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#### Abstract

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# The use of a common location measure in the invariant coordinate selection and projection pursuit 

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#### Abstract

Invariant coordinate selection (ICS) and projection pursuit (PP) are two methods that can be used to detect clustering directions in multivariate data by optimizing criteria sensitive to non-normality. In particular, ICS finds clustering directions using a relative eigen-decomposition of two scatter matrices with different levels of robustness; PP is a one-dimensional variant of ICS. Each of the two scatter matrices includes an implicit or explicit choice of location. However, when different measures of location are used, ICS and PP can behave counter-intuitively. In this paper we explore this behavior in a variety of examples and propose a simple and natural solution: use the same measure of location for both scatter matrices.


Keywords: Cluster analysis, Invariant coordinate selection, Projection pursuit, Robust scatter matrices, Location measures, Multivariate mixture model

## 1. Introduction

Consider a multivariate dataset, given as an $n \times p$ data matrix $X$, and suppose we want to explore the existence of any clusters. One way to detect clusters is by projecting the data onto a lower dimensional subspace for which the data are maximally non-normal. Hence, methods that are sensitive to non-normality can be used to detect clusters.

One set of methods based on this principle is invariant coordinate selection (ICS), introduced by Tyler et al. [17], together with a one-dimensional variant called projection pursuit (PP), introduced by Friedman and Tukey [5]. ICS involves the use of two scatter matrices, $S_{1}=S_{1}(X)$ and $S_{2}=S_{2}(X)$ with $S_{2}$ chosen to be more robust than $S_{1}$. An eigen-decomposition of $S_{2}^{-1} S_{1}$ is carried out. If the data can be partitioned into two clusters, then typically the eigenvector corresponding to the smallest eigenvalue is a good estimate of the clustering direction. The main choice for the user when carrying out ICS is the choice of the two scatter matrices.

However, in numerical experiments based on a simple mixture of two bivariate normal distributions, some strange behavior was noticed. In certain circumstances, ICS, and its variant PP, badly failed to pick out the right clustering direction. Eventually, it was discovered that the cause was the use of different location measures in the two scatter matrices. The purpose of this paper is to explore the reasons for this strange behavior in detail and to demonstrate the benefits of using common location measures.

Section 2 gives some examples of scatter matrices and reviews the use of ICS and PP as clustering methods. Section 3 sets out the multivariate normal mixture model with two useful standardizations of the coordinate system. Section 4 demonstrates in the population setting an ideal situation where ICS and PP work as expected and where an analytic solution is available - the two-group normal mixture model where the two scatter matrices are given by the covariance matrix and a kurtosis-based matrix. Some examples with other robust estimators are given in Sections 5-6, which show how ICS and PP can go wrong when different location measures are used and how the problem is fixed by using a common location measure. Further issues, including unbalanced mixtures and heteroscedasticity, are discussed in Section 7.

[^0]Notation. Univariate random variables, and their realizations, are denoted by lowercase letters, $x$, say. Multivariate random vectors, and their realizations, are denoted by lowercase bold letters, $\boldsymbol{x}$, say. A capital letter, $X$, say is used for $n \times p$ data matrix containing $p$ variables or measurements on $n$ observations; $X$ can be written in terms of its rows as

$$
X=\left(\boldsymbol{x}_{1}^{\top}, \ldots, \boldsymbol{x}_{n}^{\top}\right)^{\top},
$$

with $i$ th row $\boldsymbol{x}_{i}^{\top}=\left(x_{i 1}, \ldots, x_{i p}\right), i=1, \ldots, n$.

## 2. Background

### 2.1. Scatter matrices

A scatter matrix $S(X)$, as a function of an $n \times p$ data matrix $X$, is a $p \times p$ affine equivariant positive definite matrix. Following Tyler et al. [17], it is convenient to classify scatter matrices into three classes depending on their robustness.
(1) Class I: is the class of non-robust scatter matrices with zero breakdown point and unbounded influence function. Examples include the covariance matrix defined below in (1) and the kurtosis-based matrix in (2).
(2) Class II: is the class of scatter matrices that are locally robust, in the sense that they have bounded influence function and positive breakdown points not greater than $1 /(p+1)$. An example from this class is the class of multivariate M-estimators, such as the $M$-estimate for the $t$-distribution, e.g., [4, 8].
(3) Class III: is the class of scatter matrices with high breakdown points such as the Stahel-Donoho estimate, the minimum volume ellipsoid (mve) and the constrained M-estimates, e.g., [7, 18] .

Each scatter matrix has an implicit location measure. Let us look at the main examples in more detail, and note what happens in $p=1$ dimension. The labels in parentheses are used as part of the notation later in the paper.

The sample covariance matrix (var) is defined by

$$
\begin{equation*}
S=\frac{1}{n} \sum_{i=1}^{n}\left(\boldsymbol{x}_{i}-\overline{\boldsymbol{x}}\right)\left(\boldsymbol{x}_{i}-\overline{\boldsymbol{x}}\right)^{\top}, \tag{1}
\end{equation*}
$$

where for convenience here a divisor of $1 / n$ is used, and where $\overline{\boldsymbol{x}}$ is the sample mean vector. The implicit measure of location is just the sample mean.

The kurtosis-based matrix (kmat) is defined by

$$
\begin{equation*}
K=\frac{1}{n} \sum_{i=1}^{n}\left\{\left(\boldsymbol{x}_{i}-\overline{\boldsymbol{x}}\right)^{\top} S^{-1}\left(\boldsymbol{x}_{i}-\overline{\boldsymbol{x}}\right)\right\}\left(\boldsymbol{x}_{i}-\overline{\boldsymbol{x}}\right)\left(\boldsymbol{x}_{i}-\overline{\boldsymbol{x}}\right)^{\top} . \tag{2}
\end{equation*}
$$

Note that outlying observations are given higher weight than for the covariance matrix, so that $K$ is less robust than $S$. Again the implicit measure of location is just the sample mean. When $p=1$, the scatter matrix $S^{-1} K$ reduces to 3 plus the usual univariate kurtosis.

The $M$-estimator of scatter based on the multivariate $t_{v}$-distribution for fixed $v$ is the maximum likelihood estimate obtained by maximizing the likelihood jointly over scatter matrix $\Sigma$ and location vector $\mu$. If both parameters are unknown and $v \geq 1$, then under mild conditions on the data, the mle of $(\mu, \Sigma)$, is is the unique stationary point of the likelihood. Similarly, if $v \geq 0$ and $\mu$ is known, the mle of $\Sigma$ is the unique stationary point of the likelihood; see Kent et al. [8]. In either case, an iterative numerical algorithm is needed. Note that when $\boldsymbol{\mu}$ is to be estimated as well as $\Sigma$, the mle of $\mu$ is the implicit measure of location for this scatter matrix. For this paper we limit attention to the choice $v=2$ (and label it below by t 2 ).

The minimum volume ellipsoid (mve) estimate of scatter $S_{\text {mve }}$, introduced by Rousseeuw [14], is the ellipsoid that has the minimum volume among all ellipsoids containing at least half of observations, and its implicit estimate of location, $\overline{\boldsymbol{x}}_{\text {mve }}$, say, is the center of that ellipsoid. Calculating the exact mve requires extensive computation. In practice, it is calculated approximately by considering only a subset of all subsamples that contain $50 \%$ of the observations, e.g., $[9,18]$. If the location vector is specified, the search is limited to ellipsoids centered at this location measure.

When $p=1$, the mve reduces to the lshorth, defined as the length of the shortest interval that contains at least half of observations. The corresponding estimate of location, $\overline{\boldsymbol{x}}_{\text {lshorth }}$, say, is the midpoint of this interval. Calculating the lshorth around a known measure of location is trivial; just find the length of the interval that contains half of observations centered at this location measure. The lshorth was introduced by Grubel [6], building on an earlier suggestion of Andrews et al. [3] to use $\overline{\boldsymbol{x}}_{\text {Ishorth }}$, which they called the shorth, as a location measure.

The minimum covariance determinant estimate of scatter (mcd), $S_{\mathrm{mcd}}$, say, is defined as the covariance matrix of half of observations with the smallest determinant. The mcd location measure, $\overline{\boldsymbol{x}}_{\mathrm{mcd}}$, say, is the sample mean of those observations. The mcd can be calculated approximately by considering only a subset of all subsamples that contain at least half of observations, e.g., Rousseeuw and Driessen [15]. The mcd estimate of scatter with respect to a known location measure $\boldsymbol{\mu}$ is defined as the covariance matrix about $\boldsymbol{\mu}$ of half of observations with the smallest determinant. Recall that the covariance matrix about $\boldsymbol{\mu}$ for a dataset is given by $S+(\boldsymbol{\mu}-\overline{\boldsymbol{x}})(\boldsymbol{\mu}-\overline{\boldsymbol{x}})^{\top}$, where $S$ and $\overline{\boldsymbol{x}}$ are the sample covariance matrix and mean vector of the dataset.

When $p=1$, the mcd reduces to a truncated variance, $v_{\text {trunc }}$, say, defined as the smallest variance of half the observations. Its implicit measure of location, $\bar{x}_{\text {trunc }}$, say, is the sample mean of that interval. Also, a modified definition of $v_{\text {trunc }}$ using a known location measure is trivial and does not require any search; just find the interval that contains half of observations centered at the given location measure and calculate the variance.

Routines are available in R [13] to compute (at least approximately) these robust covariance matrices and their implicit location measures, in particular, tM from the package ICS [10] for the multivariate $t$-distribution, cov.rob from the package MASS [19] for mve, and CovMcd from the package rrcov [16] for mcd. Modified versions of these routines have been written by us to deal with the case of known location measures.

### 2.2. Invariant coordinate selection and projection pursuit

Given an $n \times p$ data matrix $X$, the ICS objective function is given by the ratio of quadratic forms

$$
\begin{equation*}
\kappa_{\mathrm{ICS}}(\boldsymbol{a})=\frac{\boldsymbol{a}^{\top} S_{1} \boldsymbol{a}}{\boldsymbol{a}^{\top} S_{2} \boldsymbol{a}}, \quad \boldsymbol{a} \in \mathbb{R}^{p}, \tag{3}
\end{equation*}
$$

where $S_{1}=S_{1}(X)$ and $S_{2}=S_{2}(X)$ are two scatter matrices. By convention, $S_{2}$ is chosen to be more robust than $S_{1}$. The intuition behind this convention is as follows. Under a balanced elliptically symmetric model, the population center is always uniquely defined. In the clustering direction the data will appear to have shorter tails, for the same reason that kurtosis is negative in this direction (see Section 4) than in the perpendicular directions, and hence we expect a more robust estimator to give a larger estimate of scatter, relative to a less robust estimator, in this direction than in the perpendicular direction.

For exploratory statistical analysis, attention is focused on the choices for $\boldsymbol{a}$ maximizing or minimizing $\kappa_{\mathrm{ICS}}(\boldsymbol{a})$. These values can be calculated analytically as the eigenvectors of $S_{2}^{-1} S_{1}$ corresponding to the maximum/minimum eigenvalues.

The original ICS method did not make a strong distinction between the largest and the smallest eigenvalues. However for clustering purposes between two groups, when the mixing proportion is not too far from $1 / 2$, it is the minimum eigenvalue which is of interest; see Section 4.

The method of PP can be regarded as a one-dimensional version of ICS. It looks for a linear projection $\boldsymbol{a}$ to maximize or minimize the criterion,

$$
\begin{equation*}
\kappa_{\mathrm{PP}}(\boldsymbol{a})=\frac{s_{1}(X \boldsymbol{a})}{s_{2}(X \boldsymbol{a})}, \tag{4}
\end{equation*}
$$

where $s_{1}=s_{1}(X \boldsymbol{a})$ and $s_{2}=s_{2}(X \boldsymbol{a})$ are two one-dimensional measures of spread. In general, optimizing $\kappa_{\mathrm{PP}}(\boldsymbol{a})$ must be carried out numerically. Searching for a global optimum is computationally expensive, and the complexity of the search increases as the dimension $p$ increases. Alternatively, we can search for a local optimum starting from a sensible initial solution, such as the ICS optimum direction.

Both ICS and PP are equivariant under affine transformations. That is, if $X$ is transformed to $U=\mathbf{1}_{n} \boldsymbol{h}^{\top}+X Q^{\top}$, where $Q(p \times p)$ is nonsingular and $\boldsymbol{h}$ is a translation vector in $\mathbb{R}^{p}$, then for both ICS and PP the new optimal vector $\boldsymbol{b}$, say, for $U$ is related to the corresponding optimal vector $\boldsymbol{a}$ for $X$ by

$$
\begin{equation*}
\boldsymbol{b} \propto Q^{-\top} \boldsymbol{a} . \tag{5}
\end{equation*}
$$

For numerical work it is convenient to have an explicit notation for the different choices in ICS and PP. If Scat 1 and Scat2 are the names of two types of multivariate scatter matrix, each computed with its own implicit location measure, then the corresponding versions of ICS and PP will be denoted

$$
\text { ICS : Scat } 1: \text { Scat } 2, \quad \text { and } \quad \text { PP }: \text { Scat } 1: \text { Scat } 2 .
$$

Note that PP is based on the univariate versions of Scat 1 and Scat2. For example, ICS based on the covariance matrix and the minimum volume ellipsoid will be denoted by ICS:var:mve. Other choices for scatter matrices have been summarized in Section 2.

When a common location measure is imposed on Scat1 and Scat2, then this restriction will be indicated by the augmented notation
ICS : Scat1 : Scat2 : Loc,
and similarly for PP. In this paper the only choice used for the location measure is the sample mean (mean). For example, ICS based on the covariance matrix and the minimum volume ellipsoid, both computed with respect to the mean vector, is denoted
ICS : var : mve : mean.

## 3. The two-group multivariate normal mixture model

The simple model used to demonstrate the main points of this paper is the two group multivariate normal mixture model, with density

$$
f(\boldsymbol{x})=q \phi_{p}\left(\boldsymbol{x}, \boldsymbol{\mu}_{1}, \Omega\right)+(1-q) \phi_{p}\left(\boldsymbol{x}, \boldsymbol{\mu}_{\mathbf{2}}, \Omega\right),
$$

where $\phi_{p}$ is the multivariate normal density, $\mu_{1}$ and $\mu_{2}$ are two mean vectors, $\Omega$ is a common covariance matrix, and $0<q<1$ is the mixing proportion. Even in this simple case, major problems with ICS and PP can arise.

Since ICS and PP are affine equivariant, we may without loss of generality choose the coordinate system so that

$$
\mu_{1}=\alpha \boldsymbol{e}_{1}, \quad \mu_{2}=-\alpha e_{1}, \quad \Omega=I_{p},
$$

where $\boldsymbol{e}_{\boldsymbol{1}}=(1,0, \ldots, 0)^{\top}$ is a unit vector along the first coordinate axis, and $\alpha>0$. That is, $\boldsymbol{\mu}_{\boldsymbol{1}}$ and $\boldsymbol{\mu}_{\mathbf{2}}$ lie equally spaced about the origin along the first coordinate axis, and the covariance matrix of each component equals the identity matrix.

A random vector $\boldsymbol{x}$ from the mixture model can also be given a stochastic representation,

$$
\boldsymbol{x}=\alpha \boldsymbol{s} \boldsymbol{e}_{1}+\boldsymbol{\epsilon},
$$

where $\boldsymbol{\epsilon} \sim \mathcal{N}_{p}\left(0, I_{p}\right)$ independently of an indicator variable $s$,

$$
s=\left\{\begin{array}{rl}
1 & \text { with probability } q \\
-1 & \text { with probability }(1-q)
\end{array} .\right.
$$

Moments under the mixture model are calculated most simply in terms of this stochastic representation. In particular,

$$
\boldsymbol{\mu}_{x}=\mathrm{E}(\boldsymbol{x})=q \boldsymbol{\mu}_{1}+(1-q) \boldsymbol{\mu}_{2}=(2 q-1) \alpha \boldsymbol{e}_{1}, \quad \mathrm{E}\left(\boldsymbol{x} \boldsymbol{x}^{\top}\right)=\alpha^{2} \boldsymbol{e}_{1} \boldsymbol{e}_{1}^{\top}+I_{p},
$$

so that the covariance matrix is

$$
\begin{equation*}
\Sigma_{x}=\operatorname{var}(\boldsymbol{x})=\mathrm{E}\left(\boldsymbol{x} \boldsymbol{x}^{\top}\right)-\boldsymbol{\mu}_{x} \boldsymbol{\mu}_{x}^{\top}=4 q(1-q) \alpha^{2} \boldsymbol{e}_{1} \boldsymbol{e}_{1}^{\top}+I_{p} . \tag{6}
\end{equation*}
$$

For practical work it is also convenient to consider a standardization for which the overall covariance matrix is the identity matrix. That is, define a new random vector

$$
\begin{equation*}
y=C^{-1} \boldsymbol{x}, \tag{7}
\end{equation*}
$$

where $C^{-1}=\operatorname{diag}\left(1 / c_{1}, \ldots, 1 / c_{p}\right)$, where $c_{1}=\left\{1+4 q(1-q) \alpha^{2}\right\}^{1 / 2}$, and $c_{2}=\ldots=c_{p}=1$. Then $\boldsymbol{y}$ has a stochastic representation

$$
\boldsymbol{y}=\delta s \boldsymbol{e}_{1}+\boldsymbol{\eta},
$$

where

$$
\begin{equation*}
\delta=\alpha /\left\{1+4 q(1-q) \alpha^{2}\right\}^{1 / 2}, \tag{8}
\end{equation*}
$$

and

$$
\boldsymbol{\eta} \sim \mathcal{N}_{p}\left(0, \operatorname{diag}\left(\sigma_{\eta}^{2}, 1, \ldots, 1\right)\right)
$$

where the first diagonal term $\sigma_{\eta}^{2}$ has two equivalent formulas,

$$
\sigma_{\eta}^{2}=\left\{1+4 \alpha^{2} q(1-q)\right\}^{-1} \quad \text { or } \quad \sigma_{\eta}^{2}=1-4 q(1-q) \delta^{2}
$$

The first two moments of $\boldsymbol{y}$ are

$$
\boldsymbol{\mu}_{y}=(2 q-1) \delta \boldsymbol{e}_{1}, \quad \Sigma_{y}=I_{p} .
$$

## 4. A population example: PP based on the kurtosis and ICS based on the kurtosis-based matrix and the covariance matrix

In this section we look at ICS:kmat:var and PP:kmat:var in the population case. In this setting it is possible to derive analytic results. Note that since kmat is based on fourth moments it is less robust than the variance matrix; hence kmat is listed first.

Recall the kurtosis of a univariate random variable $u$, say, with mean $\mu_{u}$, is defined by

$$
\operatorname{kurt}(u)=\frac{\mathrm{E}\left\{\left(u-\mu_{u}\right)^{4}\right\}}{\left[\mathrm{E}\left\{\left(u-\mu_{u}\right)^{2}\right\}\right]^{2}}-3 .
$$

The univariate kurtosis is zero when the random variable has normal distribution. For non-normal distributions the kurtosis lies in the interval $[-2, \infty]$ and is often nonzero. In particular, the kurtosis takes the following possible values:
(1) $\operatorname{kurt}(u)=0$; satisfied under normality.
(2) $\operatorname{kurt}(u)<0$; this case is called sub-Gaussian.
(3) $\operatorname{kurt}(u)>0$; this case is called super-Gaussian.

The sub-Gaussian case appears in distributions flatter than the normal and have thinner tails; one example is the uniform distribution. On the other hand, the super-Gaussian case appears in distributions that are more peaked than the normal distribution and have longer tails; examples include $t$, and Laplace distributions.

Define a balance parameter $\psi(q)=|q-1 / 2|$. Peña and Prieto [11] studied the population version of PP:kmat:var and showed that when the mixing proportion is not too far from $1 / 2$, more precisely, if $q(1-q)>1 / 6$, i.e., $\psi(q)<1 / \sqrt{12}$, then minimizing the PP objective function picks out the correct clustering direction. Similarly, if $q$ is far from half, i.e., $\psi(q)>1 / \sqrt{12}$, then maximizing the objective function picks out the correct clustering direction.

Their result can be derived simply as follows. Let $\boldsymbol{a} \in \mathbb{R}^{p}$ be a unit vector. Write $\boldsymbol{a}^{\top} \boldsymbol{x}=\alpha a_{1} s+v$, where $v=\boldsymbol{a}^{\top} \boldsymbol{\epsilon} \sim \mathcal{N}(0,1)$ is independent of $s$. The moments of $s$ are $\mathrm{E}(s)=\mathrm{E}\left(s^{3}\right)=m$, say, where

$$
\begin{equation*}
m=2 q-1 \text {, } \tag{9}
\end{equation*}
$$

and $\mathrm{E}\left(s^{2}\right)=\mathrm{E}\left(s^{4}\right)=1$. Hence, $\operatorname{var}(s)=\sigma^{2}$, say, where

$$
\begin{equation*}
\sigma^{2}=4 q(1-q) \tag{10}
\end{equation*}
$$

Then

$$
\operatorname{kurt}(s)=-6+4 / \sigma^{2}
$$

It can be checked that $\operatorname{kurt}(s)<0$ provided $\phi(q)<1 / \sqrt{12}$.

Next, we use the property that if $u_{1}, u_{2}$ are independent random variables with the same variance, and if $\delta_{1}, \delta_{2}$ are coefficients satisfying $\delta_{1}^{2}+\delta_{2}^{2}=1$, then

$$
\operatorname{kurt}\left(\delta_{1} u_{1}+\delta_{2} u_{2}\right)=\delta_{1}^{4} \operatorname{kurt}\left(u_{1}\right)+\delta_{2}^{4} \operatorname{kurt}\left(u_{2}\right)
$$

Applying this result to $\boldsymbol{a}^{\top} \boldsymbol{x}$ yields

$$
\begin{equation*}
\operatorname{kurt}\left(\boldsymbol{a}^{\top} \boldsymbol{x}\right)=\frac{a_{1}^{4} \alpha^{4} \sigma^{4}}{\left(\alpha^{2} a_{1}^{2} \sigma^{2}+1\right)^{2}} \operatorname{kurt}(s) \tag{11}
\end{equation*}
$$

Provided $\operatorname{kurt}(s)<0,(11)$ is minimized when $a_{1}^{2}$ is maximized, that is, if $a_{1}^{2}=1$, so that $\boldsymbol{a}= \pm e_{1}$ picks out the first coordinate axis.

The ICS calculations proceed similarly. First note that $\mathrm{E}\left(x_{1}\right)=\alpha m$, and the first diagonal term in $\Sigma_{x}$, defined in (6), can be expressed in terms of $\sigma^{2}$, defined in (10), as $\alpha^{2} \sigma^{2}+1$.

The first factor in the population version of $K$ defined in (2), $K_{x}$, say, is given by

$$
\left(\boldsymbol{x}-\boldsymbol{\mu}_{x}\right)^{\top} \Sigma_{\boldsymbol{x}}^{-1}\left(\boldsymbol{x}-\boldsymbol{\mu}_{x}\right)=\frac{\left(x_{1}-\alpha m\right)^{2}}{1+\alpha^{2} \sigma^{2}}+x_{2}^{2}+\ldots+x_{p}^{2}=D^{2}, \text { say },
$$

where $m$ is defined in (9). Note that $D^{2}$ is an even function in $x_{2}, \ldots, x_{p}$. Hence by symmetry all the off-diagonal terms in $K_{x}$ vanish. The first diagonal term is given by

$$
\mathrm{E}\left\{D^{2}\left(x_{1}-\alpha m\right)^{2}\right\}=\left(1+\alpha^{2} \sigma^{2}\right)(p+2)+\frac{\alpha^{4} \sigma^{4} \operatorname{kurt}(s)}{\left(1+\alpha^{2} \sigma^{2}\right)}
$$

The remaining diagonal terms, $j=2, \ldots, p$ are given by

$$
\mathrm{E}\left(D^{2} x_{j}^{2}\right)=p+2
$$

Hence $\Sigma_{x}^{-1} K_{x}$ reduces to

$$
\operatorname{diag}\left\{p+2+\frac{\operatorname{kurt}(s) \alpha^{4} \sigma^{4}}{\left(1+\alpha^{2} \sigma^{2}\right)}, p+2, \ldots, p+2\right\}
$$

These diagonal values are the eigenvalues. Hence provided $\operatorname{kurt}(s)<0, \kappa_{\mathrm{ICS}}$ is minimized when $\boldsymbol{a}=\boldsymbol{e}_{1}$, that is, when $a$ picks out the clustering direction.

If $p=2$, we can write a unit vector as $\boldsymbol{a}=(\cos \theta, \sin \theta)^{\top}$, and since $\boldsymbol{a}$ and $-\boldsymbol{a}$ define the same axis, we can parameterize the ICS and PP objective functions in terms of $\theta,-\pi / 2 \leq \theta \leq \pi / 2$. Plots of $\kappa_{\mathrm{ICS}}(\theta)$ and $\kappa_{\mathrm{PP}}(\theta)$ for $\alpha=3$ and $q=1 / 2,0.85$ and $1 / 2+1 / \sqrt{12}$ are shown in Figure 1.

For numerical work, especially when the underlying mixture model is unknown, the only feasible standardization is to ensure the overall variance matrix $\Sigma_{y}$ is the identity rather than the within-group variance matrix. In terms of the population model of this section, it means working with $\boldsymbol{y}$ from (7) rather than $\boldsymbol{x}$. If $p=2$ and $\boldsymbol{b} \propto(\cos \phi, \sin \phi)^{\top}$, say, is also written in polar coordinates, then from (5) and (7) $\boldsymbol{a}$ and $\boldsymbol{b}$ are related by

$$
b \propto C a
$$

hence, $\phi$ and $\theta$ are related by

$$
\binom{\cos \phi}{\sin \phi} \propto\left(\begin{array}{cc}
c_{1} & 0 \\
0 & c_{2}
\end{array}\right)\binom{\cos \theta}{\sin \theta} .
$$

Thus,

$$
\tan \phi=c \tan \theta
$$

where $c=c_{2} / c_{1}$.
The plot of the ICS and PP objective functions in Figure 2 shows that there is a sharper minimum in $\phi$ coordinates than in $\theta$ coordinates because under our mixture model $c$ is less than 1 . If $\boldsymbol{x}$ is scaled as in (7) with $c_{1}>c_{2}$, i.e., $c>1$, then there will be a wider minimum in $\phi$.


Figure 1: Plot of the population criteria $\kappa_{\mathrm{ICS}}(\theta)$ (red dotted line), and $\kappa_{\mathrm{PP}}(\theta)$ (solid black line) versus $\theta$, for $q=1 / 2,0.85$ and $1 / 2+1 / \sqrt{12}$, and $\alpha=3$.


Figure 2: Plot of the population criteria $\kappa_{\mathrm{ICS}}(\phi)$ (red dotted line), and $\kappa_{\mathrm{PP}}(\phi)$ (solid black line) versus $\phi$, for $q=1 / 2$, and $\delta=0.95$.

## 5. The effect of using a common location measure on ICS and PP

As mentioned earlier in Section 2.2, the ICS and PP criteria are expected to have similar behavior to the kurtosisbased criteria in Section 4. Namely, they are expected to be minimized in the clustering direction when the mixing proportion is not too far from $1 / 2$.

However, when applying ICS with at least one robust estimate of scatter (mainly from Class III), some peculiar behavior was observed on many datasets. In particular, the ICS criterion was often maximized in the clustering direction rather than minimized.

Here is an explanation. Under the two-group mixture model with one group slightly bigger than the other, a class III scatter matrix will typically home in on the larger group, with its corresponding location measure at the center of this group and its estimate of the scatter matrix capturing the spread of this group. The other scatter matrix (Class I or II) will measure the overall scatter of the data with its corresponding location measure at the overall center of the data. The result is erratic behavior in $\kappa_{\mathrm{ICS}}$ and $\kappa_{\mathrm{PP}}$.

Imposing a common location measure on the two scatter matrices fixes this problem. Here is a population example in $p=2$ dimensions to illustrate the issues in greater detail.

In this example we look at ICS:var:mve for the population bivariate normal mixture model in Section 3, with $q=1 / 2$ and any value of $\alpha>0$, i.e., $0 \leq \delta \leq 1$, where $\delta$ is given in (8). Standardize the coordinate system so that the overall covariance matrix is the identity, $\Sigma_{y}=I_{2}$. Let $\Sigma_{\text {mve }}$ denote the population minimum volume ellipsoid scatter matrix.

Then it turns out that $\Sigma_{\text {mve }}$ is the within-group covariance matrix for (either) one of the groups,

$$
\Sigma_{\mathrm{mve}}=\left(\begin{array}{cc}
1-\delta^{2} & 0  \tag{12}\\
0 & 1
\end{array}\right)
$$

where $0 \leq \delta \leq 1$ is given in (8). The implicit estimate of the center of the data will be given by the center of either group, $\pm \delta \boldsymbol{e}_{1}$; both values fit equally well.


Figure 3: For $\delta=0.9$, plots of the population criterion of: (a) ICS:var:mve vs. $\phi$, and (b) ICS:var:mve:mean .
Figure 3 (a) shows that the ICS:var:mve estimate of clustering direction is $(0,1)^{\top}$, i.e., $\phi= \pm \pi / 2$. However, the true direction of group separation direction is $(1,0)^{\top}$, i.e., $\phi=0$.

Next consider ICS:var:mve:mean, i.e., the common mean version of the previous example. The overall mean of the data is at the origin. When $\Sigma_{\text {mve }}$ is constrained to have its location measure at the origin, then the ICS criterion now picks out the true clustering direction. In order to give an analytic proof of this result, we restrict attention to the the limiting case of the balanced mixture model, i.e., when $\delta=1, q=1 / 2$. Hence, the group components will lie on two parallel vertical lines with means

$$
\mu_{1}=(1,0)^{\top}, \quad \mu_{2}=(-1,0)^{\top},
$$

and within-group covariance matrix

$$
\left(\begin{array}{ll}
0 & 0 \\
0 & 1
\end{array}\right) .
$$

In this setting, the following theorem gives population version of the MVE matrix.
Theorem 1. Consider the limiting balanced bivariate normal mixture model,

$$
\boldsymbol{y}=s \boldsymbol{e}_{1}+z \boldsymbol{e}_{2},
$$

where $s= \pm 1$, each with probability $1 / 2$, independent of $z \sim \mathcal{N}(0,1)$, and $\boldsymbol{e}_{1}=(1,0)^{\top}, \boldsymbol{e}_{2}=(0,1)^{\top}$. This model is standardized with respect to the "total" coordinates; i.e., $\mathrm{E}(\boldsymbol{y})=\mathbf{0}$ and $\operatorname{var}(\boldsymbol{y})=I_{2}$. The model can also be described in terms of a mixture of two normal distributions, concentrated on the vertical lines $y_{1}=1$ and $y_{1}=-1$ as shown in Figure 4.

The minimum volume ellipsoid mve of $\boldsymbol{y}, \Sigma_{\text {mve }}$, say, takes the form

$$
\Sigma_{m v e}=c_{t} \Sigma_{t}=\left(\begin{array}{cc}
2 & 0 \\
0 & 2 d^{2}
\end{array}\right)
$$

where $d=\Phi^{-1}(.75)=0.674$, the 75 th quantile of the standard normal distribution. Hence the dominant eigenvector is $\boldsymbol{e}_{1}$.

Theorem 1 is proved in the Appendix. The ellipse of $\Sigma_{\text {mve }}$ is plotted in Figure 4. Figure 3 (b) shows that the criterion of ICS:var:mve:mean, $\kappa_{\mathrm{ICS} ; \mu}(\phi)$ picks out the correct clustering direction $\boldsymbol{e}_{1}$.


Figure 4: Plot of the ellipse of $\Sigma_{\text {mve }}$ with its location measure forced at the origin superimposed on a mixture of two normal distributions concentrated on the vertical lines $y_{1}=1$ and $y_{1}=-1$.

Like ICS, PP can fail to detect the clustering direction if applied using different location measures. If the projection direction separates the data into two groups with one slightly bigger than the other, then the more robust measure of spread will measure the spread of the larger group. In Section 6, we give a detailed numerical example of the problem arising from using two different location measures in PP:var:mcd, and how the problem is fixed by using a common location measure.

## 6. Numerical examples

## Overview

In this section, we give numerical examples that demonstrate different ways in which ICS and/or PP can go wrong. We also show the beneficial effect of using common location measures in these examples. We use one simulated data set and apply different ICS and PP methods, with and without imposing a common location measure (the mean).

A two-dimensional data set of size $n=500$ is generated from the balanced mixture model, defined in Section 3, with $q=1 / 2$, and $\alpha=3$, so that $\delta=0.95$. Thus the two groups are well-separated and no sensible statistical method should have any problem finding the two clusters. All calculations are done after standardization with respect to the "total" coordinates. That is, the data matrix $Y(500 \times 2)$ is standardized to have sample mean $\mathbf{0}$ and sample covariance matrix $I_{2}$.

The ICS and PP methods used are:
(1) (PP,ICS):var:t2 with corresponding criteria $\kappa_{\mathrm{ICS}}^{1}$, and $\kappa_{\mathrm{ICS}}^{1}$.
(2) (PP,ICS):var:mcd with corresponding criteria $\kappa_{\mathrm{ICS}}^{2}$, and $\kappa_{\mathrm{PP}}^{2}$.
(3) (PP,ICS):var:mve with corresponding criteria $\kappa_{\text {ICS }}^{3}$, and $\kappa_{\text {PP }}^{3}$.
(4) (PP,ICS):t2:mcd with corresponding criteria $\kappa_{\mathrm{ICS}}^{4}$, and $\kappa_{\mathrm{PP}}^{4}$.
(5) (PP,ICS):t2:mve with corresponding criteria $\kappa_{\mathrm{ICS}}^{5}$, and $\kappa_{\mathrm{PP}}^{5}$.

When imposing the mean as the common location measure, the ICS and PP criteria will be denoted by $\kappa_{\mathrm{ICS}: m e a n}^{j}$ and $\kappa_{\text {PP:mean }}^{j}$, where $j=1, \ldots, 5$.

To understand the behavior of ICS and PP, their criteria are plotted against $-\pi / 2 \leq \phi \leq \pi / 2$. The plots are shown in Figure 5. From the panels in Figure 5, we make the following remarks based on the simulated data set:
(1) Panel (a) shows that ICS:var:t2 and PP:var:t2 work well since $\overline{\boldsymbol{y}}$ and $\overline{\boldsymbol{y}_{t 2}}$ are approximately equal. Hence, imposing a common location measure has little effect, as shown in (b).
(2) Panels (c), (e), (g), (i) show examples when ICS and/or PP go wrong because of the difference in the location measures.
(3) Using a common location measure fixes the problem in panel (d) for (PP, ICS):var:mcd, panel (f) for (PP, ICS):var:mve, and panel(h) for (PP, ICS):t2:mcd.
(4) From panel (j), using a common location measure in PP:t2:mve:mean does not seem to work well. The reason might be due to the unstable behavior of the mve and lshorth.
(5) The plots generally suggest that PP will be more accurate than ICS, since the PP plots are narrower at the clustering direction than the ICS plot. This property has been confirmed empirically in Alashwali [2] for certain multivariate normal mixture models and choices of scatter matrix.
(6) Similar patterns are seen with most simulated data sets from this model.


Figure 5: For $\delta=0.95$ and $q=1 / 2$, plots of different ICS (red dashed curve) and PP (black solid curve) criteria without (left) and with imposing a common location measure (right).

## Behavior of ICS:var:mcd

To gain a deeper understanding of the behavior of ICS:var:mcd in panel 5 (c) and the effect of forcing a common location measure on mcd in panel (d), we plot the ellipse of $S_{\text {mcd }}$ (both with and without imposing a common location measure) and superimpose it on the data points of our example. The plots are shown in panels 6 (a) and (b). The behavior in this example agrees with the interpretation given for the population example in Section 5 .


Figure 6: Plots of the ellipses of mcd scatter matrix based on (a) mcd location measure, and (b) the sample mean, superimposed on data of size $n=500$, distributed as mixtures of two normal distributions.

## Behavior of PP:var:mcd

The objective function for PP:var:mcd, has a similar problem to ICS; it is maximized rather than minimized near the correct clustering direction.

To understand this behavior in more detail, we plot in Figure 7 one-dimensional histograms after projections by the following choices for the angle $\phi: 0^{\circ}, 15^{\circ}, 30^{\circ}$, and $90^{\circ}$. For each histogram, we plot the $50 \%$ of the data that has the smallest variance, and the corresponding location measure $\bar{x}_{\text {trunc }}$. The plots are repeated where the location measure is constrained at the sample mean $\bar{x}=0$. Note that the shape of the histograms depends on of the projection directions. Also, as $v_{\text {trunc }}$ gets smaller, the PP criterion $\kappa_{\text {PP }}$ gets larger. From the panels of Figure 7, we make the following remarks:
(1) The $0^{\circ}$ projection produces two widely separated groups with one group is slightly bigger than the other. In this case, $\bar{x}_{\text {trunc }}$ is at the larger group and $v_{\text {trunc }}$ is essentially the variance of this group. Hence $v_{\text {trunc }}$ takes its smallest value and $\kappa_{\mathrm{PP}}$ is largest.
(2) The $15^{\circ}$ projection produces two slightly separated groups with within-group variance is larger than in the $0^{\circ}$ projection. The value of $v_{\text {trunc }}$ is larger than for $0^{\circ}$.
(3) The $30^{\circ}$ projection produces one group, with a pseudo-uniform distribution. The value of $v_{\text {trunc }}$ is larger than for $15^{\circ}$.
(4) The $90^{\circ}$ projection produces one normally distributed group. The value for $v_{\text {trunc }}$ becomes small again.

Constraining the mean to be at the origin fixes the problem. The value of $v_{\text {trunc }}$ steadily decreases from $0^{\circ}$ to $90^{\circ}$.


Figure 7: Histograms of $0^{\circ}, 15^{\circ}, 30^{\circ}$ and $90^{\circ}$ projections. Left panels show the vectors of $50 \%$ of data with the smallest variance (the blue lines), and its location measure (the red lines), right panels show the $50 \%$ of data with the smallest variance computed around the mean 0 .

Table 1: Estimates of $\hat{\theta}_{I C S}$ in degrees for simulated data sets with $n=500, q=0.6$ and $0.85, \alpha=3$, and equal covariance matrices.

| Method | $q=0.6(\mathrm{~min})$ | $q=0.85(\max )$ |
| :---: | :---: | :---: |
| ICS:var:t2 | 1.02 | -2.05 |
| ICS:var:t2:mean | 1.09 | -0.05 |
| ICS:var:mcd | 88.87 | -1.29 |
| ICS:var:mcd:mean | 2.90 | 19.31 |
| ICS:var:mve | 33.00 | 0.13 |
| ICS:var:mve:mean | 0.89 | 0.98 |
| ICS:t2:mcd | 89.44 | -1.04 |
| ICS:t2:mcd:mean | 3.77 | 23.58 |
| ICS:t2:mve | 88.53 | 0.65 |
| ICS:t2:mve:mean | 0.77 | 1.26 |

## 7. Further issues

So far, we have investigated the importance of using a common location measure in the performance of ICS based on robust estimates of scatter under mixtures of two balanced normal distributions. In this section, we discuss some further issues regarding ICS performance including lack of balance, heteroscedasticity, and the importance of robust estimates.

## Lack of balance

Recall from Section 4 that under mixtures of two normal distributions with $S_{1}=K$ and $S_{2}=S$, if $q$ is close to half, then $\kappa_{\mathrm{ICS}}$ is minimized in the clustering direction, whereas if $q$ is far from half then $\kappa_{\mathrm{ICS}}$ is maximized in the clustering direction. In this section, we want to explore the extent to which this behavior continues to hold for other choices of $S_{1}$ and $S_{2}$.

Several data sets were simulated from the mixture model defined in Section 3 with $n=500, \alpha=3$, and different choices of $q$. After standardizing the data as in (7), the following ICS methods are applied: ICS:var:t2, ICS:var:t2:mean, ICS:var:mcd, ICS:var:mcd:mean, ICS:var:mve, ICS:var:mve:mean, ICS:t2:mcd, ICS:t2:mcd:mean, ICS:t2:mve, and ICS:t2:mve:mean for $q=0.6$ (near half), 0.85 (far from half),. Table 1 shows a comparison of the clustering direction estimates of the ICS methods. The simulation results can be summarized as follows:
(1) if $q$ is close enough to $1 / 2$, then minimization is still appropriate.
(2) if $q$ is far enough from $1 / 2$, then maximization is appropriate. In this case, forcing a common location measure is unnecessary, because the Class II and III estimates of location will be at the center of the larger group, and the Class I estimate of location will be close to the center of the larger group.
(3) several simulations for different values of $q$ suggest that robust ICS methods have the same balance parameter $\phi(q)=1 / \sqrt{12}$ as discussed in Section 4.

## Heteroscedasticity

Following Peña et al. [12], consider the heteroscedstic model:

$$
q \mathcal{N}\left(\mu_{1}, \Omega\right)+(1-q) \mathcal{N}\left(\mu_{2}, \Omega+\Delta \Omega\right)
$$

where $\Delta \Omega$ is the added perturbation. Without loss of generality assume $\mu_{1}=(\alpha, 0)^{\top}, \mu_{2}=(-\alpha, 0)^{\top}, \Omega=I_{2}$.


Figure 8: Plot of $\hat{v}(\hat{\theta})$ for estimates of clustering directions estimated by the methods ICS:kmat:var:mean, ICS:var:t2:mean, ICS:var:mcd:mean, and ICS:var:mve:mean versus $\alpha=1,2$ and 3 for four different heteroscedastic models labeled by $j=1, \ldots, 4$.

To investigate the effect of heteroscedasticity, restrict attention to the balanced case ( $q=1 / 2$ ) in $p=2$ dimensions, with three different scenarios for $\Delta_{j}, j=1, \ldots, 4$,

$$
\Delta_{1}=\operatorname{diag}(0.5,1.5), \Delta_{2}=\operatorname{diag}(1,1.5), \Delta_{3}=\operatorname{diag}(1,3), \text { and } \Delta_{4}=\operatorname{diag}(2,1.5) .
$$

In the simulation study, $N=500$ datasets of size $n=500$ were simulated under each scenario for $\alpha=1,2$, and 3 . All data set are standardized as in (7) to have the identity matrix as the total covariance matrix. The following methods are applied: ICS:kmat:var, ICS:var:t2:mean, ICS:var:mcd:mean, ICS:var:mve:mean. Note that the different location measures version of the used ICS methods have the same problems that appear under equal covariance mixture model (see Section 6). Each method gives a set of estimates of the clustering direction as follows: $\hat{\theta}_{1}, \ldots, \hat{\theta}_{500}$, with the true clustering direction at $\theta_{0}=0$. To compare the performances of the four methods, we use the following measure of spread:

$$
\begin{equation*}
\hat{v}(\hat{\theta})=\frac{1}{N} \sum_{k=1}^{N} \sin ^{2}\left(\hat{\theta}_{k}-\theta_{0}\right), \tag{13}
\end{equation*}
$$

If the distribution of $\hat{\theta}$ is concentrated around $\theta_{0}$, then $v(\hat{\theta})=0$. If the distribution of $\hat{\theta}$ is concentrated around $\theta_{0}+\pi / 2$ or $\theta_{0}+3 \pi / 2$, then $v(\hat{\theta})=1$. If $\hat{\theta}$ is uniformly distributed, then $v(\hat{\theta})=1 / 2$. Figure 8 shows plots of $\hat{v}(\hat{\theta})$ for the
four different methods. The plots show that forcing a common location measure works well under the heteroscedastic
model. Also, the methods ICS:kmat:var and ICS:var:t2 have the best performance for all $\Delta_{j}$ among all other methods used in this study.

## Importance of robust estimators

In this section, we compare the performance of different ICS methods using robust estimates of scatter versus ICS:kmat:var under mixtures of long-tailed distributions.

The data sets used in this section are simulated from the following model. Suppose that the clustering direction is along the first coordinate axis. Let $\boldsymbol{x}=\left(x_{1}, x_{2}\right)^{\top}$ be a bivariate random vector, where $x_{1}$ follows a balanced mixture of two $t$ distributions with $v$ degrees of freedom, and $x_{2}$ follows a standard normal distribution. The random variable $x_{1}$ can be written as:

$$
x_{1}=\alpha s+z
$$

where $\alpha$, and $s$ are defined in Section 3, and $z$ is a $t$ random variable with $v$ degrees of freedom. The first and third moments of $z$ are equal to zero, the second and fourth moments are given by, e.g., Ahsanullah et al. [1],

$$
\mathrm{E}\left(z^{2}\right)=\frac{v}{v-2}, \mathrm{E}\left(z^{4}\right)=\frac{3 v^{2}}{(v-2)(v-4)} .
$$

The kurtosis of $z$ is $6 /(v-4)$ for $v>4$. Following our model in Section 3, we first standardize with respect to the within-group variance, i.e., $x_{1}$ can be written as:

$$
x_{1}=\alpha s+u,
$$

where $u=z \sqrt{(v-2) / v}$. The second moment of $u$ is 1 and its fourth moment is $3(v-2) /(v-4)$. The kurtosis of $u$ is $6 /(v-4)$.

The kurtosis of $x_{1}$ is given by:

$$
\begin{aligned}
\operatorname{kurt}\left(x_{1}\right) & =\frac{\alpha^{4}}{\left(\alpha^{2}+1\right)^{2}} \operatorname{kurt}(s)+\frac{1}{\left(\alpha^{2}+1\right)^{2}} \operatorname{kurt}(u) \\
& =-\frac{2 \alpha^{4}}{\left(\alpha^{2}+1\right)^{2}}+\frac{1}{\left(\alpha^{2}+1\right)^{2}}\left(\frac{6}{v-4}\right) .
\end{aligned}
$$

We want to explore settings in which each mixture component has positive kurtosis and the mixture has zero or negative kurtosis. Let $v=7$; then the kurtosis of each mixture component is 9.8 and the kurtosis of $x_{1}$ is

$$
\operatorname{kurt}\left(x_{1}\right)=\frac{1}{\left(\alpha^{2}+1\right)^{2}}\left(-2 \alpha^{4}+2\right) .
$$

For $\alpha=1$, the kurtosis equals to zero, and as $\alpha$ increases the kurtosis decreases (takes negative values).
The simulation is repeated $N=500$ times for each $\alpha=1,2$, and 3, and sample size $n=500$. The following ICS methods are applied: ICS:kmat:var; ICS:var:t2:mean; ICS:var:mcd:mean; ICS:var:mve:mean. To compare the performances of the ICS methods, we use (13). Figure 9 shows plots of $\hat{v}(\hat{\theta})$ versus $\alpha=1,2$, and 3 . The plots show that for small $\alpha$, robust ICS methods especially ICS:var:t2:mean are more accurate than ICS:kmat:var.

## 8. Conclusion

This paper has clarified several issues about role of the location measure when ICS and PP are used for two-group cluster analysis. The key observation is that if the mixing proportion $q$ is near $1 / 2$ (the balanced case) and the two scatter measures use different location measures, then ICS and PP are prone to erratic behavior. This problem is most severe when one scatter matrix comes from Class I and the other comes from Class II or III. The solution is to modify the definition of the scatter matrices to ensure they both use the same measure of location. The clustering direction can be found by minimizing the ICS and PP criteria, respectively.


Figure 9: Plot of $\hat{v}(\hat{\theta})$ for estimates of clustering directions estimated by the methods ICS:kmat:var, ICS:var:t2:mean, ICS:var:mcd:mean, and ICS:var:mve:mean versus $\alpha=1,2$ and 3 for balanced mixtures of two $t_{7}$ distributions.

In the unbalanced case when $q$ is far from $1 / 2$, the situation is simpler. The clustering direction is found by maximizing the ICS or PP criteria, respectively, and in this case it does not matter whether or not a common location parameter is used.

Most of paper focuses on the use of normal distributions for the mixture components. It is also possible to reach some conclusions when the mixture components have longer tails. In this setting it is beneficial for one of the scatter matrices to be robust. In particular, if $q=1 / 2$ then ICS:var:t2:mean outperforms ICS:kmat:var.

## Appendix

In this appendix we shall prove Theorem 1. In particular, we show that the population version of the mve, constrained to be centered at the origin, is given by

$$
\Sigma_{\mathrm{mve}}=\left[\begin{array}{cc}
2 & 0 \\
0 & d^{2}
\end{array}\right]
$$

where $d=\Phi^{-1}(.75)$ in terms of the cumulative distribution function of the $\mathcal{N}(0,1)$ distribution.
First let $u_{1}<u_{2}$ be two possible values for $y_{2}$ and consider an ellipse based on a matrix $\Sigma$ with inverse $\Sigma^{-1}=\Omega$,

$$
\begin{equation*}
y^{\top} \Omega y=1 \tag{A.1}
\end{equation*}
$$

which intersects the vertical line passing through $(1,0)^{\top}$, at these points,

$$
\left[\begin{array}{ll}
1 & u_{1}
\end{array}\right] \Omega\left[\begin{array}{c}
1  \tag{A.2}\\
u_{1}
\end{array}\right]=1, \quad\left[\begin{array}{ll}
1 & u_{2}
\end{array}\right] \Omega\left[\begin{array}{c}
1 \\
u_{2}
\end{array}\right]=1
$$

By symmetry the ellipse also intersects the points $\left(-1,-u_{1}\right)^{\top}$ and $\left(-1,-u_{2}\right)^{\top}$. Note that $\Sigma$ will be a candidate for the mve matrix if the interior of the ellipse covers $50 \%$ of the probability mass, that is,

$$
\begin{equation*}
\Phi\left(u_{2}\right)=\Phi\left(u_{1}\right)+1 / 2 . \tag{A.3}
\end{equation*}
$$

If $u_{1}$ and $u_{2}$ are finite, then necessarily $u_{1}<0$ and $u_{2}>0$.
The proof will proceed in two stages. First, for fixed $u_{1}, u_{2}$ satisfying (A.3), we choose $\Sigma$ to minimize $\operatorname{det}(\Sigma)$ (or equivalently maximize $\operatorname{det}(\Omega)$ ). Secondly, we optimize over the choice of $u_{1}, u_{2}$.

Thus, start with a fixed pair of values $u_{1}, u_{2}$ satisfying (A.3). If $\boldsymbol{y}=(1, u)^{\top}$ represents a point on one of the vertical lines, then the intersection with the ellipse (A.1) can be written

$$
\omega_{11}+2 \omega_{12} u+\omega_{22} u^{2}=1
$$

or equivalently as the quadratic equation in $u$,

$$
A u^{2}+B u+C=0,
$$

where $A=\omega_{22}, B=2 \omega_{12}, C=\omega_{11}-1$. If this ellipse passes through $\left(1, u_{1}\right)^{\top}$ and $\left(1, u_{2}\right)^{\top}$, then then $u_{1}, u_{2}$ are roots of the quadratic equation, so

$$
\begin{equation*}
u_{1}, u_{2}=\frac{-B \pm \sqrt{B^{2}-4 A C}}{2 A} \tag{A.4}
\end{equation*}
$$

In particular, setting $M=\left(u_{1}+u_{2}\right) / 2$ to be the mean of the roots, and $P=u_{1} u_{2}$ to be the product of the roots, we have

$$
\begin{equation*}
M=-\frac{B}{2 A}=-\frac{\omega_{12}}{\omega_{22}}, \quad P=\frac{C}{A}=\frac{\omega_{11}-1}{\omega_{22}} . \tag{A.5}
\end{equation*}
$$

Let us try to maximize $\operatorname{det}(\Omega)$ subject to the ellipse satisfying (A.2). Start with an arbitrary $\omega_{22}>0$. Then (A.5) determines the remaining elements of $\Omega$,

$$
\omega_{12}=-M \omega_{22}, \quad \omega_{11}=1+P \omega_{22}
$$

Hence

$$
\operatorname{det}(\Omega)=\omega_{11} \omega_{22}-\omega_{12}^{2}=\omega_{22}-Q \omega_{22}^{2},
$$

where

$$
\begin{equation*}
Q=M^{2}-P=\frac{1}{4}\left(u_{1}-u_{2}\right)^{2}>0 . \tag{A.6}
\end{equation*}
$$

Maximizing $\operatorname{det}(\Omega)$ with respect to the choice of $\omega_{22}$ leads to $\omega_{22}=1 /(2 Q)$ and

$$
\operatorname{det}(\Omega)=1 /(4 Q)
$$

The remaining task is to choose $u_{1}<0$ (which determines $u_{2}>0$ by (A.3)) to maximize $\operatorname{det}(\Omega)$, or equivalently, to minimize $Q$ in (A.6).

Recall a basic result from calculus. If $t=f(u)$ and $u=g(t)$ are monotone functions which are inverse to one another, then $g(f(u))=u$. Differentiating two times yields the relation between the derivatives,

$$
g^{\prime}=1 / f^{\prime}, \quad g^{\prime \prime}=-f^{\prime \prime} /\left\{f^{\prime}\right\}^{3} .
$$

In particular, consider $f(u)=\Phi(u)$, with derivatives $f^{\prime}(u)=\phi(u)$ and $f^{\prime \prime}(u)=-u \phi(u)$, where $\phi(u)$ is the probability density function of $\mathcal{N}(0,1)$. Then $g(t)=\Phi^{-1}(t)$ with derivatives $g^{\prime}(t)=1 / \phi(u)$ and $g^{\prime \prime}(t)=u /\{\phi(u)\}^{2}$, where $u=$ $\Phi^{-1}(t)$.

With this notation, write $u_{1}=g(t)$ for $0<t<1 / 2$. Then $u_{2}=g(t+1 / 2)$. Write $\phi_{1}=\phi\left(u_{1}\right), \phi_{2}=\phi\left(u_{2}\right)$. The quantity $Q$ in (A.6), treated as a function of $t$, has derivatives

$$
\begin{aligned}
Q^{\prime} & =\frac{1}{2}\left\{u_{1} u_{1}^{\prime}-u_{1} u_{2}^{\prime}-u_{1}^{\prime} u_{2}+u_{2} u_{2}^{\prime}\right\} \\
& =\frac{1}{2}\left\{u_{1}\left(1 / \phi_{1}-1 / \phi_{2}\right)+u_{2}\left(1 / \phi_{2}-1 / \phi_{1}\right)\right\}, \\
Q^{\prime \prime} & =\frac{1}{2}\left\{u_{1} u_{1}^{\prime \prime}+\left(u_{1}^{\prime}\right)^{2}-u_{1} u_{2}^{\prime \prime}-2 u_{1}^{\prime} u_{2}^{\prime}-u_{1}^{\prime \prime} u_{2}+u_{2} u_{2}^{\prime \prime}+\left(u_{2}^{\prime}\right)^{2}\right\} \\
& =\frac{1}{2}\left\{u_{1}^{2} / \phi_{1}^{2}+1 / \phi_{1}^{2}-u_{1} u_{2} / \phi_{2}^{2}-2 /\left(\phi_{1} \phi_{2}\right)-u_{1} u_{2} / \phi_{1}^{2}+u_{2}^{2} / \phi_{2}^{2}+1 / \phi_{2}^{2}\right\} \\
& =\frac{1}{2}\left\{\left(1 / \phi_{1}-1 / \phi_{2}\right)^{2}+u_{1}^{2} / \phi_{1}^{2}-u_{1} u_{2} /\left(1 / \phi_{1}^{2}+1 / \phi_{2}^{2}\right)+u_{2}^{2} / \phi_{2}^{2}\right\} .
\end{aligned}
$$

If $u_{1}=-d$, then $u_{2}=d$ and $\phi_{1}=\phi_{2}$ so that the first derivative vanishes. For all $(0<t<1 / 2)$, the second derivative is positive, so the function is convex. Hence $Q$ is minimized for $u_{1}=-d, u_{2}=d$. Then $M=0, Q=-P=d^{2}$ and the optimal $\Sigma$ becomes

$$
\Sigma=\Omega^{-1}=\left[\begin{array}{cc}
2 & 0 \\
0 & 2 d^{2}
\end{array}\right]
$$

as required.

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