

APPENDIX A

Selected Statistical Tables

Table A.1: Chi-square critical values (selected)

df	$\alpha = 0.10$	$\alpha = 0.05$	$\alpha = 0.01$
1	2.71	3.84	6.63
2	4.61	5.99	9.21
3	6.25	7.81	11.34
4	7.78	9.49	13.28
5	9.24	11.07	15.09

Table A.2: Standard normal (z) critical values

Confidence level	One-sided z	Two-sided z
90%	1.282	1.645
95%	1.645	1.960
99%	2.326	2.576

Table A.3: Conventional LOD score interpretation (Chapters 8 and 17)

LOD score, Z	Interpretation
$Z \geq 3.0$	Significant evidence for linkage
$2.0 \leq Z < 3.0$	Suggestive evidence for linkage
$-2.0 < Z < 2.0$	Inconclusive
$Z \leq -2.0$	Significant evidence against linkage

Table A.4: Coefficient of relationship (r) for common relative pairs (Chapter 6)

Relationship	r
Parent–offspring	1/2
Full siblings	1/2
Half-siblings	1/4
Grandparent–grandchild	1/4
Uncle/aunt–nephew/niece	1/4
First cousins	1/8
Double first cousins	1/4

Table A.5: Conventional significance thresholds in genome-wide and rare-variant studies (Chapters 18 and 20)

Setting	Conventional threshold
Genome-wide significance (common-variant GWAS)	$p < 5 \times 10^{-8}$
“Suggestive” genome-wide association	$p < 1 \times 10^{-5}$
Exome-wide significance (gene-based rare-variant tests, $\approx 20,000$ genes)	$p < 2.5 \times 10^{-6}$
Rare variant (minor allele frequency)	MAF < 0.01 (sometimes < 0.05)
Common variant (minor allele frequency)	MAF ≥ 0.05

Table A.6: Imputation quality (INFO/ r^2) rule-of-thumb thresholds (Chapter 19)

INFO / r^2 range	Typical use
≥ 0.8	High-confidence; suitable for primary analysis
$0.3 - 0.8$	Usable with caution; often retained in large meta-analyses
< 0.3	Generally excluded from primary association analysis