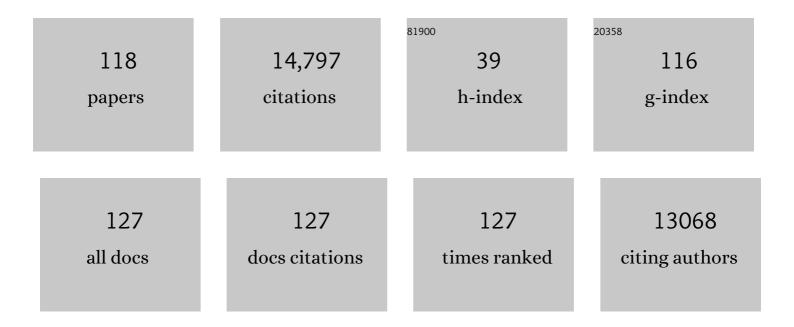
## Glen A Satten

List of Publications by Year in descending order

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#	Article	IF	CITATIONS
1	Declining Morbidity and Mortality among Patients with Advanced Human Immunodeficiency Virus Infection. New England Journal of Medicine, 1998, 338, 853-860.	27.0	8,991
2	Estimated Risk of Transmission of the Human Immunodeficiency Virus by Screened Blood in the United States. New England Journal of Medicine, 1995, 333, 1721-1725.	27.0	334
3	Age-associated DNA methylation in pediatric populations. Genome Research, 2012, 22, 623-632.	5.5	326
4	Inference on Haplotype Effects in Case-Control Studies Using Unphased Genotype Data. American Journal of Human Genetics, 2003, 73, 1316-1329.	6.2	235
5	Accounting for Unmeasured Population Substructure in Case-Control Studies of Genetic Association Using a Novel Latent-Class Model. American Journal of Human Genetics, 2001, 68, 466-477.	6.2	231
6	Microdeletions of 3q29 Confer High Risk for Schizophrenia. American Journal of Human Genetics, 2010, 87, 229-236.	6.2	215
7	Dysbiosis, inflammation, and response to treatment: a longitudinal study of pediatric subjects with newly diagnosed inflammatory bowel disease. Genome Medicine, 2016, 8, 75.	8.2	211
8	Time course of viremia and antibody seroconversion following human immunodeficiency virus exposure. American Journal of Medicine, 1997, 102, 117-124.	1.5	202
9	Marginal Analyses of Clustered Data When Cluster Size Is Informative. Biometrics, 2003, 59, 36-42.	1.4	187
10	Late postnatal mother-to-child transmission of HIV-1 in Abidjan, Côte d'Ivoire. Lancet, The, 1997, 349, 1054-1059.	13.7	158
11	Rank-Sum Tests for Clustered Data. Journal of the American Statistical Association, 2005, 100, 908-915.	3.1	158
12	A Simple and Improved Correction for Population Stratification in Case-Control Studies. American Journal of Human Genetics, 2007, 80, 921-930.	6.2	150
13	Performance Characteristics of a New Less Sensitive HIV-1 Enzyme Immunoassay for Use in Estimating HIV Seroincidence. Journal of Acquired Immune Deficiency Syndromes (1999), 2003, 33, 625-634.	2.1	142
14	Validity of the Aalen–Johansen estimators of stage occupation probabilities and Nelson–Aalen estimators of integrated transition hazards for non-Markov models. Statistics and Probability Letters, 2001, 55, 403-411.	0.7	134
15	The Kaplan–Meier Estimator as an Inverse-Probability-of-Censoring Weighted Average. American Statistician, 2001, 55, 207-210.	1.6	123
16	HIV Infection among Patients in U.S. Acute Care Hospitals. New England Journal of Medicine, 1992, 327, 445-452.	27.0	110
17	Effect of interventions to control sexually transmitted disease on the incidence of HIV infection in female sex workers. Aids, 2001, 15, 1421-1431.	2.2	104
18	Markov Chains With Measurement Error: Estimating the `True' Course of a Marker of the Progression of Human Immunodeficiency Virus Disease. Journal of the Royal Statistical Society Series C: Applied Statistics, 1996, 45, 275.	1.0	98

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19	Subtype-specific Transmission Probabilities for Human Immunodeficiency Virus Type 1 among Injecting Drug Users in Bangkok, Thailand. American Journal of Epidemiology, 2002, 155, 159-168.	3.4	87
20	Comparison of prospective and retrospective methods for haplotype inference in case-control studies. Genetic Epidemiology, 2004, 27, 192-201.	1.3	82
21	Nonparametric Maximum Likelihood Estimation for Competing Risks Survival Data Subject to Interval Censoring and Truncation. Biometrics, 2001, 57, 74-80.	1.4	81
22	Investigating Childhood Leukemia in Churchill County, Nevada. Environmental Health Perspectives, 2007, 115, 151-157.	6.0	81
23	Standardization and denoising algorithms for mass spectra to classify whole-organism bacterial specimens. Bioinformatics, 2004, 20, 3128-3136.	4.1	75
24	MALDI-TOF mass spectrometry as a tool for differentiation of invasive and noninvasive <i>Streptococcus pyogenes</i> isolates. FEMS Immunology and Medical Microbiology, 2008, 53, 333-342.	2.7	75
25	A Signedâ€Rank Test for Clustered Data. Biometrics, 2008, 64, 501-507.	1.4	73
26	Testing hypotheses about the microbiome using the linear decomposition model (LDM). Bioinformatics, 2020, 36, 4106-4115.	4.1	73
27	Genetic Association Analysis Using Data from Triads and Unrelated Subjects. American Journal of Human Genetics, 2005, 76, 592-608.	6.2	69
28	Informative Missingness in Genetic Association Studies: Case-Parent Designs. American Journal of Human Genetics, 2003, 72, 671-680.	6.2	67
29	Changes in vaginal community state types reflect major shifts in the microbiome. Microbial Ecology in Health and Disease, 2017, 28, 1303265.	3.5	66
30	Estimation of Integrated Transition Hazards and Stage Occupation Probabilities for Non-Markov Systems Under Dependent Censoring. Biometrics, 2002, 58, 792-802.	1.4	63
31	A Permutation Procedure to Correct for Confounders in Case-Control Studies, Including Tests of Rare Variation. American Journal of Human Genetics, 2012, 91, 215-223.	6.2	62
32	Inferences About Exposure-Disease Associations Using Probability-of-Exposure Information. Journal of the American Statistical Association, 1993, 88, 200-208.	3.1	61
33	Estimating the marginal survival function in the presence of time dependent covariates. Statistics and Probability Letters, 2001, 54, 397-403.	0.7	58
34	Inference Based on Imputed Failure Times for the Proportional Hazards Model with Interval-Censored Data. Journal of the American Statistical Association, 1998, 93, 318-327.	3.1	57
35	Evaluation of a Sensitive/Less-Sensitive Testing Algorithm Using the 3A11-LS Assay for Detecting Recent HIV Seroconversion among Individuals with HIV-1 Subtype B or E Infection in Thailand. AIDS Research and Human Retroviruses, 2001, 17, 453-458.	1.1	57
36	Characterization of Bacterial Communities in Selected Smokeless Tobacco Products Using 16S rDNA Analysis. PLoS ONE, 2016, 11, e0146939.	2.5	55

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37	Late Preterm Birth and Risk of Developing Asthma. Journal of Pediatrics, 2010, 157, 74-78.	1.8	52
38	Genetic Studies of a Cluster of Acute Lymphoblastic Leukemia Cases in Churchill County, Nevada. Environmental Health Perspectives, 2007, 115, 158-164.	6.0	51
39	Modification of nonequilibrium fluctuations by interaction with surfaces. Physical Review A, 1982, 26, 940-949.	2.5	46
40	Inferences About Exposure-Disease Associations Using Probability-of- Exposure Information. Journal of the American Statistical Association, 1993, 88, 200.	3.1	41
41	Vaginal Microbiome Composition in Early Pregnancy and Risk of Spontaneous Preterm and Early Term Birth Among African American Women. Frontiers in Cellular and Infection Microbiology, 2021, 11, 641005.	3.9	41
42	Inverse Probability of Censoring Weighted U-statistics for Right-Censored Data with an Application to Testing Hypotheses. Scandinavian Journal of Statistics, 2010, 37, 680-700.	1.4	40
43	Modelling the female-to-male per-act HIV transmission probability in an emerging epidemic in Asia. Statistics in Medicine, 1994, 13, 2097-2106.	1.6	39
44	HIV Seroincidence Among Patients at Clinics for Sexually Transmitted Diseases in Nine Cities in the United States. Journal of Acquired Immune Deficiency Syndromes (1999), 2002, 29, 478-483.	2.1	37
45	The incubation period to AIDS in injecting drug users estimated from prevalent cohort data, accounting for death prior to an AIDS diagnosis. Aids, 1998, 12, 1537-1544.	2.2	36
46	Conditional and Unconditional Categorical Regression Models with Missing Covariates. Biometrics, 2000, 56, 384-388.	1.4	34
47	Use of immunological markers and continuous-time Markov models to estimate progression of HIV infection in homosexual men. Aids, 1996, 10, 649-656.	2.2	33
48	Fitting Semi-Markov Models to Interval-Censored Data with Unknown Initiation Times. Biometrics, 1999, 55, 507-513.	1.4	32
49	Stability of the vaginal, oral, and gut microbiota across pregnancy among African American women: the effect of socioeconomic status and antibiotic exposure. PeerJ, 2019, 7, e8004.	2.0	31
50	Discrete-Time Nonparametric Estimation for Semi-Markov Models of Chain-of-Events Data Subject to Interval Censoring and Truncation. Biometrics, 1999, 55, 514-522.	1.4	30
51	Marginal estimation for multi-stage models: waiting time distributions and competing risks analyses. Statistics in Medicine, 2002, 21, 3-19.	1.6	30
52	Heavy metals, organic solvents, and multiple sclerosis: An exploratory look at gene-environment interactions. Archives of Environmental and Occupational Health, 2016, 71, 26-34.	1.4	30
53	A novel haplotypeâ€sharing approach for genomeâ€wide caseâ€control association studies implicates the calpastatin gene in Parkinson's disease. Genetic Epidemiology, 2009, 33, 657-667.	1.3	29
54	Estimating the Extent of Tracking in Interval-Censored Chain-Of-Events Data. Biometrics, 1999, 55, 1228-1231.	1.4	27

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55	Nonparametric Estimation for the Three-Stage Irreversible Illness-Death Model. Biometrics, 2000, 56, 841-847.	1.4	27
56	Maternal smokeless tobacco use in Alaska Native women and singleton infant birth size. Acta Obstetricia Et Gynecologica Scandinavica, 2012, 91, 93-103.	2.8	27
57	Estimation of Incidence of HIV Infection Using Cross-Sectional Marker Surveys. Biometrics, 1994, 50, 675.	1.4	26
58	Testing Rare-Variant Association without Calling Genotypes Allows for Systematic Differences in Sequencing between Cases and Controls. PLoS Genetics, 2016, 12, e1006040.	3.5	26
59	Critical phenomena in randomly stirred fluids: Correlation functions, equation of motion, and crossover behavior. Physical Review A, 1986, 33, 3415-3432.	2.5	24
60	HIV seroconverting donors delay their return: screening test implications. Transfusion, 2002, 42, 414-421.	1.6	24
61	Locally-efficient robust estimation of haplotype-disease association in family-based studies. Biometrika, 2005, 92, 559-571.	2.4	21
62	Inference on haplotype/disease association using parentâ€affectedâ€child data: the projection conditional on parental haplotypes method. Genetic Epidemiology, 2007, 31, 211-223.	1.3	21
63	Control for Confounding in Case-Control Studies Using the Stratification Score, a Retrospective Balancing Score. American Journal of Epidemiology, 2011, 173, 752-760.	3.4	21
64	Stratificationâ€Score Matching Improves Correction for Confounding by Population Stratification in Caseâ€Control Association Studies. Genetic Epidemiology, 2012, 36, 195-205.	1.3	21
65	A Statistical Approach for Rare-Variant Association Testing in Affected Sibships. American Journal of Human Genetics, 2015, 96, 543-554.	6.2	21
66	PhredEM: a phred-score-informed genotype-calling approach for next-generation sequencing studies. Genetic Epidemiology, 2017, 41, 375-387.	1.3	21
67	Estimating future stage entry and occupation probabilities in a multistage model based on randomly right-censored data. Statistics and Probability Letters, 2000, 50, 89-95.	0.7	20
68	SAMPLE SIZE REQUIREMENTS FOR INTERVAL ESTIMATION OF THIS ODDS RATIO. American Journal of Epidemiology, 1990, 131, 177-184.	3.4	19
69	Sample size determination for pair-matched case-control studies where the goal is interval estimation of the odds ratio. Journal of Clinical Epidemiology, 1990, 43, 55-59.	5.0	19
70	HFE genotype and transferrin saturation in the United States. Genetics in Medicine, 2003, 5, 304-310.	2.4	19
71	Statistical Models for Haplotype Sharing in Case-Parent Trio Data. Human Heredity, 2007, 64, 35-44.	0.8	19
72	A rarefaction-based extension of the LDM for testing presence–absence associations in the microbiome. Bioinformatics, 2021, 37, 1652-1657.	4.1	18

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73	Analysis of Dynamic Cohort Data. American Journal of Epidemiology, 2001, 154, 366-372.	3.4	17
74	Kaplan–Meier representation of competing risk estimates. Statistics and Probability Letters, 1999, 42, 299-304.	0.7	15
75	California Very Preterm Birth Study: design and characteristics of the population―and biospecimen bankâ€based nested case–control study. Paediatric and Perinatal Epidemiology, 2012, 26, 250-263.	1.7	15
76	Effects of maternal smokeless tobacco use on selected pregnancy outcomes in Alaska Native women: a case-control study. Acta Obstetricia Et Gynecologica Scandinavica, 2013, 92, 648-655.	2.8	15
77	Utilizing Population Controls in Rare-Variant Case-Parent Association Tests. American Journal of Human Genetics, 2014, 94, 845-853.	6.2	15
78	Impact of the 5As brief counseling on smoking cessation among pregnant clients of Special Supplemental Nutrition Program for Women, Infants, and Children (WIC) clinics in Ohio. Preventive Medicine, 2015, 81, 438-443.	3.4	14
79	Steady-state calculation of the risk of HIV infection from transfusion of screened blood from repeat donors. Mathematical Biosciences, 1997, 141, 101-113.	1.9	13
80	Validating Marker-Based Incidence Estimates in Repeatedly Screened Populations. Biometrics, 1999, 55, 1224-1227.	1.4	13
81	Random error and undercounting in birth defects surveillance data: Implications for inference. Birth Defects Research Part A: Clinical and Molecular Teratology, 2003, 67, 610-616.	1.6	13
82	Upper and Lower Bound Distributions That Give Simultaneous Confidence Intervals for Quantiles. Journal of the American Statistical Association, 1995, 90, 747-752.	3.1	12
83	Effect of population stratification on the identification of significant single-nucleotide polymorphisms in genome-wide association studies. BMC Proceedings, 2009, 3, S13.	1.6	12
84	Restoring the Duality between Principal Components of a Distance Matrix and Linear Combinations of Predictors, with Application to Studies of the Microbiome. PLoS ONE, 2017, 12, e0168131.	2.5	12
85	Inference Based on Imputed Failure Times for the Proportional Hazards Model with Interval-Censored Data. Journal of the American Statistical Association, 1998, 93, 318.	3.1	12
86	Consistency and Asymptotic Normality of Estimators in a Proportional Hazards Model with Interval Censoring and Left Truncation. Annals of the Institute of Statistical Mathematics, 2000, 52, 160-172.	0.8	11
87	Midrank unification of rank tests for exact, tied, and censored data. Journal of Nonparametric Statistics, 2002, 14, 569-581.	0.9	11
88	The S-U algorithm for missing data problems. Computational Statistics, 2000, 15, 243-277.	1.5	10
89	Conditional Regression Analysis of the Exposure-Disease Odds Ratio Using Known Probability-of-Exposure Values. Biometrics, 1993, 49, 429.	1.4	9
90	Genome-wide association analysis of rheumatoid arthritis data via haplotype sharing. BMC Proceedings, 2009, 3, S30.	1.6	9

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91	The Effect of Antiretroviral Therapy for the Treatment of Human Immunodeficiency Virus (HIV)-1 in Pregnancy on Gestational Weight Gain. Clinical Infectious Diseases, 2022, 75, 665-672.	5.8	9
92	Robust estimation and testing of haplotype effects in case ontrol studies. Genetic Epidemiology, 2008, 32, 29-40.	1.3	8
93	Multisample adjusted Uâ€statistics that account for confounding covariates. Statistics in Medicine, 2018, 37, 3357-3372.	1.6	8
94	Fluctuations in finite systems: Time reversal symmetry, surface onsager reciprocal relations and fluctuating hydrodynamics. Physica A: Statistical Mechanics and Its Applications, 1984, 125, 281-301.	2.6	7
95	Bootstrap calibration of TRANSMIT for informative missingness of parental genotype data. BMC Genetics, 2003, 4, S39.	2.7	7
96	Scoreâ€based adjustment for confounding by population stratification in genetic association studies. Genetic Epidemiology, 2010, 34, 383-385.	1.3	7
97	Integrative analysis of relative abundance data and presence–absence data of the microbiome using the LDM. Bioinformatics, 2022, 38, 2915-2917.	4.1	7
98	How special is a 'special' interval: modeling departure from length-biased sampling in renewal processes. Biostatistics, 2004, 5, 145-151.	1.5	6
99	Response to Lee etÂal American Journal of Human Genetics, 2008, 82, 526-528.	6.2	6
100	A Regressionâ€based Association Test for Caseâ€control Studies that Uses Inferred Ancestral Haplotype Similarity. Annals of Human Genetics, 2009, 73, 520-526.	0.8	6
101	SNPs in CAST are associated with Parkinson disease: A confirmation study. American Journal of Medical Genetics Part B: Neuropsychiatric Genetics, 2010, 153B, 973-979.	1.7	6
102	Marginal estimation for multi-stage models: waiting time distributions and competing risks analyses. Statistics in Medicine, 2002, 21, 3-19.	1.6	6
103	A rarefaction-without-resampling extension of PERMANOVA for testing presence–absence associations in the microbiome. Bioinformatics, 2022, 38, 3689-3697.	4.1	6
104	Robust testing of haplotype/disease association. BMC Genetics, 2005, 6, S69.	2.7	5
105	Robust Regression Analysis of Copy Number Variation Data based on a Univariate Score. PLoS ONE, 2014, 9, e86272.	2.5	5
106	Improved association analyses of disease subtypes in case-parent triads. Genetic Epidemiology, 2006, 30, 209-219.	1.3	4
107	Association mapping via a class of haplotype-sharing statistics. BMC Proceedings, 2007, 1, S123.	1.6	4
108	Marginal Analyses of Multistage Data. Handbook of Statistics, 2003, 23, 559-574.	0.6	3

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109	Fast and Robust Association Tests for Untyped SNPs in Case-Control Studies. Human Heredity, 2010, 70, 167-176.	0.8	3
110	Populationâ€Based Association and Gene by Environment Interactions in Genetic Analysis Workshop 18. Genetic Epidemiology, 2014, 38, S49-56.	1.3	3
111	Hold everything! Holding policies for protecting plasma supplies. Mathematical Biosciences, 1999, 160, 159-173.	1.9	2
112	Upper and Lower Bound Distributions that Give Simultaneous Confidence Intervals for Quantiles. Journal of the American Statistical Association, 1995, 90, 747.	3.1	2
113	Efficient estimation of indirect effects in caseâ€control studies using a unified likelihood framework. Statistics in Medicine, 2022, 41, 2879-2893.	1.6	2
114	Associations between microbial communities and key chemical constituents in U.S. domestic moist snuff. PLoS ONE, 2022, 17, e0267104.	2.5	2
115	Inference on Clustered Survival Data Using Imputed Frailties. Journal of Computational and Graphical Statistics, 2003, 12, 640-662.	1.7	1
116	Percentage of Gestational Diabetes Mellitus Attributable to Overweight and Obesity. Obstetrical and Gynecological Survey, 2010, 65, 617-618.	0.4	1
117	Estimation of Stage Occupation Probabilities in Multistage Models. , 2003, , 493-505.		0
118	[Backcalculation of HIV Infection Rates]: Comment. Statistical Science, 1993, 8, .	2.8	0