Genetic correlations between sites via fully random-effects model

In this approach, we create subsets of our plot data. Each subset contains the information of only two sites. Since we have 10 sites, there are 45 different site pairs and thus 45 subsets we need to analyze. For each subset, we fit a model that allows for a genetic correlation between sites as:

L.corr

As a result e.g. for the site pair Bharisal-Bhanga we obtain the variance component estimates above. This pair has a genetic correlation of 0.599. After looping through all 45 site pairs, we obtain these genetic correlations:

	Barisal	Bhanga	Comilla	Gazipur	Habiganj	Kustia	Rajshahi	Rangpur	Satkhira	Sonagazi
Barisal		0,599	0,698	0,641	0,498	0,307	0,544	0,155	0,772	0,548
Bhanga			0,564	0,247	0,773	0,117	0,48	0,534	0,666	0,322
Comilla				0,512	0,876	0,387	0,245	0,362	0,797	0,604
Gazipur					0,516	0,41	0,196	0,134	0,246	0,015
Habiganj						0,302	0,371	0,734	0,646	0,591
Kustia							0,013	0,049	0,563	0,007
Rajshahi								0,633	0,376	-0,149
Rangpur									0,262	0,012
Satkhira										0,673
Sonagazi										