


Objective

> BiocManager::install("nnSVG")

Weber et al. (2023) proposed nnSVG, a scalable approach to identify spatially variable genes (SVGs) in spatially-resolved transcriptomics data based on nearest-neighbor Gaussian processes (NNGP). $\{y(s); s \in \mathbb{R}^k\}$

Methods

$\mathbf{y}_g = (y_{g1}, \dots, y_{gN})^\top$, normalized and transformed (*logcounts*) gene expression levels, for gene $g = 1, \dots, G$ across the finite set of N spatial locations $\mathbf{S} = (\mathbf{s}_1^\top, \dots, \mathbf{s}_N^\top)^\top$. $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boxed{\mathbf{b} + \boldsymbol{\epsilon}}$, $\mathbf{b} \sim \mathcal{N}_N(\mathbf{0}, \sigma_s^2 \cdot \mathbf{K}) \perp \boldsymbol{\epsilon} \sim \mathcal{N}_N(\mathbf{0}, \tau^2 \cdot \mathbf{I})$

Response NNGP Model	$\mathbf{y} \sim \mathcal{N}_N(\boldsymbol{\mu}, \boldsymbol{\Sigma})$	(1)
SpatialDE (spatial differential expression):	$\boldsymbol{\Sigma} = \sigma_s^2 \cdot \mathbf{K} + \tau^2 \cdot \mathbf{I}$	(2)
 Squared Exponential Kernel Function	$K_{ij} = \exp \left\{ -d_{ij}^{\frac{2}{\alpha}} / \frac{2}{\alpha} l^{\frac{2}{\alpha}} \right\}$ for $i, j \in \{1, \dots, N\}$	(3)
nnSVG: a scalable approximation to Eq. 2, Stan	$\tilde{\boldsymbol{\Sigma}}^{-1} = (\mathbf{I} - \mathbf{L})^\top \mathbf{D}^{-1} (\mathbf{I} - \mathbf{L})$ <small>sparse</small>	(4)

l : Length scale (bandwidth) hyperparameter. $l \nearrow$, $K_{ij} \nearrow$, Smoothness \nearrow

How rapidly does the covariance decay as a function of the Euclidean norm $d_{ij} = \|\mathbf{s}_i - \mathbf{s}_j\|$?

σ_s^2 : Spatial component of variance in gene expression.

Identified highly variable genes (HVGs) using $\mathbf{y} = \mathbf{X}\boldsymbol{\beta} + \boldsymbol{\epsilon}$ that assumes $\mathcal{H}_0: \sigma_s^2 = 0$. (5)

τ^2 : Nugget, the non-spatial component of variance in gene expression.

$\sigma_s^2 / (\sigma_s^2 + \tau^2)$ defines the *effect size* per gene (Svensson et al., 2018).

Separability between $\boldsymbol{\epsilon}$ and latent \mathbf{b} (resolution; Allen et al., 2023, p. 1785; Shang & Zhou, 2022, p. 12).

- Fitted a separate model for each gene and obtained maximum likelihood estimates for l , σ_s^2 , and τ^2 using the fast optimization algorithms in the “BRISC” (bootstrap for rapid inference on spatial covariances, $N > 100$) R package.
- Performed a likelihood ratio (LR) test comparing the fitted model using (4) against the baseline model (5).
- Ranked genes by the estimated LR statistics and calculated multiple-testing (Benjamini-Hochberg) adjusted approximate p -values for statistical significance per gene using an asymptotic χ^2_2 -distribution. p. 9

Highlights

“nnSVG” v1.5.3+

- Identified genes that vary in expression continuously across the entire tissue ($\boldsymbol{\mu} = \boldsymbol{\mu}_g \cdot \mathbf{1}$, mostly) or within *a priori* defined **spatial domains** (regions of the tissue slide corresponding to anatomical features or tissue types; Fig. 2) by including the spatial domains as covariates within the model where $\boldsymbol{\mu} = \mathbf{X}\boldsymbol{\beta}$; See also Tbl. 1;
- Used flexible **gene-specific** estimates of l_g within the models (one model per gene; See Fig. 1b; $\phi = l_g^{-1}$); (unlike SPARK-X which uses pooled l for all g and may lose sensitivity to spatial patterns);
- Scaled the computational complexity and runtime **linearly** with N , i.e., $\mathcal{O}(Nm^3)$ flops, where m is the number of NNs, See Fig. 3; and, thus, applied to large transcriptome-wide datasets, e.g., $N > 1,000$, high-throughput; (unlike SpatialDE and SpatialDE2 which scale cubically and quadratically). By default, $m = 10 \ll N$.

Limitations $y_i \sim \text{Pois}(\lambda_i)$ or $B(n_i, p_i)$, $\ln \lambda_i$ or $\text{logit}(p_i) = \mathbf{x}_i^T \boldsymbol{\beta} + \boxed{b_i + \epsilon_i}$, $\mathbf{b} = (b_1, \dots, b_N)^T \sim \mathcal{N}(\mathbf{0}, \sigma_s^2 \cdot \mathbf{K}) \perp \epsilon_i \stackrel{\text{i.i.d.}}{\sim} \mathcal{N}(0, \tau^2)$

SpatialDE, SpatialDE2, and nnSVG typically transform raw count data into **normalized** data before DE analysis, which can result in a potential loss of power due to failing in accounting for the mean-variance relationship that exists in raw counts (Guo et al., 2023, p. 4). **Error: zeros** or low-expressed/quality. *SCTransform*.

nnSVG scaled better with the number of spatial locations than SpatialDE but was slower on datasets with **many genes** (Chen et al., 2024, p. 11). nnSVG managed to achieve linear time inference but was still the second slowest method. SpatialDE overtakes nnSVG at 10,000 cells but is faster for fewer cells in part because it runs on a **GPU** (Fig. 5; Jones et al., 2023, p. 7-8).

nnSVG and SOMDE (**self-organizing map**) did not identify any significant peaks (spatially variable peaks [**SVPs**]), indicating their limitations in capturing spatial variability in this context (Li et al., 2023, p. 15).

Discussion

1. Nonstationary spatial modeling based on the Matérn kernel.

$$K_{ij} = \frac{2^{1-\nu}}{\Gamma(\nu)} \left(\frac{\sqrt{2\nu} d_{ij}}{l} \right)^\nu \cdot K_\nu \left(\frac{\sqrt{2\nu} d_{ij}}{l} \right),$$

where $K_\nu(\cdot)$ is the modified Bessel function of the second kind, e.g., $\nu \rightarrow +\infty$ and $\nu = 1/2$.

Different kernels make different assumptions about smoothness, periodicity, and other properties.

Stationarity - statistical properties such as mean and variance are constant over space

Isotropy - these properties are uniform in all directions

2. High power of nnSVG in detecting biologically informative genes? Benchmarking.

Performance compared to HVGs (*“scrn”*), *deviance residuals* from a binomial regression model (*“scry”*), and Moran’s *I* (a measure of spatial autocorrelation; *“Rfast2”*).

p. 10

$$\text{Global } I = \frac{N}{\sum_{i=1}^N \sum_{j=1}^N w_{ij}} \frac{\sum_{i=1}^N \sum_{j=1}^N w_{ij} (y_i - \bar{y})(y_j - \bar{y})}{\sum_{i=1}^N (y_i - \bar{y})^2}, \text{ where } w_{ij} \text{ are the spatial weights } (w_{ii} = 0).$$

3. The key idea of the NNGP: to model the data, we often don’t need to model the influence between all pairs of points; instead we can just consider a few of each point’s “neighbors” (Jones, 2021; Vecchia, 1988).

$$p(\mathbf{y}) = p(y_1, \dots, y_N) = p(y_1) \cdot p(y_2 | y_1) \cdot \dots \cdot p(y_N | y_1, \dots, y_{N-1}) = p(y_1) \prod_{i=2}^N p(y_i | \{y_j\}_{j=1}^{i-1}) \approx \prod_{i=1}^N p(y_i | \mathbf{y}_{N(s_i)})$$

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Future Work: (1) genes not independent; (2) Bayes factors