

EDITORIAL RESPONSIBILITIES:

Editorial Board, Human Genetics, 1994-1999
Editorial Board, Genetic Epidemiology, 1996-2012
Editorial Board, The American Journal of Human Genetics, 2006-2010
Editor, Genetic Analysis Workshop 11, Genetic Epidemiology, vol. 17, supplement 1999
Senior Editor, Genetic Analysis Workshop 12, Genetic Epidemiology, vol. 21, supplement 2001
Editor, Genetic Analysis Workshop 15, 2007
Editor, Genetic Analysis Workshop 19, BMC Proceedings vol. 10, Supplement 7, 2014-2016
Faculty of 1000, 2013-present

MONITORING BOARDS/ADVISORY PANELS:

Member, Policy and monitoring board of:
NIH NHLBI "The collaborative studies on the genetics of asthma"
NIH NHLBI Determinants of high blood pressure data and safety monitoring board, 1996-2005.
NIH NIA, Member, Genetic Epidemiology Advisory Group.
NIH NIMH, Member, Genetics Research Planning Panel, 1998
NIH NHLBI, Member, Jackson Heart Study, "Emerging Science Genetics advisory panel", 2005-2011
NIH NHLBI, Member, Candidate gene association resource Committee, 2005-2011
NIA Board of Scientific counselors, Member, 2006-2010; ad hoc, 2011
NIH NHLBI, Member, National Registry for Genetically Triggered Thoracic Aortic Aneurysms and Cardiovascular Conditions (GENTAC), observational study monitoring board, 2007-2015,
Genetic Analysis Workshop Advisory board member, 2010-2014

INVITED TALKS AND PARTICIPATION

1. "Rule-based haplotype construction in pedigrees". University of California - Los Angeles, October 1986.
2. "Automated haplotype analysis". Department of Medicine, University of Washington, December 1986.
3. "The effects of model misspecification on the results of linkage analysis of familial Alzheimer's disease".
Second International Symposium on Familial Alzheimer's Disease, May 1989.
4. Participant, Banbury meeting on Molecular Genetics and the Biology of Alcoholism, October 1989.
5. "Linkage Analysis of Alzheimer's disease". Oregon Health Sciences University, December 1989.
6. Participant, Thalassemia in Asian Americans, Costa Mesa, CA, June 1990.
7. Participant, University of Washington Law School workshop on DNA fingerprinting, April 1992.
8. "Complex genetic analysis in human genetics". Institute of Mathematical Statistics annual meeting (WNAR), Corvallis Oregon, June 1992.
9. "All you wanted to know about the genetics of Alzheimer's disease, but forgot to ask". Neyman Seminar invited talk, Statistics Department, Berkeley CA, October 1992.
10. "Special problems associated with linkage analysis in familial Alzheimer's disease". Society for Neuroscience meeting, October 1992.
11. "Alzheimer's disease genes". The American Geriatrics Society annual meeting, May 1994.
12. "Statistical issues and approaches in the genetics of AD". Adler Foundation Symposium, September 1994.
13. "Monte Carlo Methods in Genetics and Epidemiology: opportunities and problems". Joint Statistical Meetings, August 1995.
14. Participant, National Heart, Lung, and Blood Institute sponsored workshop on the genetics of asthma, "Phenotypic issues in studies of asthma genetics", September 1995.
15. "Mapping genes for Alzheimer's disease - a late onset disorder with multiple etiologies", University of Toronto, Lunenfeld Research Institute seminar series, May 1996.
16. "Mapping genes for Alzheimer's disease", Wellcome trust center for human genetics, Oxford University July 1996.
17. "Linkage disequilibrium: a case study leading to the identification of the Werner's syndrome locus". Department of Biostatistics, University of Michigan, Ann Arbor, Michigan, November 1996.
18. "Monte Carlo Markov chain methods and model selection for complex traits." Urbana, Illinois. Allerton II meeting, November 1996.
19. "Linkage disequilibrium: a case study leading to the identification of the Werner's syndrome locus". NHGRI, National Institutes of Health, January 1997.

20. "Finding genes for Alzheimer's disease: a disease of complex etiology". AMSIE'97, AAAS annual meeting, Seattle, February 1997.
21. "Monte Carlo Markov chain methods and model selection in genetic epidemiology". Second World Congress of the International Association for Statistical Computing, Pasadena, February 1997.
22. Participant, Institute for Mathematics and its Applications, "Statistics in the Health sciences - Genetics", Minneapolis, July 1997.
23. "Finding genes for Alzheimer's disease: a disease of complex etiology". Department of Biostatistics and Epidemiology, Case Western Reserve University, Cleveland, November 1997.
24. "Finding genes for Alzheimer's disease: a disease of complex etiology". Memorial Sloan Kettering Cancer Institute, January 1988.
25. Participant, "Genetics of Autism meeting", National Institutes of Health. January 1998.
26. "Linkage studies in genetic epidemiology", Centre de recherches mathématiques, Montreal, May 1998.
27. "Statistical and computational contributions to gene mapping: history and current developments", Mathematical Sciences Research Institute, Berkeley, May 1998.
28. "Perspectives on pedigree and case-control designs for mapping genes contributing to complex disease", National Cancer Institute workshop, Seattle, May 1998.
29. "Penetrance: what is it?" Joint Statistics Meetings, Dallas, August 1998.
30. "Issues with mapping genes for complex traits in humans", Department of Epidemiology, University of Minnesota, December 1998.
31. "Issues with finding genes for complex traits in humans, with special reference to Alzheimer's disease", Exelixis, South San Francisco, California, March 1999
32. Society for Epidemiological Research meetings, Baltimore, Maryland, Invited speaker, "Under what genetic models and population histories are case-control studies useful?", June 1999.
33. Sackler McDonnell foundation meeting on Molecular genetics and developmental psychopathology, Invited speaker, "Methods and designs for studying autism", August 1999.
34. International Genetic Epidemiology Society meeting, St. Louis, Missouri, Invited speaker, "Under what conditions are association studies more efficient than family studies for gene mapping?", September 1999.
35. Marshfield Medical Foundation, "Mapping genes for complex traits: perspectives on pedigree-based vs. case-control approaches", May 2000.
36. Gordon Conference, Quantitative genetics and genomics, "Complex traits and complex models in human gene discovery", February 2001.
37. American Society of Human Genetics, "More powerful methods for family studies of atherosclerotic risk factors", Invited session on Dissecting the genetic contributions to complex disease: Atherosclerosis, October 2001.
38. Washington University, Division of Biostatistics, "From case-control to large pedigrees: genetic analysis of complex traits", November 2001.
39. Workshop in Statistical Genetics and Computational Molecular Biology, University of Washington, "Gene finding in human populations", December 2001
40. University of California – Los Angeles, Department of Genetics, "From case-control to large pedigrees: genetic analysis of complex traits", January 2002
41. University of Alberta – Edmonton, Department of Human Genetics, "From Case-Control to Large Pedigree Designs", January 2003
42. University of Michigan – Ann Arbor, Department of Biostatistics, "Complex traits and complex models in human gene discovery: pedigree vs. case-control designs", January 2004
43. Toronto, Symposium on Genetic findings in reading disabilities and related cognitive processes, "Use of phenotypic subtypes and complex trait models in genetic analysis of dyslexia", June 2005
44. American Society of Human Genetics, "Genetic basis of communication disorders", invited session organizer and moderator, October 2005
45. Keystone Meeting, Alzheimer's Disease: Genes, Cellular Pathways and Therapies, "Complex models in the search for late-onset AD genes", invited speaker, February 2006
46. Emory University, Department of Human Genetics, "Complex traits dissected by complex models: Case studies in cardiovascular disease, Alzheimer's disease, and learning disabilities", February 2006
47. Banbury meeting, "Multilocus models and analysis of component phenotypes" invited speaker, March 2006

48. Toronto, First Canadian Genetic Epidemiology and Statistical Genetics Workshop, “Building capacity in genetic epidemiology and statistical genetics: challenges and perspectives”, invited speaker, March 2006
49. Bethesda, “National Cancer Institute – National Genome Research Institute working group on replication in association studies”, invited participant, November 2006
50. Seattle, International Meeting for Autism Research, “Statistical genetic approaches for analysis of autism and autism endophenotypes”, invited speaker, May 2007
51. Bethesda, “Genetics of Alzheimer’s disease”, invited participant, August 2007.
52. American Society of Human Genetics, “Evaluating potential bias in and interpreting results from epidemiologic designs for genome-wide association studies”, invited speaker, October 2007.
53. Bethesda, “Frontiers in Population Genomics Meeting”, invited discussant, December 2007.
54. Case Western Reserve University, Department of biostatistics and epidemiology, “Complex traits vs. complex models: searching for disease genes”, February 2008.
55. Vanderbilt University, Department of Genetics, “Complex traits vs. complex models: searching for disease genes”, March 2008.
56. Fourth Annual Canadian Genetic Epidemiology and Statistical Genetics Meeting, “Population Genetics Informs Genetic Epidemiology”, May 2009.
57. Fifth Annual Canadian Genetic Epidemiology and Statistical Genetics meeting, “Why are pedigrees still relevant in an era of genomic technologies?”, April, 2010.
58. Alzheimer’s Association International Conference on Alzheimer’s Disease 2010, “Family based approaches to analysis of GWAS data in the NIA-LOAD/NCRAD sampe”, July 2010.
59. American Society of Human Genetics meeting, “Cardiovascular quantitative trait loci: Challenges and opportunities in the search for rare variants”, November 2010.
60. International Genetic Epidemiology Society meeting, “Sequencing in family-based projects”, September 2011.
61. Hospital for Sick Kids, Toronto, Canada, “There be dragons here: what we learned from genetic studies in multi-site Alzheimer’s disease samples”, December 2011.
62. University of Toronto, Toronto, Canada, “New genomics technologies and complex traits: what do we gain and what are the challenges?”, December 2011.
63. Montreal, Canada, Montreal Spring School of Population Genomics and Genetic Epidemiology, “There be dragons here: population genetics meetings genetic epidemiology in a GWAS of Alzheimer’s disease”, May 2012
64. Boston University, Boston, Massachusetts, Department of Biostatistics, “There be dragons here: challenges in the analysis of large genomics studies”, April 2013
65. Banff International Research Station for Mathematical Innovation and Discovery, Banff, Canada, “Genotype imputation from sequence data in pedigrees: rare and common variants in complex traits”, June 2014
66. University of Texas, Houston, Division of Epidemiology, Human Genetics, and Environmental Sciences, “New genomics technologies and complex traits in human genetics: what do we gain and what are the challenges?”, September 2014
67. Harvard University, Boston, Department of Biostatistics, “Complex genetic traits in an era of high-throughput genomics technologies”, April 2015
68. Rutgers University, Department of Genetics, “Complex genetic traits in an era of high-throughput genomics technologies”, May 2015
69. American Society of Human Genetics, Baltimore, “How do you know you have it if you can’t measure it?”, October 2015
70. Alzheimer’s Association International Conference, “The Alzheimer’s Disease Sequencing Project: Family-based analyses”, invited speaker, Toronto, Canada, July 2016.
71. University of Wisconsin, Madison, WI, “James F Crow and Human Genetics”, September 2016.

BIBLIOGRAPHY

Manuscripts

1. **Wijsman** EM (1984) The effect of mutagenesis on competitive ability in *Drosophila*. *Evolution* 38:571-581.
2. **Wijsman** EM, Zei G, Moroni A, Cavalli-Sforza LL (1984) Surnames in Sardinia II. Computation of migration matrices from surname distributions in different periods. *Annals of Human Genetics* 48:65-78.

3. **Wijsman** EM (1984) Techniques for estimating genetic admixture and applications to the problem of the origin of the Icelanders and the Ashkenazi Jews. *Human Genetics* 67:441-448.
4. **Wijsman** EM (1984) Optimizing selection of restriction enzymes in the search for DNA variants. *Nucleic Acids Research* 12:9209-9226.
5. Astolfi P, Pagnacco G, **Wijsman** EM (1985) Estimation of racial mixture in a native Italian Cattle breed. *Journal of Animal Breeding and Genetics* 1102:56-64.
6. Feder J, Yen L, **Wijsman** E, Wang L, Wilkins L, Schroder J, Spurr N, Cann H, Blumenberg M, Cavalli-Sforza LL (1985) A systematic approach for detecting high frequency restriction fragment length polymorphisms using large genomic probes. *American Journal of Human Genetics* 37:635-649.
7. **Wijsman** EM, Neves WA (1986) The use of nonmetric variation in estimating human population admixture: a test case with Brazilian Blacks and Whites. *American Journal of Physical Anthropology* 70:395-405.
8. **Wijsman** EM (1987) A deductive method of haplotype analysis in pedigrees. *American Journal of Human Genetics* 41:356-373.
9. Bowcock AM, Hebert JM, Christiano AM, **Wijsman** E, Cavalli-Sforza LL, Boyd CD (1987) The pro alpha 1 (IV) collagen gene is linked to the D13S3 locus at the distal end of human chromosome 13q. *Cytogenetics and Cell Genetics* 45:234-236.
10. Bowcock AM, Hebert JM, **Wijsman** E, Gadi I, Cavalli-Sforza LL, Boyd CD (1988) High recombination between two physically close human basement membrane collagen genes at the distal end of chromosome 13q. *Proceedings of the National Academy of Sciences USA* 85:2701-2705.
11. Schellenberg GD, Bird TD, **Wijsman** EM, Moore DK, Boehnke M, Bryant EM, Lampe TH, Nochlin D, Sumi M, Deeb SS, Beyreuther K, Martin GM (1988) Absence of linkage of chromosome 21q21 markers to familial Alzheimer's disease. *Science* 241:1507-1510.
12. Darby JK, Willems PJ, Nakashima P, Johnsen J, Ferrell RE, **Wijsman** EM, Gerhard D, Dracopoli NC, Housman D, Henke J, Fowler ML, Shows TB, O'Brien JS, Cavalli-Sforza LL (1988) Restriction analysis of the structural alpha-L- fucosidase gene and its linkage to fucosidosis. *The American Journal of Human Genetics* 43:749-755.
13. Bird TD, Schellenberg GD, **Wijsman** EM, Martin GM (1989) Evidence for etiologic heterogeneity in Alzheimer's disease. *Neurobiology of Aging*. 10:432-434.
14. Schellenberg GD, Bird TD, **Wijsman** EM, Moore DK, Martin GM (1989) The genetics of Alzheimer's Disease. *Biomedicine and Pharmacotherapy* 43:463-468.
15. Raskind WH, **Wijsman** EM, Pagon RA, Cox TC, Bawden MJ, May BK, Bird TD (1991) X-linked sideroblastic anemia and ataxia: linkage to phosphoglycerate kinase at Xq13. *The American Journal of Human Genetics* 48:335-341.
16. Schellenberg GD, Pericak-Vance MA, **Wijsman** EM, Moore DK, Gaskell Jr. PC, Yamaoka LA, Bebout JL, Anderson L, Welsh KA, Clark CM, Martin GM, Roses AD, Bird TD (1991) Linkage analysis of familial Alzheimer's disease using chromosome 21 markers. *The American Journal of Human Genetics* 48:563-583.
17. **Wijsman**, EM. (1991) Recurrence risk of a new dominant mutation in children of unaffected parents. *The American Journal of Human Genetics* 48:654-661.
18. Schellenberg GD, Anderson L, O'dahl S, **Wijsman** EM, Sadovnick AD, Ball MJ, Larson EB, Kukull WA, Martin GM, Roses AD, Bird TD (1991) APP717, APP693, and PRIP gene mutations are rare in Alzheimer's disease. *The American Journal of Human Genetics* 49:511-517.
19. Austin MA, **Wijsman** E, Guo S, Krauss RM, Brunzell JD, Deeb S (1991) Lack of evidence for linkage between low-density lipoprotein subclass phenotypes and the apolipoprotein B locus in familial combined hyperlipidemia. *Genetic Epidemiology* 8:287-297.
20. Blossey H, Guo SW, McKnight B, Tierney C, Thompson E, **Wijsman** E (1992) Linkage analysis of malignant melanoma with the chromosome 1 markers D1S47 and PND. *Cytogenetics and Cell Genetics* 59:182-184.
21. Schellenberg GD, Boehnke M, **Wijsman** EM, Moore DK, Martin GM, Bird TD (1992) Genetic association and linkage analysis of the Apo CII locus and familial Alzheimer's disease. *Annals of Neurology* 31:223-227.
22. Austin MA, Horowitz H, **Wijsman** E, Krauss RM, Brunzell J (1992) Bimodality of Plasma Apolipoprotein B levels in Familial Combined Hyperlipidemia. *Atherosclerosis* 92:67-77.
23. Deeb SS, Failor RA, Brown BG, Brunzell JD, Albers JJ, Motulsky AG, **Wijsman** E (1992) Association of Apolipoprotein B gene variants with Plasma apoB and LDL Cholesterol Levels. *Human Genetics* 88:463-470.
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- Linkage and mutational analysis of familial Alzheimer's disease kindreds for the APP gene region. *American Journal of Human Genetics* 51:998-1014.
25. **Wijsman EM.** (1992) Principles of linkage analysis applied to genetic mapping of familial Alzheimer's disease. *Current Science* 63:487-491.
 26. *Schellenberg GD, Bird TD, **Wijsman EM**, Orr HT, Anderson L, Nemens E, White JA, Bonnycastle L, Weber JL, Alonso ME, Potter H, Heston LL, Martin GM (1992) Genetic linkage evidence for a familial Alzheimer disease locus on chromosome 14. *Science* 258:668-671.
 27. Jarvik GP, **Wijsman E**, Little RER, Albers JJ, Motulsky AG (1993) Host and environmental effects on plasma apolipoprotein B. *International Journal of Clinical and Laboratory Research.* 23:215-220.
 28. Olson JM, **Wijsman EM** (1993) Linkage between quantitative trait and marker loci: methods using all relative pairs. *Genetic Epidemiology* 10:87-102.
 29. Lin S, Thompson E, **Wijsman E** (1993) Achieving irreducibility of the Markov chain Monte Carlo method applied to pedigree data. *IMA J Math Appl in Med & Biol* 10:1-17.
 30. **Wijsman EM**, Bird TD, Martin GM, Schellenberg GD (1993) The Seattle Alzheimer's disease data set. *Genetic Epidemiology* 10:365-369.
 31. **Wijsman EM** (1993) Genetic analysis of Alzheimer's disease: summary of GAW8. *Genetic Epidemiology* 10:349-360.
 32. Thompson EA, Lin S, Olshen AB, **Wijsman EM** (1993) Monte Carlo segregation and linkage analysis of a large hypercholesterolemia pedigree. *Genetic Epidemiology* 10:677-682.
 33. Stephens K, Sybert VP, **Wijsman EM**, Ehrlich P, Spencer A (1993) A keratin 14 mutational hot spot for epidermolysis bullosa simplex, Dowling-Meara: implications for diagnosis. *Journal of Investive Dermatology* 101:240-243.
 34. Bonnycastle LLC, Yu C-E, **EM Wijsman EM**, Orr HT, Patterson D, Clancy KP, Goddard KAB, Alonso ME, Nemens E, White JA, Heston LL, Martin GM, Bird TD, Schellenberg GD (1993) The c-fos gene and early-onset familial Alzheimer's disease. *Neuroscience Letters* 163:33-36.
 35. Schellenberg GD, Payami H, **Wijsman EM**, Orr HT, Goddard KAB, Anderson L, Nemens E, White JA, Alonso ME, Ball MJ, Kaye J, Morris JC, Chui H, Sadovnick AD, Heston LL, Martin GM, Bird TD (1993) Chromosome 14 and late-onset familial Alzheimer disease. *American Journal of Human Genetics* 53:619-628.
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 37. Nakura J, Miki T, Nagano K, Kihara K, Ye L, Kamino K, Fujiwara Y, Yoshida S, Murano S, Fukuchi K-I, **Wijsman EM**, Martin GM, Schellenberg GD, Ogihara T (1993) Close linkage of the gene for Werner's syndrome to ANK1 and D8S87 on the short arm of chromosome 8. *Gerontology* 39 (suppl):11-15.
 38. Commenges D, Olson J, **Wijsman E** (1994) The weighted rank pairwise correlation statistic for linkage analysis: simulation study and application to Alzheimer's disease. *Genetic Epidemiology* 11:201-212.
 39. Palmer SE, Dale DC, Livingston RJ, **Wijsman EM**, Stephens K (1994) Autosomal dominant cyclic hematopoiesis: exclusion of linkage to the major hematopoietic regulatory gene cluster on chromosome 5. *Human Genetics*, 93:195-197.
 40. Lin S, Thompson EA, **Wijsman EM** (1994) Finding non-communicating sets for Markov chain Monte Carlo estimations on pedigrees. *American Journal of Human Genetics* 54:695-704.
 41. Yu C-E, Payami H, Olson JM, Boehnke M, **Wijsman EM**, Orr HT, Kukull WA, Goddard KAB, Nemens E, White JA, Alonso ME, Taylor TD, Ball MJ, Kaye J, Morris J, Chui H, Sadovnick AD, Martin GM, Larson EB, Heston LL, Bird TD, Schellenberg GD (1994) The Apolipoprotein E/CI/CII gene cluster and late-onset Alzheimer's disease. *American Journal of Human Genetics* 54:631-642.
 42. Palmer SE, Scherer SW, Kukulich M, **Wijsman EM**, Tsui L-C, Stephens K, Evans JP (1994) Evidence for locus heterogeneity in human autosomal dominant split hand/split foot malformation. *American Journal of Human Genetics* 55:21-26.
 43. Yu C-E, Oshima J, Goddard KAB, Miki T, Nakura J, Ogihara T, Poot M, Hoehn H, Fraccaro M, Piusan C, Martin GM, Schellenberg GD, **Wijsman EM** (1994) Linkage disequilibrium and haplotype studies of chromosome 8p 11.1-21.1 markers and Werner's syndrome. *American Journal of Human Genetics* 55:356-364.
 44. Olson JM, **Wijsman EM** (1994) Design and sample size considerations in the detection of linkage disequilibrium with a disease locus. *American Journal of Human Genetics* 55:574-580.

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46. Nakura J, **Wijsman EM**, Miki T, Kamino K, Yu C-E, Oshima J, Fukuchi K, Weber JL, Piussan C, Malaragno MI, Epstein CJ, Scappaticci S, Fraccaro M, Matsumura T, Murano S, Yoshida S, Fujiwara Y, Saida T, Ogihara T, Martin GM, Schellenberg GD. (1994) Homozygosity mapping of the Werner's syndrome locus (WRN). *Genomics* 23:600-608.
47. Jarvik GP, Brunzell JD, Austin MA, Krauss RM, Motulsky AG, **Wijsman EM** (1994) Genetic predictors of familial combined hyperlipidemia in four large pedigrees: influence of apolipoprotein B level major locus predicted genotype and low density lipoprotein subclass phenotype. *Arteriosclerosis, Thrombosis and Vascular Biology* 14:1687-1694.
48. Jarvik GP, Kukull WA, Schellenberg GD, Yu C, Larson EB, **Wijsman EM** (1995) Interactions of Apolipoprotein E genotype, total cholesterol level, age, and sex in prediction of Alzheimer disease in a case-control study. *Neurology* 45:1092-1096.
49. Stephens K, Zlotogorski A, Smith L, Ehrlich P, **Wijsman E**, Livingston RJ, Sybert VP (1995) Epidermolysis bullosa simplex: a keratin 5 mutation is a fully dominant allele in epidermal cytoskeleton function. *American Journal of Human Genetics* 56:577-585.
50. Goddard KAB, Jarvik GP, Graham J, McNeney B, Hsu L, Siegmund K, Grosser S, Olson J, **Wijsman EM** (1995) Analysis of quantitative risk factors for a common oligogenic disease. *Genetic Epidemiology* 12:759-764.
51. Querfurth H, **Wijsman E**, St. George-Hyslop PH, Selkoe D (1995) bAPP mRNA transcription is increased in cultured fibroblasts from the familial Alzheimer's disease-1 family. *Molecular Brain Research* 28:319-337.
52. Koller WC, Glatt SL, Hubble JP, Paolo A, Tröster AI, Handler MS, Horvat RT, Martin C, Schmidt K, Karst A, **Wijsman EM**, Yu C-E, Schellenberg GD (1995) Apolipoprotein E genotypes in Parkinson's disease with and without dementia. *Annals of Neurology* 37:242-245.
53. Brunzell JD, Austin MA, Deeb SS, Hokanson JE, Jarvik GP, Nevin DN, **Wijsman E**, Zambon A, Motulsky AG (1995) Familial combined hyperlipidemia and genetic risk for atherosclerosis. *Atherosclerosis* X:624-627.
54. Levy-Lahad E, **Wijsman EM**, Nemens E, Anderson L, Goddard KAB, Weber, JL, Bird TD, Schellenberg GD (1995) A familial Alzheimer's disease locus on chromosome 1. *Science* 269:970-973.
55. Levy-Lahad E, Wasco W, Poorkaj P, Romano DM, Oshima J, Pettingell, WH, Yu C-E, Jondro PD, Schmidt SD, Wang K, Crowley AC, Fu Y-H, Guenette SY, Galas D, Nemens E, **Wijsman EM**, Bird TD, Schellenberg GD, Tanzi RE (1995) Candidate gene for the chromosome 1 familial Alzheimer's disease locus. *Science* 269:973-977.
56. Levy-Lahad E, Lahad A, **Wijsman EM**, Bird TD, Schellenberg GD (1995) ApoE genotypes and age of onset in early-onset familial Alzheimer's disease. *Annals of Neurology* 38:678-680.
57. Olshen AB, **Wijsman EM** (1996) Pedigree Analysis Package vs. MIXD: fitting the mixed model on a large pedigree. *Genetic Epidemiology* 13:91-106.
58. Jarvik GP, Larson EB, Goddard K, Kukull WA, Schellenberg GD, **Wijsman EM** (1996) Influence of apolipoprotein E genotype on the transmission of Alzheimer disease in a community-based sample. *American Journal of Human Genetics* 58:191-200.
59. Payami H, Zarepari S, Montee KR, Sexton GJ, Kaye JA, Bird TD, Yu C-E, **Wijsman EM**, Heston LL, Litt M, Schellenberg GD (1996) Gender difference in apolipoprotein E-associated risk for familial Alzheimer disease (AD): a possible clue to the higher incidence of Alzheimer Disease in women. *American Journal of Human Genetics* 58:803-811.
60. Edland SD, Silverman JM, Pesking ER, Tsuang D, **Wijsman E**, Morris JC (1996) Increased risk of dementia in mothers of Alzheimer's disease cases: evidence for maternal inheritance. *Neurology* 47:254-256.
61. Goddard KAB, Yu C-E, Oshima J, Miki T, Nakura J, Piussan C, Martin GM, Schellenberg GD, **Wijsman EM**, and members of the International Werner's Syndrome Collaborative Group (1996) Towards localization of the Werner syndrome gene by linkage disequilibrium and ancestral haplotyping: lessons learned from analysis of 35 chromosome 8p11.1-21.1 markers. *American Journal of Human Genetics* 58:1286-1302.
62. Yu C-E, Oshima J, Fu Y-H, **Wijsman EM**, Hisama F, Alisch R, Matthews S, Nakura J, Miki T, Ouais S, Martin GM, Mulligan J, Schellenberg GD (1996) Positional cloning of the Werner's syndrome gene. *Science* 272:258-262.

63. Nakura J, Miki T, Le L, Mitsuda N, Zhao Y, Kihara K, Yu C-E, Oshima J, Fukuchi K, **Wijsman EM**, Schellenberg GD, Martin GM, Murano S, Hashimoto K, Fujiwara Y, Ogihara T (1996) Narrowing the position of the Werner syndrome locus by homozygosity analysis - extension of homozygosity. *Genomics* 36:130-141.
64. Bird TD, **Wijsman EM**, Nochlin D, Leehey M, Sumi SM, Payami H, Poorkaj P, Nemens E, Schellenberg GD (1997) Chromosome 17 and hereditary dementia: linkage studies in three non-Alzheimer families and kindreds with late-onset FAD. *Neurology* 48:949-954
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66. Yu C-E, Oshima J, **Wijsman EM**, Nakura J, Miki T, Piussan C, Matthews S, Fu Y-H, Mulligan J, Martin GM, Schellenberg GD, and members of the International Werner's Syndrome Collaborative Group (1997) Mutations in the consensus helicase domains of the Werner's syndrome gene. *American Journal of Human Genetics* 60:330-341.
67. Graham J, Chapman NH, Goddard KAB, Goode EL, **Wijsman EM**, Jarvik GP (1997) Segregation and linkage analysis of a quantitative versus a qualitative trait in large pedigrees. *Genetic Epidemiology* 14:999-1004.
68. Heath SC, Snow GL, Thompson EA, Tseng C, **Wijsman EM** (1997) MCMC segregation and linkage analysis. *Genetic Epidemiology* 14:1011-1016.
69. **Wijsman EM** (1997) Monte Carlo Methods and model selection in genetic analysis. *Animal Biotechnology* 8:129-144.
70. Li H, Thompson EA, **Wijsman EM** (1998) Semiparametric estimation of major gene effects for age of onset. *Genetic Epidemiology* 15:279-298.
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72. Raskind WH, Conrad EU, Matsushita M, **Wijsman EM**, Wells DE, Chapman N, Sandell LJ, Wagner JH, Houck J (1998) Evaluation of locus heterogeneity and EXT1 mutations in 34 families with hereditary multiple exostoses. *Human Mutation* 11:231-239.
73. Snow GL, **Wijsman EM** (1998) Pedigree analysis package (PAP) vs. MORGAN: Model selection and hypothesis testing on a large pedigree. *Genetic Epidemiology* 15:355-369.
74. Edland S, **Wijsman EM**, Schoder-Ehri G, Leverenz J (1997) Little evidence of reduced survival to adulthood of apoE e4 homozygotes in Down's syndrome. *NeuroReport* 8:3463-3465.
75. **Wijsman EM**, Brunzell JB, Jarvik GP, Austin MA, Motulsky AG, Deeb SS (1998) Evidence against linkage of familial combined hyperlipidemia to the apolipoprotein AI-CIII-AIV gene complex. *Arteriosclerosis, Thrombosis, and Vascular Biology*. 18:215-226.
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