

Spatial diagnostics and network workflows

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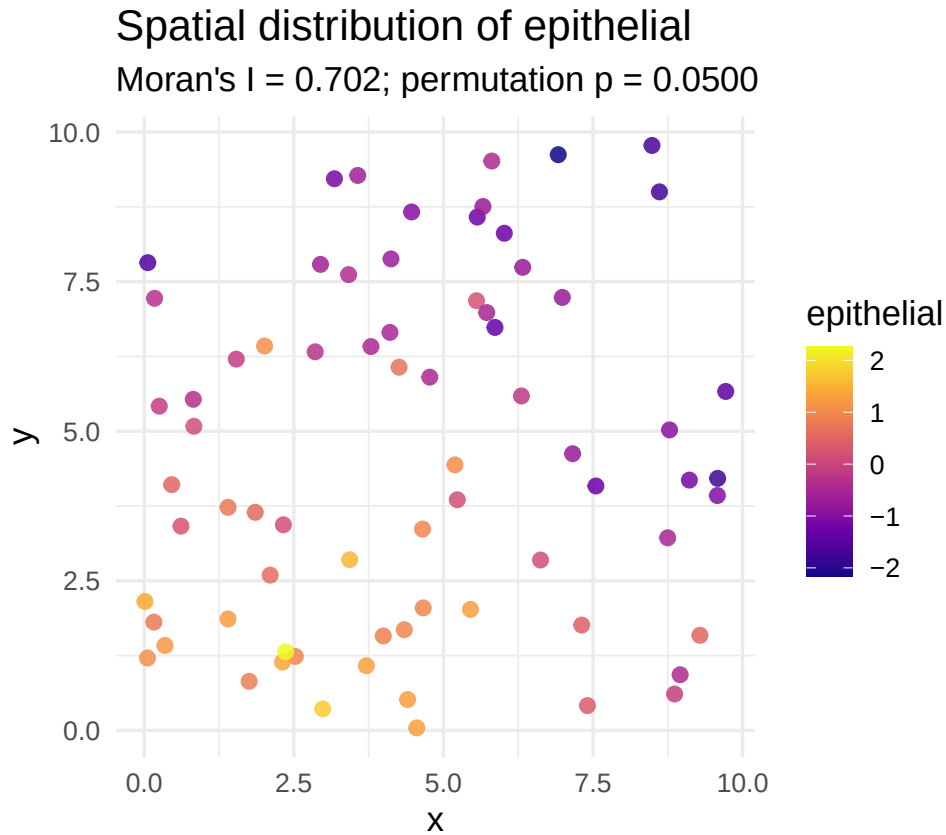
This vignette exercises the spatial and network analysis family with 72 synthetic observations. The small permutation count and compact data are intended for reproducibility checks, not final analysis settings.

```
d <- demo_spatial_data(n = 72, seed = 2026)
features <- c("epithelial", "APC", "CTL", "Treg", "T_helper")
mapping <- list(
  x = "x", y = "y", z = NULL, zone = "zone", id = "sample_id",
  outcome = "disease", exposure = "epithelial", mediator = "APC"
)
```

0.1 Spatial exploration and autocorrelation

```
spatial_qc <- run_analysis(
  "spatial_qc", d, mapping, features,
  list(feature = "epithelial", neighbors = 6, permutations = 19, seed = 2026)
)
spatial_qc$table
#>           metric      value
#> 1 Complete observations 72.0000000
#> 2           Neighbors   6.0000000
#> 3           Moran's I   0.7019779
#> 4 Permutation p-value   0.0500000

spatial_qc$plot
```



The output reports the configured neighbor graph, statistic, permutation calculation, and provenance. It does not establish a biological mechanism.

0.2 Region-aware conditional network

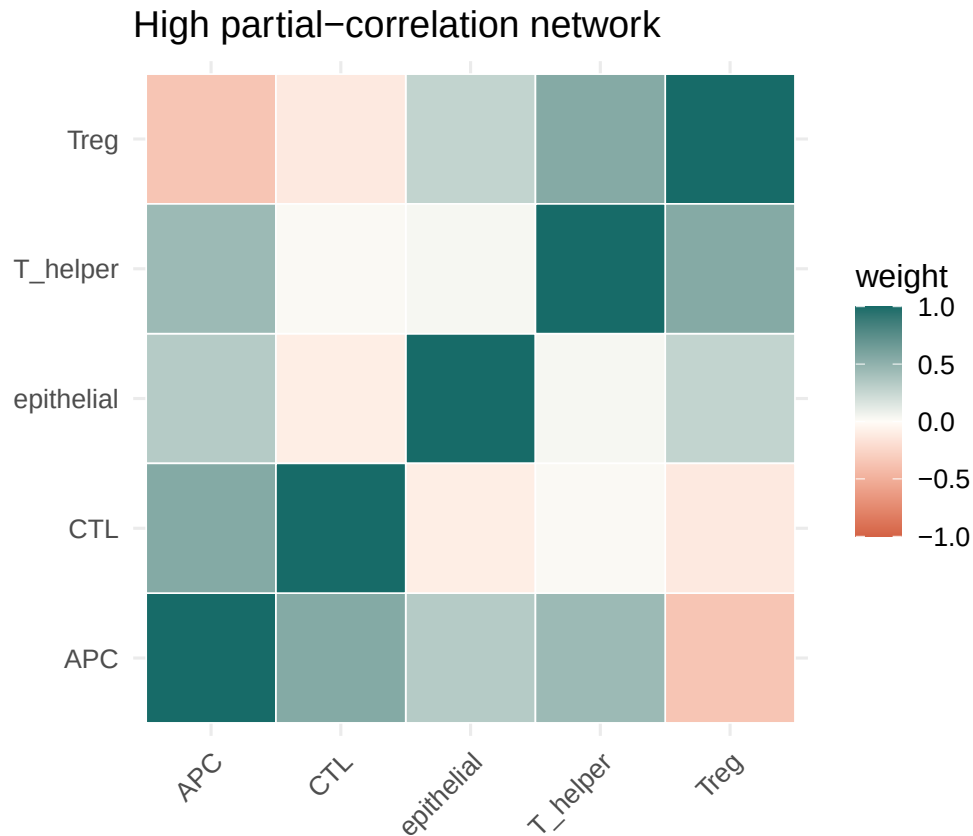
```
conditional <- run_analysis(
  "conditional_network", d, mapping, features,
  list(threshold = 0.15, ridge = 0.05, by_zone = TRUE)
)
head(conditional$table, 10)
```

#>	network	source	target	weight	sign
#> High.1	High	epithelial	APC	0.3318986	Positive
#> High.2	High	APC	CTL	0.5554517	Positive
#> High.3	High	epithelial	Treg	0.2728543	Positive
#> High.4	High	APC	Treg	-0.3581961	Negative
#> High.5	High	APC	T_helper	0.4468269	Positive
#> High.6	High	Treg	T_helper	0.5542829	Positive
#> Low.1	Low	epithelial	APC	0.4614824	Positive
#> Low.2	Low	epithelial	CTL	-0.1663843	Negative
#> Low.3	Low	APC	CTL	0.4633987	Positive
#> Low.4	Low	epithelial	Treg	0.3099184	Positive

```
conditional$summary
```

#>	networks	visible_edges	threshold	ridge
#>	3.00	23.00	0.15	0.05

```
conditional$plot
```



The stored matrices can be audited directly.

```
names(conditional$matrices)
#> [1] "High"      "Low"       "Intermediate"
vapply(conditional$matrices, nrow, integer(1))
#>      High      Low Intermediate
#>      5      5      5
```

Edges are regularized conditional-association summaries. The vignette intentionally stops at reproducible output inspection.

0.3 Public advanced engines

The following calls use the same 72-row table. They are not evaluated while building the vignette because runtime depends on the installed public engines and local hardware.

0.3.1 ISPat 2D

```
remotes::install_github("sagnikbhadury/ISPAT")

ispat <- run_analysis(
  "ispat", d, mapping, features,
  list(
    kernel = "Matern", spatial_fit = "VB", factor_fit = "CAVI",
    cores = 1L, threshold = 0.15
  )
)
```

```

)
)
ispat$summary
head(ispat$table)

```

0.3.2 GP-GHS

The short chain below is a software smoke check. Increase Monte Carlo settings and perform convergence assessment for research use.

```

remotes::install_github("sagnikbhadury/GP-GHS")

gpghs <- run_analysis(
  "gpghs", d, mapping, features,
  list(
    basis = 3L, nu = 1.5, nmc = 200L, burn = 50L, thin = 2L,
    threshold = 0.15, symmetry = "AND", cores = 1L
  )
)
gpghs$summary
head(gpghs$table)

```

Use `method_citations("ispat")` and `method_citations("gpghs")` to retrieve the required software and method references.