Perform for each trait separately

Phenotype 1

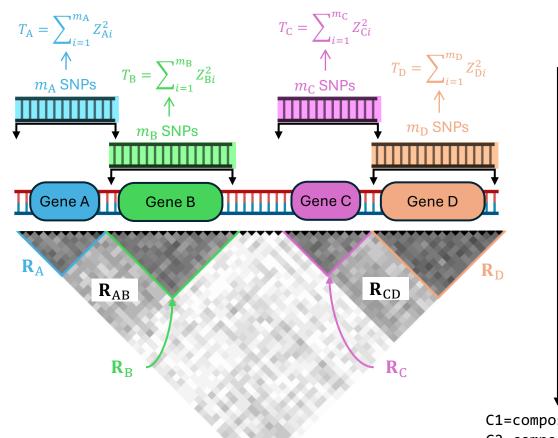
SNP Z-statistic EA

rs1	1.2	G
rs2	0.5	Α
rs3	-2.3	G
•••	•••	
rs99	5.6	Т

Phenotype 2

SNP Z-statistic EA

rs1	0.6	O
rs2	1.1	Т
rs3	-1.1	С
•••	•••	
rs99	2.4	Α



trait1

gent_sigma2_h0 gent_test_statistic

_		<u>-</u>			
	Α	5E-3	m_{A}	$2 \text{trace}(\mathbf{R}_{\mathbf{A}} \mathbf{R}_{\mathbf{A}})$	$T_{ m A}$
	В	2E-1	$m_{ m B}$	$2 \text{trace}(\mathbf{R}_{\text{B}} \mathbf{R}_{\text{B}})$	$T_{ m B}$
	С	7E-10	m_{C}	$2 trace(\mathbf{R}_{C} \mathbf{R}_{C})$	T_{C}
	D	6E-12	$m_{ m D}$	$2 \text{trace}(\mathbf{R}_{\mathrm{D}} \mathbf{R}_{\mathrm{D}})$	$T_{ m D}$
		•••	•••	•••	

trait2

(Gene	pval	m	gent_sigma2_h0	gent_test_statistic
	Α	2E-2	$m_{ m A}$	$2 trace(\mathbf{R}_{A} \mathbf{R}_{A})$	$T_{ m A}$
	В	1E-3	$m_{ m B}$	$2 trace(\mathbf{R}_{B} \mathbf{R}_{B})$	$T_{ m B}$
	С	6E-8	m_{C}	$2 trace(\mathbf{R}_{C} \mathbf{R}_{C})$	T_{C}
	D	9E-5	$m_{ m D}$	$2 \text{trace}(\mathbf{R}_{\mathrm{D}} \mathbf{R}_{\mathrm{D}})$	$T_{ m D}$
	•••	•••			

C1=compositemh(trait1) P1=posteriorgene(C1)
C2=compositemh(trait2) P2=posteriorgene(C2)

shared_count_simex(PS) ← PS=propshared(P1,P2)