

# Base Gene Interaction Matrix

Brian Jo Hsuan Lee

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Load pre-curated datasets, including sampled gene indices, gene interaction

```
gene_int = read_csv("~/Desktop/Columbia/Spring_2022/P8139-Statistical_Genetic_Modeling/Project/gene_int")
S_0 = read_csv("~/Desktop/Columbia/Spring_2022/P8139-Statistical_Genetic_Modeling/Project/s0_zero_matrix")
```

Create an undirected interaction matrix

```
gene_int_undir = graph.data.frame(gene_int, directed=F)
S_0_alt = get.adjacency(gene_int_undir, attr="combined_score", sparse=F)
```

Fill in the missing columns and rows

```
miss_col = setdiff(colnames(S_0), colnames(S_0_alt))
new_col = rep(NA, nrow(S_0_alt))
for(i in seq_len(length(miss_col))){
  S_0_alt =
    S_0_alt %>%
    cbind(new_col)
  colnames(S_0_alt)[ncol(S_0_alt)] = miss_col[i]
}

miss_row = setdiff(colnames(S_0), rownames(S_0_alt))
new_row = rep(NA, ncol(S_0_alt))
for(i in seq_len(length(miss_row))){
  S_0_alt =
    S_0_alt %>%
    rbind(new_row)
  rownames(S_0_alt)[nrow(S_0_alt)] = miss_row[i]
}
```

Reorder the columns and rows, and fill in 0s where NA is present

```
S_0_alt = S_0_alt[colnames(S_0), colnames(S_0)]
S_0_alt[is.na(S_0_alt)] = 0
```

Save the matrix upon validating the interaction dataframe is successfully converted

```
sum(S_0_alt) == 2*sum(gene_int$combined_score)
```

```
## [1] TRUE
```

```
S_0_alt = S_0_alt %>% data.frame()
write_csv(S_0_alt, file("~/Desktop/Columbia/Spring_2022/P8139-Statistical_Genetic_Modeling/Project/base_gene_interaction_matrix.csv"))
```