Robert C Elston

List of Publications by Year in Descending Order

174 papers	4,580 citations	36 h-index	63 g-index
186 ext. papers	5,005 ext. citations	4.1 avg, IF	5.19 L-index

#	Paper	IF	Citations
174	An Accidental Genetic Epidemiologist. *Annual Review of Genomics and Human Genetics*, **2020**, 21, 15-36	9.7	
173	Local Ancestry Inference in Large Pedigrees. *Scientific Reports*, **2020**, 10, 189	4.9	0
172	ONETOOL for the analysis of family-based big data. *Bioinformatics*, **2018**, 34, 2851-2853	7.2	12
171	Applying family analyses to electronic health records to facilitate genetic research. *Bioinformatics*, **2018**, 34, 635-642	7.2	5
170	How Consistent are Genetic Factors in Explaining Leisure-Time Physical Activity and Sport Participation? The Portuguese Healthy Families Study. *Twin Research and Human Genetics*, **2018**, 21, 369-377	2.2	2
169	Fisher's influence on me. *Genetic Epidemiology*, **2018**, 42, 849-853	2.6	4
168	Adjustment for covariates using summary statistics of genome-wide association studies. *Genetic Epidemiology*, **2018**, 42, 812-825	2.6	3
167	Statistical interactions and Bayes estimation of log odds in case-control studies. *Statistical Methods in Medical Research*, **2017**, 26, 1021-1038	2.3	3
166	Genomic regions associated with susceptibility to Barrett's esophagus and esophageal adenocarcinoma in African Americans: The cross BETRNet admixture study. *PLoS ONE*, **2017**, 12, e0184962	3.7	5
165	On the association analysis of CNV data: a fast and robust family-based association method. *BMC Bioinformatics*, **2017**, 18, 217	3.6	1
164	Predicting Barrett's Esophagus in Families: An Esophagus Translational Research Network (BETRNet) Model Fitting Clinical Data to a Familial Paradigm. *Cancer Epidemiology Biomarkers and Prevention*, **2016**, 25, 727-35	4	9
163	Joint modeling of longitudinal data and discrete-time survival outcome. *Statistical Methods in Medical Research*, **2016**, 25, 1512-26	2.3	7
162	A Germline Variant on Chromosome 4q31.1 Associates with Susceptibility to Developing Colon Cancer Metastasis. *PLoS ONE*, **2016**, 11, e0146435	3.7	1
161	A weighted U statistic for association analyses considering genetic heterogeneity. *Statistics in Medicine*, **2016**, 35, 2802-14	2.3	6
160	Family-Based Rare Variant Association Analysis: A Fast and Efficient Method of Multivariate Phenotype Association Analysis. *Genetic Epidemiology*, **2016**, 40, 502-11	2.6	7
159	Association Between Germline Mutation in VSIG10L and Familial Barrett Neoplasia. *JAMA Oncology*, **2016**, 2, 1333-1339	13.4	14
158	Linkage and related analyses of Barrett's esophagus and its associated adenocarcinomas. *Molecular Genetics & Genomic Medicine*, **2016**, 4, 407-19	2.3	4

157	Reply to Ashktorab et al.: Mutational landscape of colon cancers in African Americans. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, E2853	11.5	1
156	Novel approaches to the analysis of family data in genetic epidemiology. *Frontiers in Genetics*, **2015**, 6, 27	4.5	5
155	Putative linkage signals identified for breast cancer in African American families. *Cancer Epidemiology Biomarkers and Prevention*, **2015**, 24, 442-7	4	2
154	Genome-Wide Association and Trans-ethnic Meta-Analysis for Advanced Diabetic Kidney Disease: Family Investigation of Nephropathy and Diabetes (FIND). *PLoS Genetics*, **2015**, 11, e1005352	6	84
153	On the Estimation of Heritability with Family-Based and Population-Based Samples. *BioMed Research International*, **2015**, 2015, 671349	3	10
152	Novel recurrently mutated genes in African American colon cancers. *Proceedings of the National Academy of Sciences of the United States of America*, **2015**, 112, 1149-54	11.5	77
151	On the analysis of a repeated measure design in genome-wide association analysis. *International Journal of Environmental Research and Public Health*, **2014**, 11, 12283-303	4.6	5
150	Analysis pipeline for the epistasis search - statistical versus biological filtering. *Frontiers in Genetics*, **2014**, 5, 106	4.5	47
149	The association of the vanin-1 N131S variant with blood pressure is mediated by endoplasmic reticulum-associated degradation and loss of function. *PLoS Genetics*, **2014**, 10, e1004641	6	14
148	What is the significance of difference in phenotypic variability across SNP genotypes?. *American Journal of Human Genetics*, **2013**, 93, 390-7	11	29
147	Evaluation of removable statistical interaction for binary traits. *Statistics in Medicine*, **2013**, 32, 1164-90	2.3	16
146	A genome-wide search for linkage of estimated glomerular filtration rate (eGFR) in the Family Investigation of Nephropathy and Diabetes (FIND). *PLoS ONE*, **2013**, 8, e81888	3.7	23
145	Linkage-disequilibrium-based binning misleads the interpretation of genome-wide association studies. *American Journal of Human Genetics*, **2012**, 91, 965-8; author reply 969-70	11	1
144	Power of single- vs. multi-marker tests of association. *Genetic Epidemiology*, **2012**, 36, 480-7	2.6	11
143	A likelihood ratio-based Mann-Whitney approach finds novel replicable joint gene action for type 2 diabetes. *Genetic Epidemiology*, **2012**, 36, 583-93	2.6	15
142	Genetic terminology. *Methods in Molecular Biology*, **2012**, 850, 1-9	1.4	11
141	Statistical interaction in human genetics: how should we model it if we are looking for biological interaction?. *Nature Reviews Genetics*, **2011**, 12, 74	30.1	34
140	2010 William Allan Award introduction: J□g Ott. *American Journal of Human Genetics*, **2011**, 88, 262-3	11	1

139	Two-marker association tests yield new disease associations for coronary artery disease and hypertension. *Human Genetics*, **2011**, 130, 725-33	6.3	67
138	Interrogating population structure and its impact on association tests. *BMC Proceedings*, **2011**, 5 Suppl 9, S25	2.3	3
137	Testing gene-environment interactions in gene-based association studies. *BMC Proceedings*, **2011**, 5 Suppl 9, S26	2.3	3
136	Detecting genetic interactions for quantitative traits with U-statistics. *Genetic Epidemiology*, **2011**, 35, 457-68	2.6	18
135	A non-parametric method for building predictive genetic tests on high-dimensional data. *Human Heredity*, **2011**, 71, 161-70	1.1	11
134	A Note on Comparing the Power of Test Statistics at Low Significance Levels. *American Statistician*, **2011**, 65,	5	8
133	Using the optimal robust receiver operating characteristic (ROC) curve for predictive genetic tests. *Biometrics*, **2010**, 66, 586-93	1.8	12
132	Examination of association with candidate genes for diabetic nephropathy in a Mexican American population. *Clinical Journal of the American Society of Nephrology: CJASN*, **2010**, 5, 1072-8	6.9	23
131	Bagging optimal ROC curve method for predictive genetic tests, with an application for rheumatoid arthritis. *Journal of Biopharmaceutical Statistics*, **2010**, 20, 401-14	1.3	4
130	The meaning of interaction. *Human Heredity*, **2010**, 70, 269-77	1.1	100
129	Single-marker and two-marker association tests for unphased case-control genotype data, with a power comparison. *Genetic Epidemiology*, **2010**, 34, 67-77	2.6	16
128	The effect of multiple genetic variants in predicting the risk of type 2 diabetes. *BMC Proceedings*, **2009**, 3 Suppl 7, S49	2.3	12
127	Phase uncertainty in case-control association studies. *Genetic Epidemiology*, **2009**, 33, 463-78	2.6	2
126	Choosing an optimal method to combine P-values. *Statistics in Medicine*, **2009**, 28, 1537-53	2.3	90
125	Heritability of the severity of diabetic retinopathy: the FIND-Eye study **2008**, 49, 3839-45		133
124	The power of independent types of genetic information to detect association in a case-control study design. *Genetic Epidemiology*, **2008**, 32, 731-56	2.6	14
123	A unified association analysis approach for family and unrelated samples correcting for stratification. *American Journal of Human Genetics*, **2008**, 82, 352-65	11	109
122	Using the optimal receiver operating characteristic curve to design a predictive genetic test, exemplified with type 2 diabetes. *American Journal of Human Genetics*, **2008**, 82, 641-51	11	49

121	Multistage sampling for genetic studies. *Annual Review of Genomics and Human Genetics*, **2007**, 8, 327-42	9.7	21
120	Log-linear model-based multifactor dimensionality reduction method to detect gene gene interactions. *Bioinformatics*, **2007**, 23, 2589-95	7.2	72
119	Adaptive two-stage analysis of genetic association in case-control designs. *Human Heredity*, **2007**, 63, 175-86	1.1	24
118	Improving power in contrasting linkage-disequilibrium patterns between cases and controls. *American Journal of Human Genetics*, **2007**, 80, 911-20	11	36
117	Genome scan for loci predisposing to anxiety disorders using a novel multivariate approach: strong evidence for a chromosome 4 risk locus. *American Journal of Human Genetics*, **2006**, 78, 543-53	11	71
116	A powerful method of combining measures of association and Hardy-Weinberg disequilibrium for fine-mapping in case-control studies. *Statistics in Medicine*, **2006**, 25, 105-26	2.3	86
115	Advances in statistical human genetics over the last 25 years. *Statistics in Medicine*, **2006**, 25, 3049-80	2.3	22
114	Mathematical assumptions versus biological reality: myths in affected sib pair linkage analysis. *American Journal of Human Genetics*, **2005**, 76, 152-6	11	33
113	Response to letter by Veronica J. Vieland and Susan E. Hodge. *Genetic Epidemiology*, **2005**, 28, 286-287	2.6	1
112	Two-level Haseman-Elston regression for general pedigree data analysis. *Genetic Epidemiology*, **2005**, 29, 12-22	2.6	42
111	Likelihood Modelling: Genetic Mapping of Complex Traits **2005**, 339-359		
110	A review of the 'Statistical Analysis for Genetic Epidemiology' (S.A.G.E.) software package. *Human Genomics*, **2004**, 1, 456-9	6.8	33
109	A modified revisited Haseman-Elston method to further improve power. *Human Heredity*, **2004**, 57, 109-16	1.1	22
108	Linkage analysis of a complex disease through use of admixed populations. *American Journal of Human Genetics*, **2004**, 74, 1136-53	11	67
107	Regression models for linkage: issues of traits, covariates, heterogeneity, and interaction. *Human Heredity*, **2003**, 55, 86-96	1.1	38
106	Adding further power to the Haseman and Elston method for detecting linkage in larger sibships: weighting sums and differences. *Human Heredity*, **2003**, 55, 79-85	1.1	84
105	New multivariate test for linkage, with application to pleiotropy: fuzzy Haseman-Elston. *Genetic Epidemiology*, **2003**, 24, 253-64	2.6	11
104	Segregation Analysis of Gastric Cancer in a Japanese Population. *International Journal of Human Genetics*, **2001**, 1, 263-270	1	2

103	Introduction: Linkage Analyses of Single Regions. *Genetic Epidemiology*, **2001**, 21, S79-S80	2.6	
102	Segregation analysis of asthma and respiratory allergy in population-based samples of families. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S30-5	2.6	1
101	Impact of preadjusting a quantitative phenotype prior to sib-pair linkage analysis when gene x environment interaction exists. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S837-42	2.6	
100	Pooling data and linkage analysis in the chromosome 5q candidate region for asthma. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S103-8	2.6	8
99	Localization of the Q1 mutation by cladistic analysis. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S594-9	2.6	2
98	Linkage disequilibrium mapping of complex genetic diseases using multiallelic markers. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S576-81	2.6	1
97	Locating the genes underlying a simulated complex disease by discriminant analysis. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S516-21	2.6	10
96	Comparison of marker intervals and number of sib pairs used for linkage analysis on simulated nuclear family data. *Genetic Epidemiology*, **2001**, 21 Suppl 1, S748-53	2.6	1
95	Electrocardiographic prediction of abnormal genotype in congenital long QT syndrome: experience in 101 related family members. *Journal of Cardiovascular Electrophysiology*, **2001**, 12, 455-61	2.7	74
94	Segregation analyses of asthma and respiratory allergy: the Humboldt family study. *American Journal of Medical Genetics Part A*, **2001**, 104, 23-30		4
93	Transmission/disequilibrium tests for quantitative traits. *Genetic Epidemiology*, **2001**, 20, 57-74	2.6	29
92	A PROBLEM IN ASCERTAINMENT. *Communications in Statistics - Theory and Methods*, **2001**, 30, 1615-1631	0.5	
91	The Genetic Epidemiology of Age-Related Maculopathy. *International Journal of Human Genetics*, **2001**, 1, 11-24	1	2
90	On the relative sample size required for multiple comparisons. *Statistics in Medicine*, **2000**, 19, 369-72	2.3	36
89	Major gene segregation of actinic prurigo among North American Indians in Saskatchewan. *American Journal of Medical Genetics Part A*, **2000**, 92, 212-219		9
88	Two-stage global search designs for linkage analysis II: including discordant relative pairs in the study. *Genetic Epidemiology*, **2000**, 18, 111-27	2.6	18
87	Two-stage global search designs for linkage analysis I: use of the mean statistic for affected sib pairs. *Genetic Epidemiology*, **2000**, 18, 97-110	2.6	16
86	Haseman and Elston revisited. *Genetic Epidemiology*, **2000**, 19, 1-17	2.6	275

85	Model-free sib-pair linkage analysis: combining full-sib and half-sib pairs. *Genetic Epidemiology*, **2000**, 19, 30-51	2.6	5
84	Haseman and Elston revisited: the effects of ascertainment and residual familial correlations on power to detect linkage. *Genetic Epidemiology*, **2000**, 19, 456-60	2.6	27
83	Multipoint admixture mapping. *Genetic Epidemiology*, **2000**, 19, 464-7	2.6	11
82	Adding power to Haseman and Elston (1972) method. *GeneScreen*, **2000**, 1, 63-64		5
81	Genetic determinants of acute hypoxic ventilation: patterns of inheritance in mice. *Journal of Applied Physiology*, **2000**, 88, 2310-8	3.7	47
80	Major gene segregation of actinic prurigo among North American Indians in Saskatchewan **2000**, 92, 212		1
79	Linkage of chromosome 1 markers to alcoholism-related phenotypes by sib pair linkage analysis of principal components. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S271-6	2.6	10
78	Multipoint linkage disequilibrium mapping with particular reference to the African-American population. *Genetic Epidemiology*, **1999**, 17, 79-101	2.6	33
77	Fieller's theorem and linkage disequilibrium mapping. *Genetic Epidemiology*, **1999**, 17, 237-52	2.6	16
76	The study of candidate genes in drug trials: sample size considerations. *Statistics in Medicine*, **1999**, 18, 741-51	2.3	29
75	Genetic mapping of complex traits. *Statistics in Medicine*, **1999**, 18, 2961-81	2.3	24
74	Model-based and model-free multipoint genome-wide linkage analysis of alcoholism. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S175-80	2.6	1
73	Association and linkage analysis of ICD-10 diagnosis for alcoholism. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S343-7	2.6	3
72	Improving the power for disease locus detection in affected-sib-pair studies by using two-locus analysis and multiple regression methods. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S521-6	2.6	2
71	Linkage and association analyses of alcoholism using a regression-based transmission/disequilibrium test. *Genetic Epidemiology*, **1999**, 17 Suppl 1, S157-61	2.6	7
70	Authors' reply: Confidence limits based on the first occurrence of an event. V.T. George and R.C. Elton. Statistics in Medicine, 12, 685690 (1993). *Statistics in Medicine*, **1998**, 17, 945-945	2.3	
69	A multivariate logistic model (MLM) for analyzing binary family data. *American Journal of Medical Genetics Part A*, **1998**, 76, 428-37		24
68	Using family history information to distinguish true and false positive model-free linkage results. *Genetic Epidemiology*, **1998**, 15, 183-92	2.6	2

67	Analysis of Swedish male breast cancer family data: a simple way to incorporate a common sibling effect. *Genetic Epidemiology*, **1998**, 15, 201-12	2.6	5
66	Linkage and association. *Genetic Epidemiology*, **1998**, 15, 565-76	2.6	59
65	Restrictions on components of variance for epistatic models. *Theoretical Population Biology*, **1998**, 54, 161-74	1.2	17
64	A faster and more general hidden Markov model algorithm for multipoint likelihood calculations. *Human Heredity*, **1997**, 47, 197-202	1.1	47
63	Alternative test for linkage between two loci. *Genetic Epidemiology*, **1997**, 14, 117-31	2.6	8
62	Deriving components of genetic variance for multilocus models. *Genetic Epidemiology*, **1997**, 14, 1131-6	2.6	18
61	Modeling age of onset and residual familial correlations for the linkage analysis of bipolar disorder. *Genetic Epidemiology*, **1997**, 14, 675-80	2.6	4
60	Model-free age-of-onset methods applied to the linkage of bipolar disorder. *Genetic Epidemiology*, **1997**, 14, 711-6	2.6	9
59	False discoveries in genome scanning. *Genetic Epidemiology*, **1997**, 14, 779-84	2.6	15
58	False discoveries in genome scanning **1997**, 14, 779		1
57	Association within twin pairs for a dichotomous trait. *Genetic Epidemiology*, **1996**, 13, 489-99	2.6	12
56	Genetic dissection of complex traits. *Nature Genetics*, **1996**, 12, 355-6; author reply 357-8	36.3	95
55	An autosomal screen for genes that predispose to celiac disease in the western counties of Ireland. *Nature Genetics*, **1996**, 14, 329-33	36.3	153
54	Statistical validity for testing associations between genetic markers and quantitative traits in family data. *Genetic Epidemiology*, **1995**, 12, 145-61	2.6	5
53	Model-free association analysis of a rare disease. *Genetic Epidemiology*, **1995**, 12, 571-5	2.6	7
52	Effects of marker information on sib-pair linkage analysis of a rare disease. *Genetic Epidemiology*, **1995**, 12, 625-30	2.6	2
51	Testing specific hypotheses by fitting underlying distributions to categorical data. *Journal of Biopharmaceutical Statistics*, **1994**, 4, 53-64	1.3	2
50	Combining two-point genetic linkage analyses using mapping functions. *Genetic Epidemiology*, **1994**, 11, 1-17	2.6	3

49	Lods, wrods, and mods: the interpretation of lod scores calculated under different models. *Genetic Epidemiology*, **1994**, 11, 329-42	2.6	107
48	Potential role of an additive genetic component in the cause of amyotrophic lateral sclerosis and parkinsonism-dementia in the western Pacific. *American Journal of Medical Genetics Part A*, **1993**, 45, 68-76		38
47	The HGAR1 familial hypercholesterolemia pedigree. *Genetic Epidemiology*, **1993**, 10, 529-31	2.6	5
46	Statistical validity of the Haseman-Elston sib-pair test in small samples. *Genetic Epidemiology*, **1993**, 10, 593-8	2.6	42
45	Confidence limits based on the first occurrence of an event. *Statistics in Medicine*, **1993**, 12, 685-90	2.3	15
44	The Elston-Stewart algorithm for continuous genotypes and environmental factors. *Human Heredity*, **1992**, 42, 16-27	1.1	48
43	Regression toward the mean in 2 x 2 crossover designs with baseline measurements. *Statistics in Medicine*, **1992**, 11, 727-41	2.3	10
42	Effect of cohort differences in smoking prevalence on models of lung cancer susceptibility. *Genetic Epidemiology*, **1992**, 9, 261-71	2.6	29
41	Lung cancer histologic type and family history of cancer. *Cancer*, **1992**, 69, 86-91	6.4	43
40	Evidence for a dominant gene mechanism underlying coeliac disease in the west of Ireland. *Genetic Epidemiology*, **1991**, 8, 13-27	2.6	14
39	Extensions to sib-pair linkage tests applicable to disorders characterized by delayed onset. *Genetic Epidemiology*, **1990**, 7, 453-66	2.6	22
38	Generalized modulus power transformations. *Communications in Statistics - Theory and Methods*, **1988**, 17, 2933-2952	0.5	34
37	Pedigree discriminant analysis of two French Canadian Tay-Sachs families. *Genetic Epidemiology*, **1987**, 4, 77-85	2.6	1
36	Genetic etiology of gastric carcinoma: II. Segregation analysis of gastric pH, nitrate, and nitrite. *Genetic Epidemiology*, **1987**, 4, 103-14	2.6	6
35	Testing the association between polymorphic markers and quantitative traits in pedigrees. *Genetic Epidemiology*, **1987**, 4, 193-201	2.6	104
34	Association between polymorphic blood markers and risk factors for cardiovascular disease in a large pedigree. *Genetic Epidemiology*, **1987**, 4, 267-75	2.6	19
33	Segregation and linkage analyses of dopamine-beta-hydroxylase activity in a six-generation pedigree. *American Journal of Medical Genetics Part A*, **1987**, 27, 613-21		19
32	A major gene model for the familial aggregation of plasma IgA concentration. *American Journal of Medical Genetics Part A*, **1987**, 27, 857-66		6

31	Segregation analysis of hereditary nonpolyposis colorectal cancer. *Genetic Epidemiology*, **1986**, 3, 27-38	2.6	52
30	Genetic etiology of gastric carcinoma: I. Chronic atrophic gastritis. *Genetic Epidemiology*, **1986**, 3, 213-24	2.6	42
29	Description of a large pedigree with an adverse lipoprotein cholesterol phenotype: the Bogalusa Heart Study. *Genetic Epidemiology*, **1986**, 3, 241-53	2.6	10
28	Determination of the order of loci on the short arm of chromosome 11 using two and three locus linkage analyses of pedigree and sib pair data. *Genetic Epidemiology*, **1986**, 1, 147-52	2.6	20
27	Likelihood Models for Multivariate Traits in Human Genetics1. *Biometrical Journal*, **1985**, 27, 553-563	1.5	2
26	A comparison of sib-pair linkage tests for disease susceptibility loci. *Genetic Epidemiology*, **1985**, 2, 85-97	2.6	305
25	A multivariate analysis of familial associations of lipoprotein levels in the Lipid Research Clinics Collaborative Family Study: I. Familial correlation and regression analyses. *Genetic Epidemiology*, **1985**, 2, 283-300	2.6	4
24	A method to assess the environment for genetic studies: the Common Environment Index and the Household Relationships Interview. *American Journal of Medical Genetics Part A*, **1985**, 21, 325-35		2
23	Hereditary nonpolyposis colorectal cancer (Lynch syndromes I and II). I. Clinical description of resource. *Cancer*, **1985**, 56, 934-8	6.4	232
22	Hereditary nonpolyposis colorectal cancer (Lynch syndromes I and II). II. Biomarker studies. *Cancer*, **1985**, 56, 939-51	6.4	139
21	Cellular genes in the mouse regulate in trans the expression of endogenous mouse mammary tumor viruses. *Genetics*, **1985**, 111, 597-615	4	18
20	A bivariate problem in human genetics: ascertainment of families through a correlated trait. *American Journal of Medical Genetics Part A*, **1984**, 18, 435-48		13
19	Inheritance of adrenal phenylethanolamine N-methyltransferase activity in the rat. *Genetics*, **1984**, 108, 633-49	4	6
18	Power and robustness of sib-pair linkage tests and extension to larger sibships. *Communications in Statistics - Theory and Methods*, **1982**, 11, 449-484	0.5	72
17	Genetic analysis of von Willebrand's disease in two large pedigrees: a multivariate approach. *American Journal of Medical Genetics Part A*, **1980**, 6, 279-93		25
16	Confidence bands for the growth of head circumference in achondroplastic children during the first year of life. *American Journal of Medical Genetics Part A*, **1980**, 7, 529-36		15
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