fibrosis gene with molecular markers. In: Population Biology of Genes and Molecules, (Eds.) J.F. Crow and N. Takahata. Baifukan, Tokyo. pp 33–55.
11. Weir BS. 1990 Variation in sequence distances. In: Molecular Evolution, (Eds.) M.T. Clegg and S.J. O'Brien. Liss, New York. pp 281–288.
12. Weir BS. 1990. Intraspecific differentiation. In: Molecular Systematics, (Eds.) D.M. Hillis and C. Moritz. Sinauer, Sunderland, MA. pp 373–410.
13. Weir BS. 1992. Disequilibrium on chromosome 21 in some Utah families. In: Genetic Analysis Workshop 7: Issues in Gene Mapping and Detection of Major Genes, (Eds.) J.W. MacCluer, A. Chakravarti, D. Cox, D.T. Bishop and M.H. Skolnick. Cytogenetics and Cell Genetics 59:128–129.

14. Basten CJ, Weir BS. 1992. Effect of gene conversion on measures of digenic disequilibrium. In: Population Paleo-Genetics, (Ed.) N. Takahata, Japan Scientific Societies Press, Tokyo. pp 345–362.

15. Doerge RW, Zeng ZB, Weir BS. 1994. Statistical issues in the search for genes affecting quantitative traits in populations. Pp 15–26 in Analysis of Molecular Marker Data, American Society of Horticultural Science.

16. Kaplan NL, Weir BS. 1995. The use of linkage disequilibrium for estimating the recombination fraction between a marker and a disease gene. In: Mathematical Population Genetics, (Eds.) P. Donnelly and S. Tavare, Springer, New York pp 207–219.

17. Weir BS. 1996. Intraspecific differentiation. In: Molecular Systematics, second edition, (Eds.) D.M. Hillis, C. Moritz and B. Mable, Sinauer, Sunderland, MA

18. Zhu J, Weir BS. 1998. Mixed model approaches for genetic analysis of quantitative traits. Pp 321–330 in L. Chen, S. Ruan and J. Zhu (Eds). Advanced Topics in Biomathematics. World Scientific, Singapore.

19. Weir BS. 1998. Statistical methods employed in the evaluation of single-locus probe results in criminal identity cases. Pp 83–96 in P.J. Lincoln and J. Thompson (Eds) Methods in Molecular Biology 98: Forensic DNA Profiling Protocols. Humuna Press, Totowa, NJ.

20. Weir BS. 1999. Quantifying the genetic structure of populations with application to paternity calculations. pp 31–43 in M.E. Halloran and S. Geisser (Eds) Statistics in Genetics, IMA Volumes in Mathematics and its Applications, vol. 112. Springer, New York.

21. Weir BS. 2000. A statistician looks for human disease genes. Pp. 19–34 in J.P. Gustafson (editor) Genomes: 22nd Stadler Genetics Symposium' Plenum Press, New York.

22. Weir BS. 2000. The consequences of defending DNA statistics. Pp 87–97 in J.L. Gastwirth (Ed) Statistical Science in the Courtroom. Springer, New York

23. Weir BS. 2001. Forensic DNA analysis. In R. Robinson (Ed). Biology for Students. MacMillan Reference, Farmington Hills, MI.

24. Weir BS. 2001. Forensics. Pp 721–739 in D.J. Balding, M. Bishop and C. Cannings, Handbook of Statistical Genetics. Wiley, New York.

25. Lu J, Hardy S, Tao W, Muse S, Weir BS, Spruill S. 2002. Classical statistical approaches to molecular classification of cancer from gene expression profiling. Pp 97–108 in S.M. Lin and K.F. Johns (Eds) Methods of Microarray Data Analysis. Kluwer, Boston.

26. Weir BS. 2003. Forensics. Pp 830–852 in D.J. Balding, M. Bishop and C. Cannings, Handbook of Statistical Genetics (second edition). Wiley, New York.

27. Weir BS. 2005. DNA fingerprinting. Pp 255–269 in R. Peck, G. Casella, G. Cobb, R. Hoerl, D. Nolan, R. Starbuck and H. Stern, Statistics: A Guide to the Unknown, Duxbury, Belmont CA.

28. Weir BS. 2007. Forensics. Pp 1368–1392 in D.J. Balding, M. Bishop and C. Cannings, Handbook of Statistical Genetics (third edition). Wiley, New York.

29. Weir BS. 2012. Statistics for Wildlife Forensic DNA. Pp 237–252 in "Wildlife Forensics: Methods and Applications," edited by J.E. Huffman and J.R. Wallace. Wiley, New York.
30. Weir BS. 2012. Using SNPs to characterize genetic effects in clinical trials. Pp 81–91 in "Proceedings of the Fourth Seattle Symposium in Biostatistics: Clinical Trials." Lecture Notes in Statistics 1205. Edited by T.R. Fleming and B.S. Weir. Springer, New York.
31. Weir BS, Heagerty PJ. 2012. Genetic markers in clinical trials. Pp 209–245 in "Proceedings of the Fourth Seattle Symposium in Biostatistics: Clinical Trials." Lecture Notes in Statistics 1205. Edited by T.R. Fleming and B.S. Weir. Springer, New York.

6.4 Commentaries and Correspondence

1. Weir BS. 1988. Quantitative Genetics in 1987. Genetics 117:601–602. [PMCID: PMC1203234]
2. Weir BS. 1989. Building trees with DNA sequences. Biometric Bulletin 6:21–23.
3. Weir BS. 1989. Mathematical analysis of DNA sequences. Genome 31:1093–1094.
4. Weir BS. 1992. Discussion of "Statistical inference in crime investigations using DNA profiling" by D.A. Berry, I.W. Evett and R. Pinchin. Applied Statistics 41:528–529.
5. Weir BS. 1992. Population genetics in the forensic DNA debate. Proceedings of the National Academy of Sciences, USA 89:11654–11659. [PMCID: PMC50614]
6. Weir BS, Evett IW. 1992. Whose DNA? American Journal of Human Genetics 50:869. [PMCID: PMC1682623]
7. Weir BS. 1993. Forensic population genetics and the National Research Council (NRC). American Journal of Human Genetics 52: 437–440. [PMCID: PMC1682194]
8. Weir BS. 1993. DNA fingerprinting report. Science 260:473.
9. Weir BS. 1993. DNA on trial: Genetic identification and criminal justice. American Journal of Human Genetics 53:1158–1160. [PMCID: PMC1682313]
10. Weir BS. 1993. The status of DNA fingerprinting. World and I, 214–219.
11. Weir BS, Evett IW. 1993. Reply to Lewontin. American Journal of Human Genetics 52:206. [PMCID: PMC1682097]
12. Weir BS. 1994. DNA profiling on trial. Nature 369:351.
13. Weir BS. 1994. Discussion of "DNA fingerprinting: a review of the controversy" by K. Roeder. Statistical Science 9:222–278.
14. Weir BS. 1995. DNA statistics in the Simpson matter. Nature Genetics 11:365–368.
15. Weir BS. 1995. Discussion of "Inference in forensic identification" by D.J. Balding and P. Donnelly. Journal of the Royal Statistical Society. Series A. 158:21–53.
16. Weir BS. 1996. Life and hard times of a statistician: Statistics in court. STATS 16:15–17.
17. Weir BS. 1996. The second National Research Council report on forensic DNA evidence. American Journal of Human Genetics 59: 497–500. [PMCID: PMC1914912]

18. Evett IW, Gill PD, Weir BS. 1996. Reply to Morton. American Journal of Human Genetics 59:1399–1400. [PMCID: PMC1914880]

19. Kaplan NL, Martin ER, Weir BS. 1997. Reply to Sham. American Journal of Human Genetics 61:778. [PMCID: PMC1715933]

20. Shoemaker JS, Painter IS, Weir BS. 1999. Bayesian statistics in genetics: a guide for the uninitiated. Trends in Genetics 15:354–358.

21. Weir BS. 2000. Challenges facing statistical genetics. Journal of the American Statistical Association 95:319–322.

22. Evett IW, Foreman LA, Weir BS. 2000. Letter to the Editor concerning paper by A. Stockmarr. Biometrics 56:1274–1275. Response to Devlin, Biometrics 56:1277.

23. Weir BS. 2001. DNA match and profile probabilities: Comment on Budowle et al. (2000) and Fung et al. (2000). Forensic Sciences Communications, Volume 3 Number 1. http://www.fbi.gov/programs/lab/fsc

24. Weir BS. 2001. Introduction: Transmission/Disequilibrium Test/Association Group. Genetic Epidemiology 21: S421–S422.

25. Buckler E, Doebley JF, Gaut BS, Goodman MM, Kresovich S, Muse S, Weir BS. 2002. Evolutionary genomics of maize. Maize Cooperation Newsletter 76:86–88.

26. Weir BS, Hill WG. 2002. Discussion on the meeting on "Statistical modeling and analysis of genetic data." Journal of the Royal Statistical Society B: 64:737–775.

27. Weir BS. 2003. Uses of DNA and genetic markers for forensics and population studies. Theoretical Population Biology 63:171–172.

28. Weir BS. 2004. The 2004 Genetics Society of America Medal. Genetics 166:47–648. [PMCID: PMC1470721]

29. Weir BS. 2004. Statistical characterization of genetic association. Talk 18 in Genetic Epidemiology: Fundamentals, Theory, Practice and Latest Developments. Henry Stewart Talks, London.

30. Gibson GC, Weir BS. 2005. The quantitative genetics of transcription. Trends in Genetics 21:616–623.

31. Weir BS. 2006. The 2006 Thomas Hunt Morgan Medal. Genetics 172: 719–720.

32. Weir BS. 2007. QTL association mapping. Talk in Genetic Epidemiology: Latest Developments, Henry Stewart Talks Ltd, London.

33. Weir BS. 2008. Estimating the recombination parameter: a commentary on the paper 'Estimating the recombination parameter of a finite population model without selection' by Richard R. Hudson. Genetics Research 89:429–430. [PMID 18976530]

34. Weir BS, Hill WG, Zhu J, Zeng ZB. 2009. The Third International Conference of Quantitative Genetics. Genetica 136:211–212. [PMID 18777100]

35. Weir BS. 2012. Obituary for James F. Crow. Nature Genetics 44:834.

36. Weir BS. 2012. Columbus Clark Cockerham: A Biographical Memoir. http://www.nasonline.org/publications/biographical-memoirs/alphabetical-listing/memoirs-c.html

37. Buckleton J, Evett I, Weir B. 2014.

38. Buckleton J, Evett I, Weir B. 2014. Letter to the Editor in response to editorial by Risinger. Science and Justice 54:510.

6.5 Encyclopedia Entries

1. Weir BS. 1997. Encyclopedia of Human Biology: entry for Genetic Testing. Academic Press, San Diego.
2. Weir BS. 1998. Encyclopedia of Biostatistics: entries for Heterozygosity, Inbreeding, Statistical Forensics. Wiley, New York.
3. Weir BS. 1999. Encyclopedia of Forensic Sciences: entry for Genetics (c) DNA - statistical probability. Pp 545–550. Academic Press, London
4. Weir BS. 2001, 2003. Encyclopedia of the Human Genome: entry for DNA evidence: inferring identity. MacMillan, London.
5. Weir BS. 2002. Encyclopedia of Evolution: entry for Forensic DNA. Oxford University Press, New York.
6. Weir BS, Nielsen DM. 2002. Encyclopedia of Human Genetics and Genetic Epidemiology: entry for Case-only gene mapping. Wiley, New York.
7. Weir BS. 2009. Wiley Encyclopedia of Forensic Science: entry for Missing Persons and Paternity: DNA. Wiley, New York.
8. Weir BS. 2013. DNA - statistical probability. In: Siegel JA and Saukko PJ (Eds.) Encyclopedia of Forensic Sciences: Second Edition, pp. 282-286. Waltham: Academic Press.

6.6 Book Reviews

1. Weir BS. 1980. Review of: Thompson, J.N. Jr. and J.M. Thoday (Editors) 1979. Quantitative Genetic Variation. Biometrics 36:561–562.
2. Weir BS. 1980. Review of: Ewens, W.J. 1979. Mathematical Population Genetics. Biometrics 36:739–740.
3. Weir BS. 1981. Review of: Hartl, D.L. 1980. Principles of Population Genetics. Biometrics 37:414–415.
4. Weir BS. 1981. Review of: Bulmer, M.G. 1980. The Mathematical Theory of Quantitative Genetics. Biometrics 37:855–856.
5. Weir BS. 1981. Review of: Kingman, J.F.C. 1980. Mathematics of Genetic Diversity. Biometrics 37:857.
6. Weir BS. 1982. Review of: Boorman, S.A. and P.R. Levitt. 1981. The Genetics of Altruism. Biometrics 38:877–878.

7. Weir BS. 1984. Review of: Kimura, M. 1984. The Neutral Theory of Molecular Evolution. Biometrics 49:869.
8. Weir BS. 1984. Review of: MacDonald, N. 1983. Trees and Networks in Biological Models. Biometrics 40:1209–1210.
9. Weir BS. 1986. Review of: Chakravarti, A. (Editor) 1984. Human Population Genetics: The Pittsburgh Symposium. The Quarterly Review of Biology 61:264–265.
10. Weir BS. 1987. Review of: Ohta, T. and K. Aoki (Editors) 1985. Population Genetics and Molecular Evolution. Evolution 41:11354–1136.
11. Weir BS. 1987. Review of: Provine, W.B. (Editor) 1986. Evolution: Selected Papers by Sewall Wright. Kimura, M. 1983. The Neutral Theory of Molecular Evolution. The Quarterly Review of Biology 62:435–436.
12. Weir BS. 1987. Review of: Karlin, S. and E. Nevo (Editors) 1986. Evolutionary Processes and Theory. Biometrics 44:316–317.
13. Weir BS. 1988. Review of: Nei, M. 1987. Molecular Evolutionary Genetics. The Quarterly Review of Biology 63:218.
14. Weir BS. 1990. Review of: Hartl, D.L. and A.G. Clark. Principles of Population Genetics. Journal of Heredity 81:174.
15. Weir BS. 1993. Review of: Narain, P. Statistical Genetics. ASB Bulletin 38:137.
16. Weir BS. 1993. Review of: Miyamoto, M.M. and J. Cracraft (Editors). Phylogenetic Analysis of DNA Sequences. Journal of Classification 10:139–143.
17. Weir BS. 1993. Review of: Billings, P.J. (Editor). DNA on Trial: Genetic Identification and Criminal Justice. American Journal of Human Genetics 53:1158–1160.
18. Weir BS. 1998. Review of: Zeisel, H., and D. Kaye (Eds). Prove it with Figures: Empirical Methods in Law and Litigation. Journal of the American Statistical Association 93:1250.
19. Weir BS. 2007. Review of: Lucy, D. Introduction to Statistics for Forensic Scientists. Journal of the American Statistical Association.
20. Weir BS. 2009. Review of: Neale, B.M. et al. Statistical Genetics: Gene Mapping through Linkage and Association. The Quarterly Review of Biology 84:307.
21. Weir BS. 2010. Review of: Fung, W.K. Statistical DNA Forensics: Theory, Methods and Computation. Journal of Forensic Sciences

7 Funding History

7.1 Research Grants: As Principal Investigator

Period	Title, Sponsor / Amount
1984–1997	“Theoretical Population Genetics” NIH R01 GM32518
1990–2005	“Statistical and quantitative genetics” NIH P01 GM 45344
1995–1996	“Estimation of population structure parameters” NIJ 95-IJ-CX-0007
2006–2021	“Theoretical Population Genetics” NIH R01 075091
2012–2014	“Population Genetic Issues for Forensic DNA Profiles.” NIJ 2011-DN-BX-K541.
2012–2017	“Statistical and Quantitative Genetics” NIH P01 GM099568.
2015–2017	“Population Genetic Issues for Forensic DNA Profiles.” NIJ 2014-DN-BX-K028
2018-2020	“Population Genetic Issues for Forensic DNA Profiles.” NIJ 2017-DN-BX-0136.

7.2 Contracts and Cooperative Agreements: As Principal Investigator

Period	Title, Sponsor / Amount
2007-2011	“Genome Wide Association Coordinating Center (GENEVA)” NIH U01 HG 004464
2009-2012	“Randomized Clinical Trials - Whole Genome Studies Coordinating Center (GARNET).” NIH U01 HG 005157
2009-2012	“UW-GSK Cooperative Agreement.” GlaxoSmithKline
2009-2012	“Barrett’s and Esophageal Adenocarcinoma (BEAGESS).” NIH R01 CA 136725 Subcontract to Fred Hutchinson Cancer Research Center.
2009-2012	“Genome-Wide Association Study for Nonsynonymous SNPs in Colon Cancer (GECCO).” NIH R01 CA 059045. Subcontract to Fred Hutchinson Cancer Research Center.
2005-2015	“Orofacial Pain: Prospective Evaluation and Risk Assessment (OPPERA).” NIH U01 DE017018. Subcontract to University of North Carolina.
2011-2017	“UW-CIDR Cooperative Agreement.” Center for Inherited Human Disease.
2013-2016	“Omics Latinos - Genetic Analysis (OLGA)” NHLBI HHSN268201300005C
2015-2020	“Study of Latinos-Investigation of Neurocognitive Aging (SOL-INCA)” R01 AG048942 Subcontract from University of Michigan.
2015-2018	“Rare variants and NHLBI traits in deeply phenotyped cohorts.” HL R01 120393-01A1S1
2017-2022	“From Gene Regions to Whole Chromosomes: Scaling up Association-finding for Disease and Omics Outcomes in TOPMed” U01 HL137162
2017–2025	“CODIS Support.” DJ-FBI/ECS-Federal.
2017-2018	“MRI Measures of Cerebrovascular Injury and AD Atrophy in a Study of Latinos” R01 AG054548. Subcontract from University of California Davis

7.3 Outreach: As Principal Investigator

Period	Title, Sponsor / Amount
1999-2020	“Summer Institute in Statistical Genetics.” NIH R25 GM 59733
1997-2016	“Summer Institute in Statistical Genetics.” NSF DEB 9900388/0352235/1049804

7.4 Training: As Program Director/Faculty Mentor

Period	Title, Sponsor / Amount
2000-2005	"Graduate Training in Bioinformatics." NIH T32 ES 7329
2000-2005	"Graduate Industrial Traineeships." Various North Carolina Sponsors
2007-2017	"Predoctoral Research Training in Statistical Genetics." NIH T32 GM 81062
2015-2016	"Population Genetic Issues for Forensic Y-chromosome Markers." NIJ 2015-90507-WA-23
2015-2018	"What Value will Next Generation Sequencing (NGS) Bring to Complex DNA Mixture Interpretation?", NIST.
2016	"Forensic Analysis of Genetically Variant Peptides." Lawrence Livermore National Laboratory

8 Conferences and Symposia, Titles and Abstracts

1. Weir BS 1969. Equilibria under inbreeding and selection. Biometrics 25:804.

2. Weir BS, D.R. Marshall and A.H.D. Brown. 1976. Fitting and testing a neutral alleles model for finite populations. Abstracts of 9th International Biometric Conference: 81.

3. Weir BS and S.C. Choy. 1977. Nonpoisson family sizes in populations with overlapping generations. Biometrics 33:585.

4. Weir BS, A.H.D. Brown and D.R. Marshall. 1977. The distribution of a test statistic for testing the stepwise mutation model. Genetics 86:s69.

5. Marshall, D.R. and B.S. Weir. 1978. The number of neutral alleles in a finite population. Genetics 88:s63.

6. Laurie-Ahlberg, C.C. and B.S. Weir. 1978. Allozymic variation and linkage disequilibrium in laboratory populations of Drosophila. Proceedings of XIV International Congress of Genetics, Contributed Papers, Part I:466.

7. Weir BS and C.C. Cockerham. 1978. Complete characterization of disequilibria at two loci. Proceedings of XIV International Congress of Genetics, Contributed Papers, Part I:466.

8. Weir BS and D.R. Marshall. 1979. Effect of complex mixtures of hosts on the evolution of pathogens. Genetics 91:s136.

9. Laurie-Ahlberg, C.C., G.P. Maroni, J.C. Lucchesi, G.C. Bewley and B.S. Weir. 1979. Quantitative genetic variation of enzyme activities in natural populations of Drosophila melanogaster. Genetics 91:s65.

10. Weir BS 1979. Analyses of two-locus genotypic data. Resumos 10a Conferencia Internacional de Biometrica:69

11. Cockerham, C.C. and B.S. Weir. 1980. Use of sibs for studying linkage between quantitative traits. Biometrics 36:187.

12. Weir BS 1980. Variance of inbreeding. Abstracts of Joint Statistical Meetings, American Statistical Association p.245.

13. Weir BS 1981. Variances of samples from mixed self and random mating populations. Genetics 97:s112.

14. Weir BS 1981. Statistical measures for genetic structure of plant populations. Abstracts of XIII International Botanical Congress p.118.

15. Weir BS 1983. Power of a test for comparing nucleotide sequences. Genetics 104:s71.

16. Weir BS 1984. Linkage disequilibrium for restriction sites. Abstracts of Joint Statistical Meetings, American Statistical Association p.109.

17. Weir BS 1984. Linkage disequilibrium in molecular genetics. XIIth International Biometric Conference. Abstracts of Contributed Papers. p.183.

18. Weir BS and W.G. Hill. 1985. Squared linkage disequilibria for restriction sites. American Journal of Human Genetics 37:A208.

19. Weir BS, W.G. Hill and L.D. Brooks. 1986. Disequilibrium on human chromosome 11p. 7th International Congress on Human Genetics 2:684.

20. Weir BS 1987. DNA sequence comparisons. Genetics 116:(1, pt 2)viii.

21. Weir BS 1988. Statistical analysis of molecular genetic data. Statistics in Biotechnology, American Statistical Association p.62.

22. Hernandez, J.L. and B.S. Weir. 1988. A disequilibrium coefficient approach to testing for Hardy-Weinberg equilibrium. XVI International Congress of Genetics. Genome 30: Suppl. 1, 33.

23. Weir BS 1988. Temporal behavior of gene frequency correlations. XVI International Congress of Genetics. Genome 30: Suppl. 1, 33.

24. Weir BS 1988. Sampling properties of sequence statistics. 14th Int. Biometric Conference, Invited Papers P. 145.

25. Weir BS 1989. Variation in sequence distances. UCLA Symposium on Molecular and Cellular Biology, Abstract CF 002. J. Cellular Biochemistry 13C:82.

26. Weir BS and C.J. Basten. 1990. Sampling strategies for DNA sequences. Cold Spring Harbor Meeting on Genome Mapping and Sequencing. p. 190.

27. Weir BS and B. Budowle. 1990. Testing for disequilibria at VNTR loci with forensic applications. Am. J. Human Genetics 47:A148.

28. Weir BS 1990. Using RFLPs to locate genes affecting plant traits. XV International Biometric Conference Proceedings, Invited Papers p. 223.

29. Weir BS 1991. Using measures of association to find human disease genes. Australasian Gene Mapping and Molecular Genetics Symposium, Abstracts, p. 27

30. Weir BS and R.W. Doerge. 1992. Statistical issues in the search for QTLs. XVI International Biometric Conference Proceedings, Contributed Papers p. 164.

31. Weir BS and R.W. Doerge. 1993. Biometrical issues in the search for genes affecting quantitative traits.American Statistical Association Annual Meeting Abstracts p. 311

32. Weir BS 1994. Conditional genotypic frequencies. Institute of Mathematical Statistics Bulletin 23:217.

33. Weir BS, J. Chaseling and P. Reading. 1994. An evaluation of Australasian forensic databases. 12th Australian and New Zealand International Symposium on the Forensic Sciences 7.

34. Weir BS 1995. Statistical issues in DNA profiling. 16th International Congress of the International Society for Forensic Haemogenetics 179.

35. Weir BS 1996. Effect of population structure on DNA profile matches. Third International Conference on Forensic Statistics.

36. Weir BS 1996. Interpreting mixed DNA stains. 13th Australian and New Zealand Int. Symposium on the Forensic Sciences. Abstracts P. 15.85.

37. Weir BS 1996. Characterizing population structure for assigning weight to DNA matching profiles. American Academy of Forensic Sciences Annual Meeting, Abstract B87.

38. Weir BS 1997. Effects of population structure on forensic calculations. 8th Int Symp on Human Identification.

39. Weir BS 1997. Communicating the significance of DNA matches. ENAR Spring Meeting, Abstracts Book P. 160.

40. Weir BS 1997. Interpretation of mixed DNA stains: People vs Simpson. American Academy of Forensic Sciences Annual Meeting, Abstract B57.

41. Weir BS 1997. The effects of population structure on match probabilities. CHI 2nd Annual Conf. on DNA Forensics.

42. Weir BS 1997. History of Wright's F_{ST} estimation and implications for forensic scientists. 2nd Joint Mtg of the Forensic Science Society and California Association of Criminalists. Abstracts P. 25.

43. Weir BS 1998. Statistics and the search for human disease genes. Joint Statistical Meetings Abstract Book, p. 329.

44. Monks, S., B. Weir and N. Kaplan. 1998. Sibship tests of genetic association and/or linkage in the absence of parental information. Joint Statistical Meetings Abstract Book, p. 35.

45. Weir BS 1998. Missing person, remains identification, incest and parentage DNA calculations after NRC II. American Academy of Forensic Sciences Annual Meeting, Abstract B95.

46. Weir BS 1998. The structure of human populations. 16th Congress of South African Genetics Society, Abstract S4.1.

47. Weir BS 1999. Court experience in the USA. First Int. Conf. on Forensic Human Identification in the Millenium.

48. Weir BS 1999. A statistician works with genetic data. Joint Statistical Meeting, Abstracts P. 99.

49. Weir BS 1999. Identifying suspects from databases. CHI 3rd Annual Conf. on DNA Forensics.

50. Graham, J., J. Curran and B.S. Weir. 1999. Properties of match probability estimators in forensic DNA profiling. Joint Statistical Meetings, Abstracts P. 252.

51. Weir BS 1999. A statistician looks for human disease genes. New Zealand Statistical Association Annual Meeting, P. 83.

52. Weir BS 1999. Can DNA establish identity for legal purposes? ENAR Spring Meeting, Abstracts p 95.

53. Nielsen, D., M.G. Ehm and B.S. Weir. 1999. Association based tests for dissecting complex diseases. ENAR Spring Meeting, Abstracts P. 203.

54. Meng, Z., D.V. Zaykin, M.G. Ehm, M.G. and B.S. Weir. 2001. Testing the association of quantitative traits and haplotypes considering treatment effects. Am J Hum Genet 69:1286.

55. Zaykin, D.V., M.G. Ehm and B.S. Weir. 2001. Determining success of haplotyping algorithms using densely mapped genomic regions. Am J Hum Genet 69:116.

56. Liu, W. and B.S. Weir. 2001. Affected sib pair tests in inbred populations. Am J Hum Genet 69:2012.

57. Weir BS 2001. Multi-allele measures of inbreeding. New Zealand Statistical Association Annual Meeting, Abstracts P. 11.

58. Weir BS 2001. Characterizing the structure of human populations. Statistical issues in the forensic uses of DNA. 2nd Int. Symposium on Bioinformatics, Pohang, Korea.

59. Weir BS 2003. Higher order disequilibria in the human genome. 19th Int. Congress on Genetics, Abstracts P. 30.

60. Weir BS 2003. Higher order disequilibria in the human genome. European Mathematical Genetics Meeting Abstracts. Annals of Human Genetics 67,628.

61. Weir BS 2004. An evolutionary perspective for bioinformatics. International Conference on Bioinformatics, Univ Auckland. Abstracts P. 67.

62. Weir BS 2004. Individual and population relationships. 17th Australian and New Zealand Int. Symp. on the Forensic Sciences, Abstracts P. 56.

63. Weir BS, A.D. Anderson and L.R. Cardon. 2005. Sampling properties of Fst in dense SNP maps. Genomic Studies and the HapMap, Univ. Oxford.

64. Weir BS 2005. Genome structure and variation at the SNP level. CSH/Wellcome Conference on Pharmacogenomics, Hinxton UK. Abstracts P. 1.

65. Weir BS 2005. Heterogeneity of measures of population structure along the human genome. 7th Int Mtg on SNPs and Complex Genome Analysis, Hinkley UK. Abstracts P. 123.

66. Weir BS 2005. Statistical issues for DNA profiles. Joint Statistical Meetings, Abstract Book Session 496.

67. Weir BS, A.B. Hepler and A.D. Anderson. 2006. The forensic uses of SNP profiles. American Academy of Forensic Sciences Annual Meeting, Abstract B29.

68. Weir BS 2006. Impact of dense genetic marker maps on plant population genetic studies. 13th Australasian Plant Breeding Conference, Christchurch, New Zealand. Abstract Book 71.

69. Weir BS 2006. Lessons from very large SNP surveys of the human genome. National Breeders Roundtable, St Louis, MO.

70. Weir BS 2006. Use of a dense marker map to study the human genome. Workshop on Quantitative Genetics, Zheijiang University, Hangzhou, China.

71. Weir BS 2006. Heterogeneity of measures of population diversity in the human genome. Department of Genome Sciences, University of Washington.

72. Weir BS 2006. A statistician in court. IMS New Researchers Conference. University of Washington.

73. Weir BS 2006. Introductory Overview Lecture: Association mapping of human disease genes. Joint Statistical Meetings, Abstract #1.

74. Gao, X. and B.S. Weir. 2006. Human population structure detection via multilocus genotype clustering. Joint Statistical Meetings, Abstract #281.

75. Weir BS 2006. Estimating genetic relatedness. Joint Statistical Meetings, Abstract #309.

76. Samanta, S. and B.S. Weir. 2006. Estimating population structure. Joint Statistical Meetings, Abstract #426.

77. Weir BS 2006. Heterogeneity of measures of human population structure. Int. Symposium on Statistical Genetics and Genetic Epidemiology, Seoul National University, Seoul, Korea.

78. Weir BS 2006. Association mapping: statistical considerations. Joint Meetings of Am Soc Agronomy, Crop Sci Soc Am, Soil Sci Soc Am. Abstract # 76-6

79. Weir BS 2006. Estimating Relatedness. Public Health Sciences, Fred Hutchinson Cancer Research Center.

80. Weir BS 2007. Current Statistical Issues for the Interpretation of DNA Profiles. Government Laboratory, Hong Kong.

81. Weir BS 2007. The Birthday Problem and DNA Profiles. Department of Statistics, University of Auckland, New Zealand.

82. Weir BS 2007. Use of wild mice for mapping human disease genes. School of Biological Sciences, University of Auckland, New Zealand.

83. Weir BS 2007. The Birthday Problem and DNA Profiles. Department of Statistics, University of Waikato, New Zealand.

84. Lewis, K.E., B.S. Weir and M-C. King. 2008. Genomic approaches to the identification of individuals through familial database searches. American Academy of Forensic Sciences Annual Meeting, Abstract B59.

85. Weir BS 2008. The rarity of DNA profiles. Department of Statistics, University of Washington.

86. Weir BS 2008. But have you asked Dr. Hardy Weinberg? Department of Biostatistics, University of Washington.

87. Weir BS 2008. Association mapping for quantitative traits. Department of Human Genetics, University of Delhi, New Delhi, India.
88. Weir BS 2008. Statistical issues in the interpretation of DNA profiles. Department of Human Genetics, University of Delhi, New Delhi, India.
89. Weir BS 2008. Association mapping for quantitative traits. Central Potato Research Institute, Shimla, India.
90. Weir BS 2008. DNA, Genetics and Forensics. Department of Genome Sciences, University of Washington.
91. Weir BS 2008. Current statistical issues in forensic DNA analysis. University of Copenhagen, Denmark.
92. Weir BS 2008. Principal components and population structure. Banbury Center, New York.
93. Weir BS 2008. But have you asked Dr. Hardy Weinberg? Plenary Address, American Society of Human Genetics Annual Meeting.
94. Boehm, F.J., T.S. Lumley, K.M. Rice and B.S. Weir. 2008. Analysis of apparent homozygous runs in genome-wide association studies. American Society of Human Genetics Annual Meeting, Abstract 2299W.
95. Rohlfs, R.V., W.J. Swanson and B.S. Weir. 2008. Evidence for current co-evolution of fertilization genes in humans. American Society of Human Genetics Annual Meeting, Abstract 2579T.
96. Weir BS 2008. Association mapping using molecular data. New Zealand Molecular Mapping Workshop, Auckland, New Zealand.
97. Weir BS 2009. Cleaning large-scale genetic datasets. Fred Hutchinson Cancer Center, Seattle.
98. Weir BS 2009. Analysis of whole-genome SNP data. School of Biological Sciences, University of Auckland, New Zealand.
99. Weir BS 2009. What makes a good GWAS study? NIDCR Workshop on the genetics of temporomandibular joint disorders and other comorbid chronic pain conditions, Washington, DC.
100. Weir BS 2009. Current applications of the Hardy-Weinberg law. Joint Statistical Meetings, Washington, DC.
101. Weir BS and J.S. Buckleton. 2010. Lineage markers. American Academy of Forensic Sciences Annual Meeting, Abstract
102. Weir BS 2010. GWAS statistical genetics issues. Fifth Annual Canadian Genetic Epidemiology and Statistical Genetics Meeting, Toronto, Canada.
103. Weir BS 2010. Statistical genetic contributions of W.G. Hill. 9th Int Congress of Genetics Applied to Livestock Production, Leipzig, Germany.
104. Weir BS 2010. Missing heritability in GWAS studies. University of Auckland, New Zealand.

105. Weir BS 2010. The estimation of F-statistics: an historical view. Annual Meeting of the Philosophy of Science Association, Montreal, Canada.

106. Weir BS 2010. Variation in identity measures. Program in Quantitative Genomics, Harvard University, Boston, MA.

107. Weir BS 2011. Statistical genetic issues. Australasian Wildlife Forensics Conference. Auckland, New Zealand.

108. Weir BS 2011. The heritability of human height. University of Auckland, New Zealand.

109. Weir BS 2011 Population and chromosome structure revealed by SNP data. Prentice Symposium, Fred Hutchinson Cancer Center.

110. Weir BS 2012. Haplotype frequency estimation. Scientific Working Group on DNA Analysis Methods, Fredericksburg, VA.

111. Weir BS 2012. Population genetic issues for forensic DNA profiles. NIJ Grantees' Meeting, Atlanta, GA.

112. Weir BS 2012. The heritability of human height. University of Washington, Department of Biostatistics.

113. Weir BS 2012. The heritability of human height. University of Sao Paulo - Sao Paulo, Brazil, Department of Statistics.

114. Weir BS 2012. The heritability of human height. University of Sao Paulo - Piracicaba, Brazil, Department of Statistics.

115. Weir BS 2012. Population and chromosome structure revealed by SNP data. University of Sao Paulo - Sao Paulo, Brazil, Department of Genetics.

116. Weir BS 2012. Population and chromosome structure revealed by SNP data. University of Sao Paulo - Piracicaba, Brazil, Department of Genetics.

117. Weir BS 2012. The heritability of human height. Symposium, National Institute of Environmental Health Sciences, RTP, NC.

118. Weir BS, J.S. Buckleton and J. Curran. 2012. Incorporating uncertainty into likelihood ratios for DNA evidence. Joint Statistical Meetings, San Diego, CA.

119. Zheng X, Shen J, Cox C, Wakefield J, Ehm M, Nelson M, Weir BS. 2012. HIBAG - HLA genotype imputation with attribute bagging. Annual Meeting of the American Society of Human Genetics.

120. Weir BS, Ballantyne, J., Bright, J-A., Buckleton, J.S., Curran, J., Laurie, C.A., Moretti, T. and Myers S. 2013. Y-STR matching: A population-genetic perspective. 25th International Society of Forensic Genetics Congress, Melbourne, Australia.

121. Weir BS 2013. What have we learned from the GENEVA project? 59th Congress of the Brazilian Genetics Society, Aguas de Lindoia, Brazil.

122. Weir BS 2013. Y-STR matching: A population-genetic perspective. 59th Congress of the Brazilian Genetics Society, Aguas de Lindoia, Brazil.

123. Weir BS 2013. Characterizing the genetic structure of populations: Application to Y-STR profiles. Department of Biostatistics, Harvard University.

124. Weir BS 2013. Unweighted estimation for Fst. Impact of Large-scale Genomic Data on Statistical and Quantitative Genetics Conference, University of Washington.

125. Weir BS 2014. Population structure and parentage calculations. Ribeiro Preto SP, Brazil

126. Weir BS 2014. Population structure and association mapping. EMBRAPA, Sete Lagoas MG, Brazil

127. Weir BS 2014. What have GWAS data told us about genome and population structure? Department of Medical Genetics, UNIAMP. Campinas SP, Brazil

128. Weir BS 2014. What have GWAS data told us about genome and population structure? UNIAMP. Department of Genetics, University of Sao Paul, Sao Paulo SP, Brazil

129. Weir BS Estimating F-statistics: Updating Weir and Cockerham Evolution 38:1538-1570 (19844). Society for the Study of Evolution Annual Meeting, Raleigh NC.

130. Weir BS 2014. Using match probabilities to characterize the effects of population structure on the Strengths of DNA Evidence. International Conference on Forensic Statistics and Inference. Leiden, The Netherlands.

131. Weir BS 2014. Characterizing population structure with F-statistics: relatedness on an evolutionary time scale. International Centre for Mathematical Sciences Workshop on Statistical and computational methods for relatedness and relationship inference from genetic marker data. Edinburgh, UK.

132. Weir BS 2014. A population genetic approach to calculating match probabilities for autosomal and lineage forensic DNA profiles. School of Criminal Science, University of Lausanne.

133. Weir BS 2014. Estimating F-statistics for the characterization of population structure. Department of Ecology and Evolution, University of Lausanne.

134. Weir BS 2014. Statistical interpretation of whole-genome SNP data. Department of Statistics, University of Lausanne.

135. Weir BS 2014. A population genetic approach to calculating DNA match probabilities. Institute of Legal Medicine, University of Copenhagen.

136. Weir BS 2014. Estimating F-statistics for the characterization of population structure. Department of Biochemistry, SUNY Buffalo.

137. Weir BS 2014. Characterizing the genetic structure of populations. Department of Ecology and Evolution, University of California at Irvine.

138. Weir BS 2015. SNPs and SNVs in Forensic Science. International Congress on Forensic Genetics. Krakow, Poland.

139. Weir BS 2015. Should elephant-poachers worry about Hardy-Weinberg equilibrium? PHS Postdoc Discussion Group, Fred Hutchinson Cancer Research Center, Seattle.

140. Weir BS 2015. Effects of population structure on matching probabilities. Washington State Patrol, Seattle.

141. Weir BS 2016. A unified characterization of population structure and relatedness. North Carolina State University (Cockerham Lecture).

142. Weir BS 2016. Measuring population structure and relatedness with genomic data. 5th International Conference on Quantitative Genetics, Madison, WI.

143. Weir BS 2016. How should we interpret Y-chromosome evidence? Isaac Newton Institute for Mathematical Sciences, Cambridge, UK.

144. Weir BS 2016. Uncertainty in likelihood ratios for DNA evidence. Royal Statistical Society Annual International Conference, Manchester, UK.

145. Weir BS, Goudet J. 2016. A unified characterization of population structure and relatedness. American Society of Human Genetics Annual Meeting, Vancouver, BC.

146. Hall TO, Weir BS. 2016. A compendium of worldwide surveys of population-specific FST for forensic Y-STR markers. American Society of Human Genetics Annual Meeting, Vancouver, BC.

147. Graffelman J, Nelson S, Gogarten SM, Weir BS. 2016. Statistical tests for Hardy-Weinberg equilibrium at X-chromosomal genetic markers. American Society of Human Genetics Annual Meeting, Vancouver, BC.

148. Zheng X, Gogarten S, Lawrence M, Stilp A, Levine D, Weir BS. 2016. SeqArray - A storage-efficient high-performance data format for WGS variant calls. American Society of Human Genetics Annual Meeting, Vancouver, BC.

149. Weir BS. 2017. A unified characterization of population structure and relatedness. Statistical Genetics Research Symposium, University of Queensland, Brisbane, Australia.

150. Weir BS. 2017. Y-STR Interpretation. American Academy of Forensic Sciences Annual Meeting, New Orleans, LA.

151. Weir BS. 2017. Some challenges of large-scale genomic studies. ESR Research Conference, Wellington, New Zealand.

152. Weir BS. 2017. Statistical caveats with siblingship analyses. International Symposium on Human Identification (ISHI), Seattle, WA.

153. Rice K, Zheng X, Gogarten S, Sofer T, Laurie CA, Laurie CC, Weir BS, Thornton TA, Szpiro A, Bis J, Brody J. 2017. We didn't see this in GWAS: Understanding and fixing unfamiliar problems in association analyses, when pooling whole genome sequence data from multiple studies. American Society of Human Genetics Annual Meeting, Orlando, FL.

154. Weir BS. 2018. Multi-locus match probabilities. NIJ Forensic Research and Development Symposium. Seattle, WA.

155. Graffelman J, Weir BS, Puig X, Ginebra J. 2018. Recent methodological developments for a Hardy-Weinberg analysis of X-chromosomal variants. Internat. Biometric Conf. Resp4, Barcelona, Spain.

156. Goudet J, Weir BS. 2018. How to estimate kinship. Joint Evolution Meetings, Montpellier, France.

157. Weir BS. 2018. Estimating Relatedness and Population Structure. University of Auckland, New Zealand.

158. Weir BS. 2018. UW Genetic Analysis Center. Seattle Childrens Reseach Institute, Seattle, WA.

9 University of Washington Service

2006–14	Member, School of Public Health Executive Committee
2006–	Member, Graduate Certificate in Statistical Genetics Executive Committee
2006–14	Member, Internal Advisory Committee, Center for Ecogenetics and Environmental Health
2006–11	Member, Internal Advisory Board, Institute for Public Health Genetics
2008–13	Associate Director, Northwest Institute for Genetic Medicine
2008–14	Member, Internal Advisory Board, Center for Biomedical Statistics
2011–12	Member, School of Public Health Strategic Planning Committee
2012, 2015–17	Chair, School of Public Health Genomics Search Committee
2015–	Director, Institute for Public Health Genetics
2015–	Director, Graduate Program in Public Health Genetics
2015–	Director, Genetic Analysis Center
2016–17	Member, Faculty Council, School of Public Health
2018–	Member, School of Public Health Leadership Group

10 Professionally Related Community Service

2018. Talk to Advanced Statistics Class, Bainbridge Island High School.

11 Other Pertinent Information

None

12 Teaching History

12.1 Formal Courses at University of Washington

Year	Qtr	Cours Number	Credits	Course Name
2006	AUT	BIOST 580B	1	Statistical Genetics Seminar
2007	WIN	BIOST 551	3	Statistical Genetics II
	AUT	BIOST 5810B	1	Statistical Genetics Seminar
2008	WIN	BIOST 551	3	Statistical Genetics II
	SPR	BIOST 578B	3	Special Topics, Association Mapping
	AUT	BIOST 581	1	Statistical Genetics Seminar
	AUT	BIOST 551	3	Statistical Genetics II
2009	SPR	BIOST 578D	3	Special Topics: Association Mapping
	AUT	BIOST 581	1	Statistical Genetics Seminar
	AUT	BIOST 551	3	Statistical Genetics II
2010	AUT	BIOST 581	1	Statistical Genetics Seminar
	AUT	BIOST 551	3	Statistical Genetics II
2011	WIN	BIOST 581	1	Statistical Genetics Seminar
	SPR	BIOST 581	1	Statistical Genetics Seminar
	AUT	BIOST 551	3	Statistical Genetics II
2012	AUT	BIOST 581	1	Statistical Genetics Seminar
	AUT	BIOST 516	3	Statistical Methods for Genetic Epidemiology
2013	AUT	BIOST 581	1	Statistical Genetics Seminar
2014	SPR	PHG/BIOST 302	3	Forensic Genetics
2015	WIN	BIOST 581	1	Statistical Genetics Seminar
	WIN	PHG 511/EPI 517	3	Genetic Epidemiology
	SPR	PHG 302/BIOST 302	3	Forensic Genetics
	AUT	BIOST 551/STAT 551	3	Statistical Genetics II
2016	WIN	PHG 511/EPI 517	3	Genetic Epidemiology
	SPR	PHG 302/BIOST 302	3	Forensic Genetics
	AUT	BIOST 551/STAT 551	3	Statistical Genetics II
	AUT	PHG 580	1	Public Health Genetics Seminar
2017	WIN	PHG 302/BIOST 302	3	Forensic Genetics
	WIN	PHG 580	1	Public Health Genetics Seminar
	SPR	PHG 580	1	Public Health Genetics Seminar
	SPR	PHG 511/EPI 517	3	Genetic Epidemiology
	AUT	BIOST 551	3	Statistical Genetics II
	AUT	PHG 580	1	Public Health Genetics Seminar
2018	WIN	PHG 302/BIOST 302	3	Forensic Genetics
	WIN	PHG 580	1	Public Health Genetics Seminar
	SPR	PHG 580	1	Public Health Genetics Seminar
	AUT	BIOST551/STAT 551	3	Statistical Genetics II
	AUT	PHG 580	1	Public Health Genetics Seminar

12.2 Other Teaching

Year	Location	Activity
2006	University of Washington	Summer Institute in Statistical Genetics
	Seoul National University	Asian Institute in Statistical Genetics
2007	University of Washington	Summer Institute in Statistical Genetics
	University of Liege	European Institute in Statistical Genetics
2008	University of Washington	Summer Institute in Statistical Genetics
	University of Auckland	Australasian Institute in Statistical Genetics
2009	University of Washington	Summer Institute in Statistical Genetics
	University of Liege	European Institute in Statistical Genetics
2010	University of Washington	Summer Institute in Statistical Genetics
	Peking University	Asian Institute in Statistical Genetics
	US Wildlife Forensic Sci	Statistical Genetics for Forensic Science
	Canadian Soc Forensic Sci	Statistical Genetics for Forensic Science
2011	University of Washington	Summer Institute in Statistical Genetics
	University of Liege	European Institute in Statistical Genetics
2012	University of Washington	Summer Institute in Statistical Genetics
	University of Edinburgh	European Institute in Statistical Genetics
2013	University of Washington	Summer Institute in Statistical Genetics
2014	University of Sao Paulo	Brazilian Summer Institute in Statistical Genetics
	University of Washington	Summer Institute in Statistical Genetics
	University of Lausanne	Swiss Summer Institute in Statistical Genetics
2015	University of Washington	Summer Institute in Statistical Genetics
	Academia Sinica	Taiwan Institute in Statistical Genetics
2016	University of Washington	Summer Institute in Statistical Genetics
	University of Algarve	Portugese Institute in Statistical Genetics
2017	New York University Abu Dhabi	Abu Dhabi Winter Institute in Statistical Genetics
	University of Queensland	Brisbane Summer Institute in Statistical Genetics
	University of Washington	Summer Institute in Statistical Genetics
	University of Lausanne	Swiss Institute in Statistical Genetics
2018	University of Washington	Summer Institute in Statistical Genetics

13 Advising and Formal Mentoring

13.1 Current Advising and Mentoring

Name	Program	Role
Sanne Aalbers	Biostatistics m	NIST Fellow
Yuxin Guo	Public Health Genetics	Visiting Scholar
Yunqi Li	Public Health Genetics	Advisor
Pearl Liu	Biostatistics	RA Supervisor
Charles Wolock	Biostatistics	RA Supervisor
Lluvia Xia	Epidemiology	RA Supervisor
Edward Zhao	Biostatistics	RA Supervisor

13.2 PhD Dissertation Chair Completed

	Year	Name	Dissertation / Present Position
1	1976	V.J. Thomas	"The application of matrix theory to optimal design of experiments."
2	1977	Sam Choy	"One- and two-locus inbreeding for recurrent selection and overlapping generations."
3	1981	John Reynolds	"Genetic distance and coancestry." Now Biostatistics Director for Alfred Health, Melbourne, Australia.
4	1986	Kenneth Dodds	"Resampling methods in genetics and the effect of family structure in genetic data." Now at AgResearch, New Zealand
5	1988	Jaime Hernandez	"Testing genetic hypotheses."
6	1989	Jun Zhu	"Estimation of genetic variance components in the general mixed model." Now Professor at Zheijiang University.
7	1993	Spencer Muse	"Testing for equality of nucleotide substitution rates." Now Professor at North Carolina State University.
8	1993	Rebecca Doerge	"Statistical methods for locating quantitative trait loci with molecular markers." Now Dean of Science, Carnegie Mellon University.
9	1993	Paul Maiste	"Comparison of statistical tests for independence at genetic loci with many alleles."
10	1996	Lauren McIntyre	"DNA fingerprinting and Hardy-Weinberg equilibrium: a continuous analysis VNTR data." Now Professor at University of Florida.
11	1996	Yi-Ju Li	"Characterizing the structure of genetic populations." Now Associate Professor at Duke University.
12	1997	Eden Martin	"Extensions of the transmission/disequilibrium test for identifying human disease genes." Now Professor at University of Miami.
13	1998	Jennifer Shoemaker	"A Bayesian characterization of genetic disequilibria."
14	1999	Stephanie Monks	"Family-based methods which rely on association for the mapping of genes in human populations." Now S. Santorico, Associate Professor at University of Colorado
15	1999	Dahlia Nielsen	"An examination of association based tests for localizing genes in outbred populations." Now Associate Professor at North Carolina State University
16	1999	Dmitri Zaykin	"Statistical analysis of genetic associations." Now at National Institute of Environmental Health Science
17	2001	Shu-Pang Huang	"Robust methods for estimating allele frequencies." Now at Bristol-Myers-Squibb

	Year	Name	Dissertation / Present Position
18	2002	Tzu-Ming Chu	“Statistical nonparametric and linear mixed model analyses of oligonucleotide DNA chips data.” Now at SAS Inc.
19	2002	Wenlei Liu	“Development of linkage and association methods to map disease genes.” Now at Eli Lilly
20	2003	Wendy Czika	“Accounting for within- and between-locus dependencies in marker association tests.” Now at SAS Inc.
21	2003	Zhaoling Meng	“Statistical topics in disease gene mapping.” Now at Sanofi-Aventis
22	2004	Xiang Yu	“Statistical methods for the analysis of genetic marker and microarray data.” Now at Merck
23	2004	Li Li	“Disease gene mapping in general pedigrees.” Now at GlaxoSmithKline
24	2004	Andrea Johnson	“Estimation and sampling properties of gene diversity, heterozygosity and F_{ST}.” Now at CardioDx
25	2005	Amanda Hepler	“Improving forensic identification using Bayesian networks and relatedness estimation.” Now at Innovative Decisions
26	2005	Weichun Huang	“Computational methods for identifying and characterizing the human gene regulatory regions.” Now at National Institute of Environmental Health Sciences
27	2006	Gary Beecham	“Statistical methods for the analysis of forensic DNA mixtures.” Now Assistant Professor at University of Miami
28	2006	Xiaoyi Gao	“Statistical methods in genetic association studies.” Now Associate Professor at University of Illinois at Chicago.
29	2006	Xi Chen	“Characterizing the genetic structure of populations.” Now Associate Professor at Vanderbilt University
30	2010	Rori Rohlfs	“The role of null distributions in statistical genetics.” Now Assistant Professor at San Francisco State University.
31	2010	Yoonha Choi	“Case-control association testing with unknown multilevel relationships: cryptic relatedness and population structure.” Now at Veracyte.
32	2013	Xiuwen Zheng	“Statistical prediction of HLA alleles and relatedness analysis in genome-wide association studies.” Now Postdoctoral student at University of Washington.
33	2014	Matthew Conomos (co-advisor)	“Inferring, estimating, and accounting for population and pedigree structure in genetic analyses.” Now Research Scientist in Genetic Analysis Center, UW
34	2016	Taryn Hall	“The Y chromosome in forensic and public health genetics.” Now Research Scientist at Institute for Systems Biology
35	2018	Qian Zhang	“Statistical Genetic Methods and Applications for Population Structure.” Now in Medical School, University of Washington

13.3 Masters Thesis Chair Completed

Year	Student	Thesis Title
2008	Qiong Zhao	Testing for Association Between Markers and Trait Loci in a Quantitative Genetic Framework.

13.4 Postdoctoral Supervision Completed

	Years	Name	Support / Present Position
1	1982–83	J.C. Stephens	Cockerham P01 Now at Motif BioSciences
2	1985–87	L.D. Brooks	Weir R01 Now at National Human Genetics Research Institute
3	1988–90	C.J. Basten	Sloan Foundation Fellowship Now at Syngenta
4	1991–94	P.O. Lewis	NIH Fellowship Now Professor at University of Connecticut
5	1992–94	B.S. Gaut	NIH Fellowship Now Professor at University of California at Irvine
6	1994–95	N. Taylor	Weir R01 Left science
7	1996–98	K. Simonsen	Weir P01 Now Associate Professor, Purdue University
8	1996–98	I. Painter	Weir R01 Now Assistant Professor at University of Washington
9	1997–98	E. Buckler	NIH Fellowship Now Professor at Cornell University
10	1997–99	J. Curran	New Zealand Fellowship Now Professor at University of Auckland
11	1998–99	J. Graham	NISS Fellowship Now Professor at Simon Fraser University
12	1999–00	M. deLuca	Italian Fellowship Now Associate Professor at University of Alabama
13	2000–01	S. Hardy	VIGRE Fellowship Now Director of Institutional Research at University of Maine
14	2001–04	G. Skalski	NIEHS Fellowship Left science
15	2003–06	A. Anderson	VIGRE Fellowship Now Associate Professor at Western Washington University
16	2007–09	T. Bhangale	Weir R01 Now at Genentech
17	2014	S. Gittleson	Swiss NSF Now at NIST
18	2015-16	A. Thiery	NIST Now at University of Bern
19	2015-17	E. Bodah	NIEHS Fellowship Now at Progene Inc.