Effect of correlations on information - example calculation

We are interested in the impact of uniform correlations of magnitude c on the Fisher information in a population, assuming correlated Poisson variability.

Correlation matrix (*N*-dimensional):

$$\mathbf{C} = \begin{pmatrix} 1 & c & c \\ c & 1 & c \\ c & c & 1 \end{pmatrix}_{N \text{ dimensions}} = (1-c)\mathbf{I} + c\mathbf{1}\mathbf{1}^{\mathrm{T}},$$

where **I** is the identity matrix and $\mathbf{1} = (1, ..., 1)^{\mathrm{T}}$.

Fisher information in terms of the covariance matrix Σ : $I(s) = \mathbf{f}^{\mathsf{T}}(s) \Sigma^{-1}(s) \mathbf{f}'(s)$

Relation between covariance matrix and correlation matrix:

 $C_{ij} = \frac{\Sigma_{ij}}{\sigma_i \sigma_j} = \frac{\Sigma_{ij}}{\sqrt{f_i f_j}}$, since we assume Poisson variability (variance = mean). This can be

written as

$$\boldsymbol{\Sigma} = \begin{pmatrix} \sqrt{f_1} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & \sqrt{f_N} \end{pmatrix} \mathbf{C} \begin{pmatrix} \sqrt{f_1} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & \sqrt{f_N} \end{pmatrix}$$

and therefore Fisher information is

$$I = \mathbf{f}^{T} \mathbf{\Sigma}^{-1} \mathbf{f}^{T} = \mathbf{f}^{T} \begin{pmatrix} f_{1}^{-\frac{1}{2}} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & f_{N}^{-\frac{1}{2}} \end{pmatrix} \mathbf{C}^{-1} \begin{pmatrix} f_{1}^{-\frac{1}{2}} & 0 & 0 \\ 0 & \ddots & 0 \\ 0 & 0 & f_{N}^{-\frac{1}{2}} \end{pmatrix} \mathbf{f}^{T} = \begin{pmatrix} \frac{f_{1}}{\sqrt{f_{1}}} \\ \vdots \\ \frac{f_{N}}{\sqrt{f_{N}}} \end{pmatrix}^{T} \mathbf{C}^{-1} \begin{pmatrix} \frac{f_{1}}{\sqrt{f_{1}}} \\ \vdots \\ \frac{f_{N}}{\sqrt{f_{N}}} \end{pmatrix} \equiv \boldsymbol{\mu}^{T} \mathbf{C}^{-1} \boldsymbol{\mu}$$

where we denote $\boldsymbol{\mu} = \left(\frac{f_{1}}{\sqrt{f_{1}}}, \dots, \frac{f_{N}}{\sqrt{f_{N}}}\right)^{T}$.

The vector **1** is an eigenvector of **C** with eigenvalue 1 + (N-1)c.

Now observe that C is symmetric. Therefore, its eigenvectors are all orthogonal and right and left eigenvectors are the same. Any other eigenvector than 1 must be orthogonal to 1. Conversely, all vectors that are orthogonal to 1 are eigenvectors:

$$\mathbf{C}\boldsymbol{\chi} = (1-c)\mathbf{I}\boldsymbol{\chi} + c\mathbf{1}\mathbf{1}^{\mathrm{T}}\boldsymbol{\chi} = (1-c)\boldsymbol{\chi}$$

All these eigenvectors have eigenvalue 1-c. The eigenvalue 1-c has eigenspace with dimension N-1 and this space is orthogonal to the the vector **1**. All vectors orthogonal to **1** are eigenvectors and any orthogonal set of vectors which span the eigenspace can be used.

If the tuning curves are symmetric, then μ is orthogonal to 1. Therefore, μ is an

eigenvector with eigenvalue 1-*c*. We normalize it to obtain $\chi_0 = \frac{\mu}{\sqrt{\mu^T \mu}}$.

We can diagonalize **C** as $\mathbf{C} = \mathbf{X} \mathbf{\Lambda} \mathbf{X}^{-1}$, with **X** a matrix of orthonormal eigenvectors and $\mathbf{\Lambda}$ the diagonal matrix of eigenvalues. Because the eigenvectors are orthonormal, $\mathbf{X}^{\mathrm{T}} = \mathbf{X}^{-1}$ and $\mathbf{C} = \mathbf{X} \mathbf{\Lambda} \mathbf{X}^{\mathrm{T}}$, or in other words $\mathbf{C} = \sum_{i} \lambda_{i} \chi_{i} \chi_{i}^{\mathrm{T}}$. Similarly, $\mathbf{C}^{-1} = \sum_{i} \lambda_{i}^{-1} \chi_{i} \chi_{i}^{\mathrm{T}}$.

Information is therefore

$$I = \boldsymbol{\mu}^{\mathrm{T}} \mathbf{C}^{-1} \boldsymbol{\mu} = \boldsymbol{\mu}^{\mathrm{T}} \sum_{i} \lambda_{i} \boldsymbol{\chi}_{i} \boldsymbol{\chi}_{i}^{\mathrm{T}} \boldsymbol{\mu} = \frac{1}{1-c} \boldsymbol{\mu}^{\mathrm{T}} \frac{\boldsymbol{\mu} \boldsymbol{\mu}^{\mathrm{T}}}{\boldsymbol{\mu}^{\mathrm{T}} \boldsymbol{\mu}} \boldsymbol{\mu} = \frac{1}{1-c} \boldsymbol{\mu}^{\mathrm{T}} \boldsymbol{\mu}$$

For c = 0.2, the minimal variance of estimates will be 20% smaller than if c=0.

Note also that

$$I_{\text{shuffled}}\left(s\right) = \sum_{i} \frac{\left(f_{i}'(s)\right)^{2}}{f_{i}(s)} = \boldsymbol{\mu}^{\mathrm{T}}\boldsymbol{\mu}$$

This is the amount of information contained in a population in which individual neurons have the same response distributions as above, but are uncorrelated. (This is achieved by shuffling the trials.)

Furthermore,

$$I_{\text{diag}}\left(s\right) = \frac{\left(\mathbf{f}^{\mathsf{T}} \boldsymbol{\Sigma}_{\text{diag}}^{-1} \mathbf{f}^{\mathsf{T}}\right)^{2}}{\mathbf{f}^{\mathsf{T}} \boldsymbol{\Sigma}_{\text{diag}}^{-1} \boldsymbol{\Sigma} \boldsymbol{\Sigma}_{\text{diag}}^{-1} \mathbf{f}^{\mathsf{T}}} = \frac{\left(\boldsymbol{\mu}^{\mathsf{T}} \boldsymbol{\mu}\right)^{2}}{\boldsymbol{\mu}^{\mathsf{T}} \boldsymbol{\Sigma}_{\text{diag}}^{-1/2} \boldsymbol{\Sigma} \boldsymbol{\Sigma}_{\text{diag}}^{-1/2} \mathbf{h}} = \frac{\left(\boldsymbol{\mu}^{\mathsf{T}} \boldsymbol{\mu}\right)^{2}}{\boldsymbol{\mu}^{\mathsf{T}} \mathbf{C} \boldsymbol{\mu}} = \frac{\boldsymbol{\mu}^{\mathsf{T}} \boldsymbol{\mu}}{1 - c} = I(s)$$

This is the amount of information that would be extracted from the correlated population when using a suboptimal decoder that is optimal for the shuffled (decorrelated) responses.