Estimation of linkage disequilibrium in Pag and Istrian sheep breed: towards genomic optimum contribution selection

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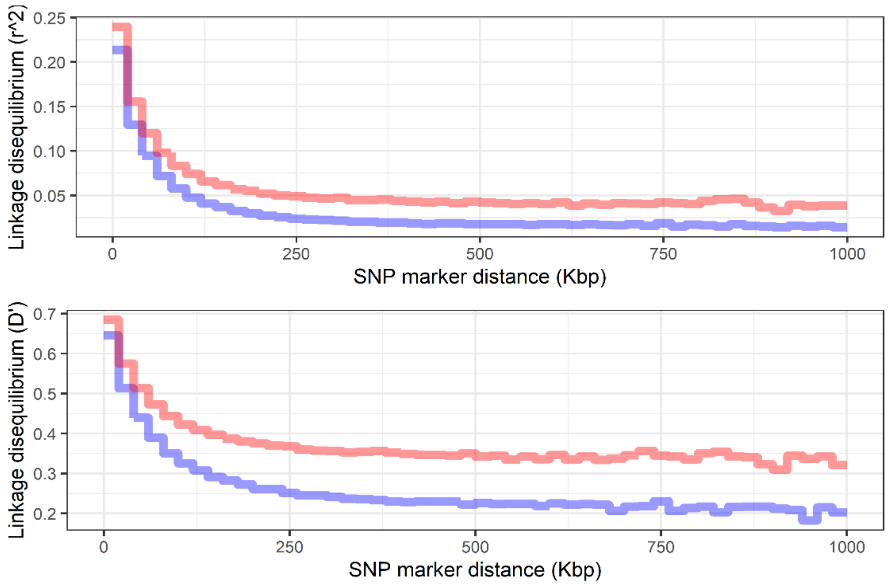
Genome wide LD classified by between-marker distance.

	Istrian sheep				Pag sheep			
Kbp	mean (r^2)	sd (r^2)	mean (D')	sd (D')	mean (r^2)	sd (r^2)	mean (D')	sd (D')
[0,100]	0.12	0.19	0.51	0.33	0.10	0.17	0.44	0.33
(100,200]	0.06	0.10	0.40	0.29	0.04	0.08	0.30	0.26
(200,300]	0.05	0.07	0.37	0.27	0.02	0.05	0.25	0.23
(300,400]	0.05	0.07	0.35	0.27	0.02	0.04	0.24	0.21
(400,500]	0.04	0.06	0.35	0.26	0.02	0.03	0.23	0.21
(500,600]	0.04	0.06	0.34	0.26	0.02	0.03	0.22	0.20
(600,700]	0.04	0.06	0.34	0.26	0.02	0.03	0.22	0.20
(700,800]	0.04	0.06	0.35	0.26	0.02	0.03	0.22	0.20
(800,900]	0.04	0.07	0.34	0.26	0.02	0.03	0.21	0.20
(900,1000]	0.04	0.05	0.33	0.26	0.02	0.03	0.21	0.20



LD decay in Istrian (red) and Pag (blue) sheep

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