

Unsupervised analysis of MS images using Cardinal

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Contents

1	Introduction	1
2	Analysis of a pig fetus whole body cross section	2
2.1	Pre-processing	3
2.1.1	Normalization	3
2.1.2	Peak picking and alignment	3
2.2	Visualizing the dataset	4
2.2.1	Visualization of molecular ion images	4
2.2.2	Exploratory analysis using PCA	4
2.3	Spatial segmentation using spatially-aware k-means clustering.	5
2.3.1	Plotting the spatial segmentation	6
2.3.2	Plotting the mean spectra of the segments	7
2.4	Spatial segmentation using spatial shrunken centroids clustering.	8
2.4.1	Plotting the spatial segmentations	10
2.4.2	Plotting the (shrunken) mean spectra of the segments	11
2.4.3	Plotting and interpreting the t-statistics of the m/z values	11
2.4.4	Identifying the number of segments.	13
2.4.5	Interpreting the spatial segmentation.	14
3	Additional example	16
3.1	Evaluation using a cardinal painting	16
4	Session info	18

1 Introduction

The goal of unsupervised analysis of mass spectrometry imaging experiments is to discover the regions of the data with distinct chemical profiles, and the masses that distinguish the chemical profiles of these regions.

Algorithmically, this means clustering the data. In imaging experiments, the resulting cluster configurations are called spatial segmentations, and the clusters are called segments.

Unsupervised analysis of MS images using Cardinal

In this vignette, an example clustering workflow in *Cardinal* is shown, along with plots of results.

2 Analysis of a pig fetus whole body cross section

This example uses the PIGII_206 dataset: a cross section of a pig fetus captured using a Thermo LTQ instrument using desorption electrospray ionization (DESI).

```
> library(CardinalWorkflows)
> data(pig206, pig206_analyses)
```

The PIGII_206 dataset is of interest for segmentation because we expect the underlying morphology of the tissue to be reflected in its chemical profile. It would be interesting, therefore, if we were able to identify abundant analytes certain physical systems such as the heart, spine, liver, or brain.

```
> image(pig206, mz = 256)
```

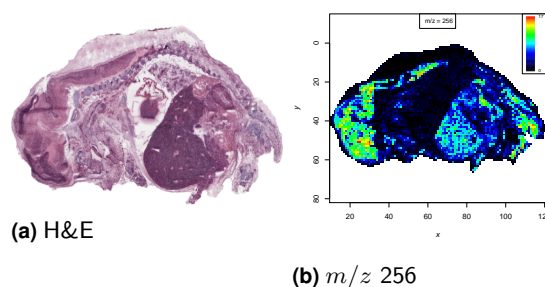


Figure 1: Optical image and a cropped ion image for the pig fetus dataset

```
> summary(pig206)

Class: MSImageSet
Features: m/z = 150.08 ... m/z = 1000 (10200 total)
Pixels: x = 72, y = 1 ... x = 83, y = 66 (4959 total)
x: 10 ... 120
y: 1 ... 66
Size in memory: 195.7 Mb
```

In the optical image shown in Figure 1a, the brain (left), heart (center), and liver (large dark region below heart) can be seen. The MS dataset has been cropped to remove the background slide pixels, leaving only the tissue section itself for analysis as seen in Figure 1b. The image contains 4959 pixels with 10200 spectral features measured at each location (m/z range from 150 to 1000).

Unsupervised analysis of MS images using Cardinal

2.1 Pre-processing

For statistical analysis, it is necessary to perform some kind of dimension reduction on the dataset as part of the pre-processing, so that computation times are reasonable. We will use peak-picking, although dimension reduction via resampling or binning is also a possible.

Note that we can perform peak-picking here for our unsupervised analysis because we do not have to worry about cross-validation as we would when performing classification (see classification workflow).

2.1.1 Normalization

In order to ensure that the spectra are comparable pixel-to-pixel, normalization is often done as a pre-processing step. A popular choice for normalization in mass spectrometry image analysis is total ion current (TIC) standardization.

```
> pig206.norm <- normalize(pig206, method = "tic")
```

2.1.2 Peak picking and alignment

For computational efficiency, it is necessary to do peak picking prior to analysing the data. As in [1], we peak pick on every 10th mass spectrum, retaining only those peaks that occur in at least 1% of the considered spectra. The selection of peaks in *Cardinal* is done using a comparison of local maxima against noise.

First, we perform peak-picking on every 10th mass spectrum using the `peakPick` method, looking for peaks with a signal-to-noise ratio (SNR) of at least 6.

```
> pig206.peaklist <- peakPick(pig206.norm, pixel = seq(1, ncol(pig206), by = 10),  
+   method = "simple", SNR = 6)
```

The peaks must be aligned using `peakAlign`. Below, the mean spectrum of the raw data is used as the reference, so the peaks will be aligned to the local maxima in the mean spectrum.

```
> pig206.peaklist <- peakAlign(pig206.peaklist, ref = pig206.norm, method = "diff",  
+   units = "ppm", diff.max = 200)
```

Now we use the `peakFilter` method to drop peaks that occur less frequently than once every 100 spectra.

```
> pig206.peaklist <- peakFilter(pig206.peaklist, method = "freq", freq.min = ncol(pig206.peaklist)/100)
```

Finally, `reduceDimension` method is used to sweep back through the full normalized dataset retrieve the identified peaks from all of the pixels.

```
> pig206.peaks <- reduceDimension(pig206.norm, ref = pig206.peaklist, type = "height")
```

```
> summary(pig206.peaks)
```

```
Class: MSImageSet  
Features: m/z = 151.33 ... m/z = 889.67 (143 total)  
Pixels: x = 72, y = 1 ... x = 83, y = 66 (4959 total)
```

Unsupervised analysis of MS images using Cardinal

```
x: 10 ... 120  
y: 1 ... 66  
Size in memory: 6.7 Mb
```

An alternative pre-processing workflow would be to perform peak-picking on all mass spectra and use these peaks directly (after alignment) rather than use `reduceDimension`. However, this would result in 0 intensities for mass spectra where certain peaks were not found, so it places a greater burden on the accuracy of the peak detection algorithm.

2.2 Visualizing the dataset

In this section, we will walk through several methods for visualizing the dataset before statistical analysis.

2.2.1 Visualization of molecular ion images

Plotting ion images is the natural first step in exploring a mass spectrometry imaging dataset.

In Figure 2 we show ion images for three selected peaks. These images have been contrast enhanced using histogram equalization [2]. Further, Gaussian smoothing is used to improve visualization of the images.

```
> image(pig206, mz = 187, contrast.enhance = "histogram", smooth.image = "gaussian")
```

```
> image(pig206, mz = 284, contrast.enhance = "histogram", smooth.image = "gaussian")
```

```
> image(pig206, mz = 537, contrast.enhance = "histogram", smooth.image = "gaussian")
```

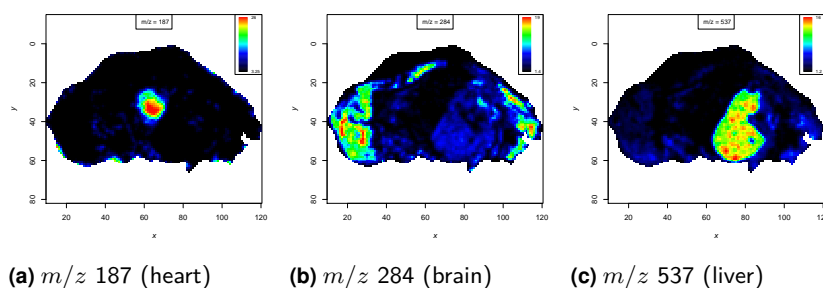


Figure 2: Ion images showing histogram equalization and Gaussian smoothing

These ion images show morphological features such as the heart (Figure 2a), brain (Figure 2b), and liver (Figure 2c) that an unsupervised analysis should identify in a spatial segmentation.

2.2.2 Exploratory analysis using PCA

Principal component analysis (PCA) is another popular method for exploring a dataset. PCA is also available in *Cardinal*. We now explore the peak-picked dataset using PCA with 5 components, fit below using the PCA method.

Unsupervised analysis of MS images using Cardinal

```
> pig206.pca <- PCA(pig206.peaks, ncomp = 5)
```

```
> summary(pig206.pca)
```

	PC1	PC2	PC3	PC4	PC5
Standard deviation	55.50312	30.40846	18.97628	18.10846	14.54119

The summary statistics show that the first 5 principal components cumulatively explain approximately 85% of the variation in the data. However, plotting the PC scores as images (as shown below in Figure 3a) shows that PCA is only somewhat helpful in visualizing the data, as the variation explained by PCA is dominated by the tissue above the spine.

```
> image(pig206.pca, column = c("PC1", "PC2", "PC3"), superpose = FALSE, col.regions = risk.colors(100),  
+       layout = c(3, 1))
```

In Figure 3b, we plot the loadings for the principal components as well.

```
> plot(pig206.pca, column = c("PC1", "PC2", "PC3"), superpose = FALSE, layout = c(3,  
+ 1))
```

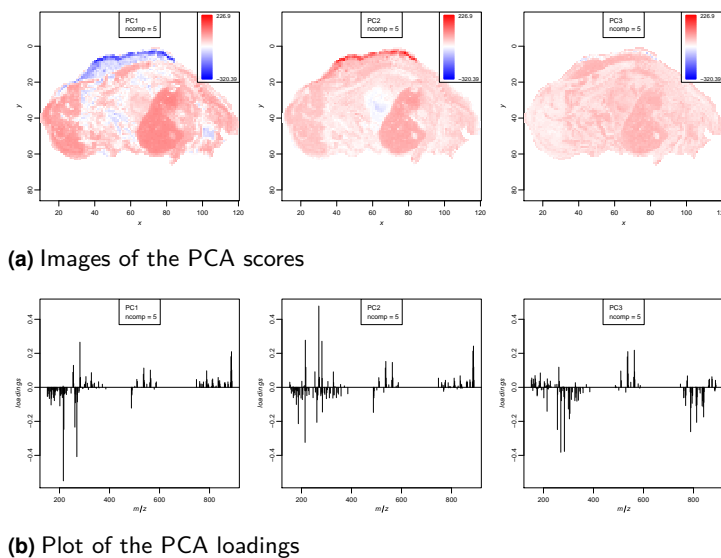


Figure 3: Principal components analysis of PIGII_206

Although PCA is widely used and can be visually useful when first exploring a dataset, it is rarely informative enough to constitute a complete analysis on its own, and additional statistical analyses are usually required to obtain more meaningful results.

2.3 Spatial segmentation using spatially-aware k-means clustering

This section demonstrates the spatially-aware clustering presented by Alexandrov and Kobarg [3], implemented in *Cardinal* in the `spatialKMeans` method.

Unsupervised analysis of MS images using Cardinal

This method uses a spatial distance function to perform dimension reduction on the mass spectra prior to clustering using ordinary k-means. The algorithm differentiates between "spatially-aware" (SA) and "spatially-aware structurally-adaptive" (SASA) clustering, which use different weights in the spatial distance function.

The "SA" variant uses simple Gaussian weights, and the "SASA" variant uses adaptive weights that often better preserves edges between segments. In *Cardinal*, these methods are differentiated by a `method` argument which can be set to either "gaussian" or "adaptive".

The parameters to be explicitly provided in the `spatialKMeans` method are:

- `r`: The neighborhood smoothing radius
- `k`: The number of segments (clusters)

The method is vectorized over these parameters, so multiple models can be fit simultaneously by giving them multiple values.

Below, we perform SA clustering with the `method="gaussian"` weights.

```
> set.seed(1)
> pig206.skmg <- spatialKMeans(pig206.peaks, r = c(1, 2), k = c(5, 10), method = "gaussian")
```

```
> summary(pig206.skmg)
```

	r	k	method	time	Within-Cluster SS	Between-Cluster SS	Total SS
1	1	5	gaussian	1.425	10250814	18077178	28327992
2	1	10	gaussian	3.354	7460608	20867384	28327992
3	2	5	gaussian	1.422	11379227	16948765	28327992
4	2	10	gaussian	3.023	8831925	19496067	28327992

Additionally, we perform SASA clustering with the `method="adaptive"` weights.

```
> set.seed(1)
> pig206.skma <- spatialKMeans(pig206.peaks, r = c(1, 2), k = c(5, 10), method = "adaptive")
```

```
> summary(pig206.skma)
```

	r	k	method	time	Within-Cluster SS	Between-Cluster SS	Total SS
1	1	5	adaptive	2.675	12066467	16261525	28327992
2	1	10	adaptive	2.950	9713476	18614516	28327992
3	2	5	adaptive	1.825	11492427	16835565	28327992
4	2	10	adaptive	2.739	9110589	19217403	28327992

Both of the resulting objects have four sets of model parameters, in the parameter space of $r = 1, 2$ and $k = 5, 10$.

2.3.1 Plotting the spatial segmentation

Cardinal has the capacity to simultaneously plot segmentations for the whole set of parameters. Figure 4a shows the SA results (Gaussian weights), and Figure 4b shows the SASA results (adaptive weights).

```
> image(pig206.skmg, key = FALSE, layout = c(2, 2))
```

Unsupervised analysis of MS images using Cardinal

```
> image(pig206.skma, key = FALSE, layout = c(2, 2))
```

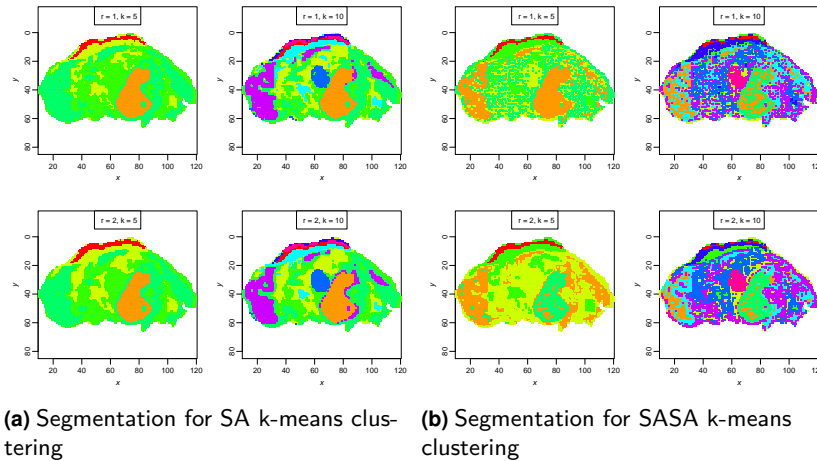


Figure 4: The spatial segmentations for spatially-aware (SA) and spatially-aware structurally-adaptive (SASA) k-means clustering with varying smoothing radii ($r = 1, 2$) and number of segments ($k = 5, 10$)

Pixels with the same color indicate membership in the same segment.

Figure 4a shows the segmentations for SA clustering and Figure 4b shows the segmentations for SASA clustering.

The segments are indicated by colors, and the additional colors used in the plots with $k = 10$ reflect the additional number of segments in those segmentations.

The noisiness in the SASA clusterings for $r = 1$ seem to suggest that it is too small a radius for use with SASA clustering for this particular dataset. In both sets of clusterings – particularly the SA clusterings with $k = 10$ – we can often see distinct segments that correspond to organs such as the brain, heart, and liver.

2.3.2 Plotting the mean spectra of the segments

Likewise, we can also plot the mean spectra for the spatial segmentations. For each parameter set, the mean spectra for all segments are overlaid in Figure 5a for SA clustering (Gaussian weights) and Figure 5b for SASA clustering (adaptive weights).

```
> plot(pig206.skmg, key = FALSE, layout = c(2, 2), type = c("p", "h"), pch = 20)
```

```
> plot(pig206.skma, key = FALSE, layout = c(2, 2), type = c("p", "h"), pch = 20)
```

Figure 5a shows the mean spectra for SA clustering and Figure 5b shows mean spectra for SASA clustering.

Like PCA, spatially-aware k-means clustering is useful for quickly visualizing an MS imaging dataset, but additional analysis is required for statistically-meaningful results.

Unsupervised analysis of MS images using Cardinal

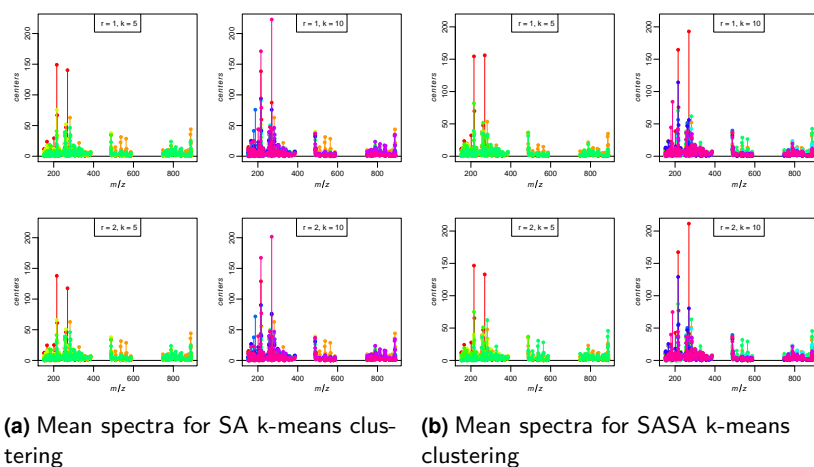


Figure 5: The mean spectra for spatially-aware (SA) and spatially-aware structurally-adaptive (SASA) k-means clustering with varying smoothing radii ($r = 1, 2$) and number of segments ($k = 5, 10$)

Colors indicate the segment from which each mean spectrum is calculated (corresponding segments can be found in Figure 4a and Figure 4b).

2.4 Spatial segmentation using spatial shrunken centroids clustering

This section demonstrates the spatial shrunken centroids clustering method for statistical analysis we introduce in *Cardinal* in the `spatialShrunkenCentroids` method.

The Gaussian and adaptive weights are retained from the spatially-aware k-means clustering [3]. In addition, we introduce statistical regularization as in nearest shrunken centroids to enforce feature sparsity [4]. This means doing feature selection, so that the analysis automatically identifies informative m/z values.

The parameters to be explicitly provided in the `spatialShrunkenCentroids` method are:

- r : The neighborhood smoothing radius
- k : The initial number of segments (clusters)
- s : The shrinkage parameter

The r parameter is the same as in `spatialKMeans`. The k parameter now specifies only the *initial* number of segments. The `spatialShrunkenCentroids` method allows the number of segments to decrease according to the data. This allows automatic selection of the number of clusters.

The s parameter is the shrinkage parameter that enforces sparsity. As s increases, fewer mass features (m/z values) will be used in the spatial segmentation, and only the informative mass features will be retained.

Typically, the number of segments will also decrease as s increases. This makes sense, because as fewer mass features are used, the fewer segments they will be able to explain.

For a detailed explanation of the shrinkage parameter s , see [4] and [5].

Now we perform spatial shrunken centroids clustering with the `method="gaussian"` weights.

Unsupervised analysis of MS images using Cardinal

```
> set.seed(1)
> pig206.sscg <- spatialShrunkenCentroids(pig206.peaks, r = c(1, 2), k = c(15,
+ 20), s = c(0, 3, 6, 9), method = "gaussian")
```

```
> summary(pig206.sscg)
```

	r	k	s	method	time	Predicted # of Classes	Mean # of Features per Class
1	1	15	0	gaussian	14.557	15	143
2	1	15	3	gaussian	25.602	10	91
3	1	15	6	gaussian	32.892	7	77
4	1	15	9	gaussian	19.852	6	63
5	1	20	0	gaussian	20.906	19	143
6	1	20	3	gaussian	28.911	11	92
7	1	20	6	gaussian	27.199	8	74
8	1	20	9	gaussian	36.020	6	62
9	2	15	0	gaussian	55.460	13	143
10	2	15	3	gaussian	42.302	10	90
11	2	15	6	gaussian	40.441	6	82
12	2	15	9	gaussian	42.164	6	62
13	2	20	0	gaussian	48.375	18	143
14	2	20	3	gaussian	77.894	9	90
15	2	20	6	gaussian	50.536	6	82
16	2	20	9	gaussian	43.045	6	60

And we perform spatial shrunken centroids clustering with the method="adaptive" weights.

```
> set.seed(1)
> pig206.ssca <- spatialShrunkenCentroids(pig206.peaks, r = c(1, 2), k = c(15,
+ 20), s = c(0, 3, 6, 9), method = "adaptive")
```

```
> summary(pig206.ssca)
```

	r	k	s	method	time	Predicted # of Classes	Mean # of Features per Class
1	1	15	0	adaptive	16.397	15	143
2	1	15	3	adaptive	32.927	9	100
3	1	15	6	adaptive	39.063	6	85
4	1	15	9	adaptive	23.927	6	62
5	1	20	0	adaptive	16.943	20	143
6	1	20	3	adaptive	28.908	11	83
7	1	20	6	adaptive	25.515	8	69
8	1	20	9	adaptive	28.771	6	62
9	2	15	0	adaptive	23.259	15	143
10	2	15	3	adaptive	41.330	9	100
11	2	15	6	adaptive	34.436	8	69
12	2	15	9	adaptive	30.122	7	55
13	2	20	0	adaptive	62.661	18	143
14	2	20	3	adaptive	46.154	10	91
15	2	20	6	adaptive	51.921	7	78
16	2	20	9	adaptive	51.214	6	66

Both of the resulting objects have sixteen sets of model parameters, in the parameter space of $r = 1, 2$, $k = 15, 20$, and $s = 0, 3, 6, 9$.

Unsupervised analysis of MS images using Cardinal

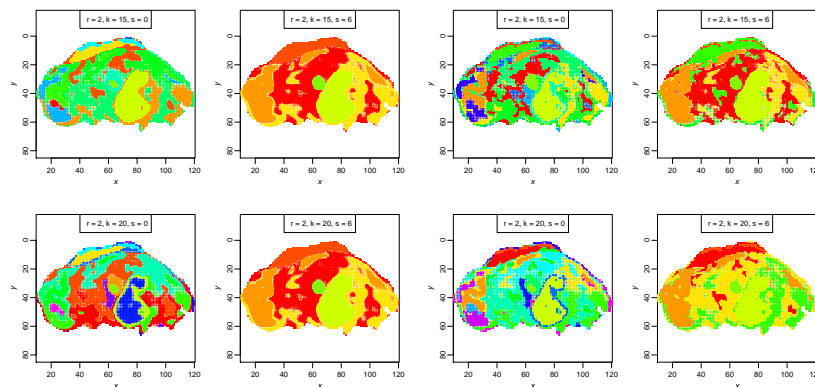
As seen in the summaries above, many of the segmentations result in fewer numbers of segments than at initialization, and the number of segments is generally lower for higher sparsity. We will show how this can be used to determine the number of segments in Section 2.4.4.

2.4.1 Plotting the spatial segmentations

We will plot four of the spatial segmentations for each of the Gaussian weights and adaptive weights. This is specified by the `model` argument, where we can list the parameters for the models we would like to plot.

```
> image(pig206.sscg, model = list(r = 2, s = c(0, 6)), key = FALSE, layout = c(2, + 2))
```

```
> image(pig206.ssca, model = list(r = 2, s = c(0, 6)), key = FALSE, layout = c(2, + 2))
```



(a) Segmentation for SSC with Gaussian weights

(b) Segmentation for SSC with adaptive weights

Figure 6: The spatial segmentations for spatial shrunken centroids clustering with Gaussian and adaptive weights, varying smoothing radii ($r = 1, 2$), initial number of segments ($k = 15, 20$), and shrinkage parameter ($s = 0, 3, 6, 9$)

Colors indicate segment membership. Opacity of the colors indicate probability of the belonging to that segment.

Figure 6a shows the segmentations for spatial shrunken centroids with Gaussian weights and Figure 6b shows the segmentations for adaptive weights.

Colors indicate segment membership, but rather than hard assignment to segments, `spatialShrunkenCentroids` produces probabilities of segment membership. We visualize these probabilistic segment assignments using opacity, where higher opacity of a color indicates higher probability of that pixel belonging to that segment.

Visualizing probabilistic segment membership is useful in quickly assessing the quality of a spatial segmentation. Low quality segmentations will yield high uncertainty in the segment assignments, resulting in low probabilities and low opacities. This means that the segmentation will appear “fuzzier” and segments will have blurry or indistinct edges. Better segmentations will have higher opacity and sharper edges.

Unsupervised analysis of MS images using Cardinal

Figure 6a and Figure 6b show that an increase the shrinkage parameter s results in fewer segments. We started the clustering iterations with both $k = 15$ and $k = 20$ initial segments, but at $s = 6$, the segmentations look very similar. For the Gaussian weights at $s = 6$, the segmentation has 6 segments for both $k = 15$ and $k = 20$. For adaptive weights at $s = 6$, both segmentations have 7 segments.

2.4.2 Plotting the (shrunk) mean spectra of the segments

As part of the feature selection process, the mean spectrum for each segment is shrunk toward the global mean spectrum. The reason for this will be discussed in Section 2.4.3. We can plot these shrunk mean spectra and interpret them by analogy to ordinary mean spectra.

```
> plot(pig206.sscg, model = list(r = 2, s = c(0, 6)), key = FALSE, layout = c(2, + 2), type = c("p", "h"), pch = 20)
```

```
> plot(pig206.ssca, model = list(r = 2, s = c(0, 6)), key = FALSE, layout = c(2, + 2), type = c("p", "h"), pch = 20)
```

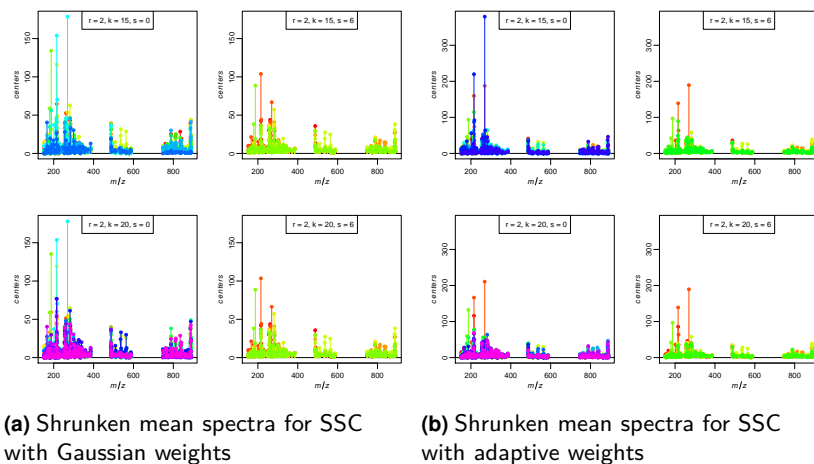


Figure 7: The shrunken mean spectra for spatial shrunken centroids for Gaussian and adaptive weights with varying smoothing radii ($r = 1, 2$), initial number of segments ($k = 5, 10$), and shrinkage parameter ($s = 0, 3, 6, 9$)

Colors indicate the segment from which each shrunken mean spectrum is calculated (corresponding segments can be found in Figure 6a and Figure 6b).

Figure 7a shows the shrunken mean spectra for spatial shrunken centroids with Gaussian weights and Figure 7b shows the shrunken mean spectra for adaptive weights.

2.4.3 Plotting and interpreting the t-statistics of the m/z values

An important goal of our approach to spatial segmentation is that we not only want a meaningful segmentation, but we also want to be able to identify and rank the important mass features that inform that segmentation. The `spatialShrunkenCentroids` method produces t-statistics for this purpose.

Unsupervised analysis of MS images using Cardinal

For each mass feature (m/z value), t-statistics are calculated for each segment as in [4] and [5], by comparison to the global mean spectrum.

Positive t-statistics correspond to systematic enrichment in that segment. Negative t-statistics correspond to systematic absence from that segment. The shrinkage parameter s is used to shrink t-statistics toward 0, and when a t-statistic is set to 0, that mass feature is no longer used to determine segment membership.

```
> plot(pig206.sscg, mode = "tstatistics", model = list(r = 2, s = c(0, 6)), key = FALSE,
+      layout = c(2, 2), type = c("p", "h"), pch = 20)
```

```
> plot(pig206.ssca, mode = "tstatistics", model = list(r = 2, s = c(0, 6)), key = FALSE,
+      layout = c(2, 2), type = c("p", "h"), pch = 20)
```

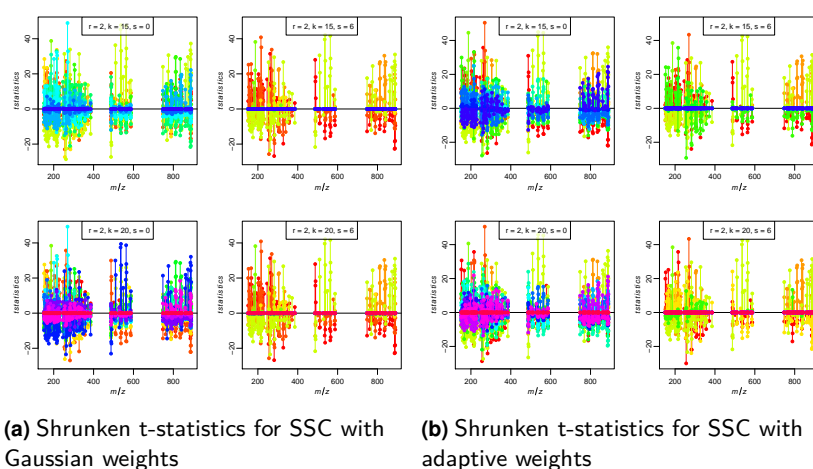


Figure 8: The shrunken t-statistics for spatial shrunken centroids for Gaussian and adaptive weights with varying smoothing radii ($r = 1, 2$), initial number of segments ($k = 5, 10$), and shrinkage parameter ($s = 0, 3, 6, 9$)

Colors indicate the segment from which the t-statistics are calculated (corresponding segments can be found in Figure 6a and Figure 6b).

Note in Figure 8a and Figure 8b that the segments that disappear as s increases from $s = 0$ to $s = 6$ generally have low t-statistics. These low t-statistics are quickly driven to 0, and their segments are removed from the model and joined with other segments.

The top m/z values for a segmentation can be queried using the `topLabels` method.

```
> topLabels(pig206.sscg, n = 20)
```

	mz	r	k	s	classes	centers	tstatistics	p.values	adj.p.values
1	269.3333	2	20	0	11	177.93947	49.26370	0	0
2	269.3333	2	15	0	11	178.60039	48.95050	0	0
3	269.3333	1	20	0	11	167.71484	48.59475	0	0
4	269.3333	1	15	0	11	168.12032	48.50941	0	0
5	537.2500	2	15	0	5	31.48324	47.73488	0	0
6	537.2500	1	15	0	5	31.72642	47.64653	0	0
7	269.3333	1	15	3	4	165.49849	47.43609	0	0
8	269.3333	1	20	3	11	165.49371	47.41058	0	0
9	563.2500	2	15	0	5	28.73309	47.40687	0	0

Unsupervised analysis of MS images using Cardinal

```
10 563.2500 1 15 0      5 28.93201  47.25001      0      0
11 537.2500 1 20 0      14 31.81774  47.21773      0      0
12 563.2500 1 20 0      14 29.01530  46.81710      0      0
13 537.2500 1 20 3      5 29.67071  45.47840      0      0
14 537.2500 1 15 3      5 29.67604  45.46918      0      0
15 269.3333 2 15 3      4 116.89795  45.39698      0      0
16 535.2500 2 15 0      5 22.89653  45.32567      0      0
17 537.2500 2 20 3      5 29.25750  45.29100      0      0
18 535.2500 1 15 0      5 23.06823  45.20485      0      0
19 537.2500 2 15 3      5 29.60737  45.15213      0      0
20 563.2500 1 20 3      5 26.98541  45.12665      0      0
```

This list can be filtered by the segment, model parameters, etc.

```
> topLabels(pig206.sscg, model = list(r = 2, s = 6, k = 20), filter = list(classes = 5))
      mz r k s classes centers tstatistics p.values adj.p.values
1 537.2500 2 20 6      5 27.35050  42.19177      0      0
2 563.2500 2 20 6      5 24.70218  41.70469      0      0
3 535.2500 2 20 6      5 19.56177  39.62103      0      0
4 887.6667 2 20 6      5 38.07015  31.04249      0      0
5 509.2500 2 20 6      5 12.68780  30.56082      0      0
6 281.6667 2 20 6      5 57.27400  29.44007      0      0
```

See `?topLabels` for details. This will be explored further in Section 2.4.5.

2.4.4 Identifying the number of segments

A unique property of our spatial shrunken centroids clustering is that it facilitates a natural way to identify an appropriate number of segments for a segmentation. We do this by plotting the number of predicted segments against the shrinkage parameter s as shown below in Figure 9a. For this dataset, adaptive weights appear to offer no advantage over Gaussian weights, so we focus on the segmentations with Gaussian weights.

```
> plot(summary(pig206.sscg), main = "Number of segments")
```

In Figure 9a, we look for the shrinkage parameter s for which the predicted number of segments match up between different initialized numbers of segments k . For $r = 2$, this occurs at $s = 6$, and we can also see from Figure 6a earlier that the final segmentations for both $k = 15$ and $k = 20$ at $s = 6$ are nearly identical. This suggests that either of these models are appropriate segmentations.

Therefore, we choose the segmentation with Gaussian weights with $r = 2, k = 20, s = 6$ for further exploration. This segmentation is plotted with custom colors in Figure 9b.

```
> mycol <- c(internal1 = "#FD9827", back = "#42FD24", internal2 = "#1995FC", brain = "#FC23D9",
+   liver = "#3524FB", heart = "#FC0D1B", bg = "#CDFD34")
> image(pig206.sscg, model = list(r = 2, k = 20, s = 6), key = FALSE, col = mycol,
+   main = "Selected segmentation")
```

Typically, we recommend choosing the segmentation with the most retained features (least sparsity) after which the predicted number of segmentations become approximately equal between different initializations of k .

Unsupervised analysis of MS images using Cardinal

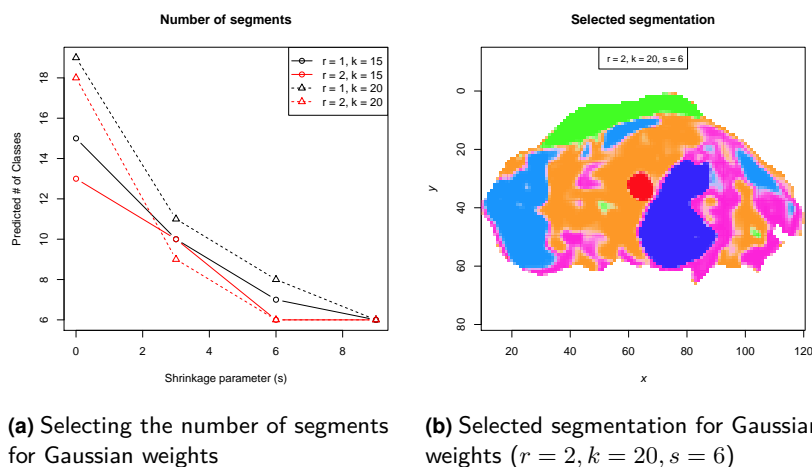


Figure 9: Plotting the predicted number of segments shows that for Gaussian weights and $r=2$, the resulting number of segments coincide after $s=6$

Therefore, we choose the segmentation for $r=2, k=20, s=6$, which results in 6 segments.

2.4.5 Interpreting the spatial segmentation

To further explore the spatial segmentation we selected in Section 2.4.4, we want to create plots that show the mass features that are important in distinguishing certain segments.

For this purpose, we write a function `summaryPlot` that will plot the probabilities for a segment, plot its shrunken mean spectrum and t-statistics, and plot the top 3 ion images associated with the segment.

```
> summaryPlots <- function(dataset, results, model, segment, name, col) {  
+   image(results, model = model, key = FALSE, column = segment, main = name,  
+     layout = c(3, 2), col = col)  
+   plot(results, model = model, key = FALSE, column = segment, mode = "centers",  
+     main = "Shrunken mean spectrum", col = col)  
+   plot(results, model = model, key = FALSE, column = segment, mode = "tstatistics",  
+     main = "Shrunken t-statistics", col = col)  
+   top <- topLabels(results, n = 3, model = model, filter = list(classes = segment))  
+   image(dataset, mz = top$mz, normalize.image = "linear", contrast.enhance = "histogram",  
+     smooth.image = "gaussian")  
+ }
```

Now we create these summary plots for the segment associated with the liver.

```
> summaryPlots(pig206, pig206.sscg, model = list(r = 2, s = 6, k = 20), segment = 5,  
+   name = "Liver segment", col = mycol)
```

From the shrunken mean spectrum and t-statistics plot in Figure 11, we can see that many of the mass features in the m/z 500–600 range and m/z 800–900 range are positively associated with the liver from their high positive t-statistics, showing that they are systematically enriched in the liver. Many of the low mass range features are negatively associated with the liver, as seen by their negative t-statistics, showing that they are systematically absent in the liver. The three top ions associated with the liver are also plotted.

Unsupervised analysis of MS images using Cardinal

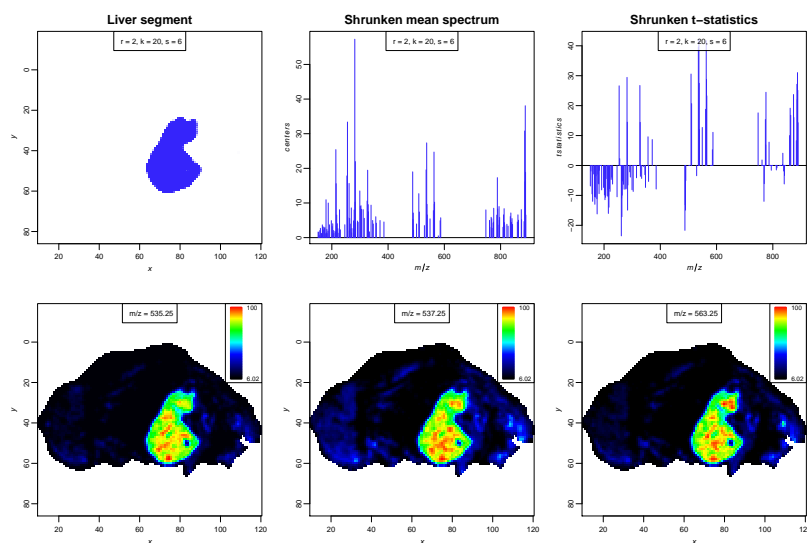


Figure 10: Summary plots of the liver segment for PIGII_206 segmentation with Gaussian weights and $r = 2, k = 20, s = 6$

To contrast with the liver segment, we do the same for the heart segment below.

```
> summaryPlots(pig206, pig206.sscg, model = list(r = 2, s = 6, k = 20), segment = 6,  
+ name = "Heart segment", col = mycol)
```

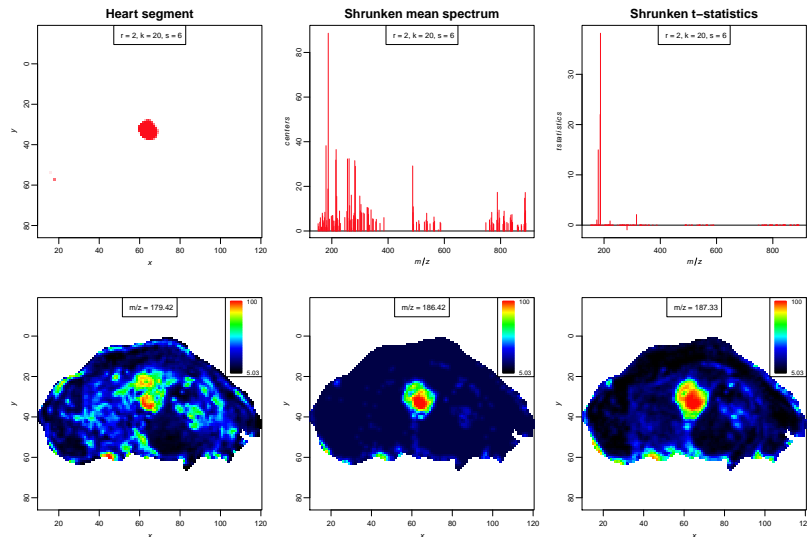


Figure 11: Summary plots of the heart segment for PIGII_206 segmentation with Gaussian weights and $r = 2, k = 20, s = 6$

Compared to the liver segment, we see that for the heart segment, only a few mass features have non-zero t-statistics. This shows that fewer ions are associated with the heart compared to the liver.

3 Additional example

A difficulty with evaluating spatial segmentation methods is that typically the ground truth is not known. Our experimental subjects are often complex biological systems, and there is usually no “gold standard” to compare with our results.

We now perform spatial segmentation on an MS image for which the ground truth is known.

3.1 Evaluation using a cardinal painting

In this first example, we present an oil painting of a cardinal, created to illustrate the utility of DESI imaging. Mass spectra were collected from the pigments in the paint, and we expect that different colors will produce unique patterns of spectral peaks, allowing for spatial segmentation.

```
> data(cardinal, cardinal_analyses)
```

We normalize the data using TIC normalization.

```
> cardinal.norm <- normalize(cardinal, method = "tic")
```

Now we perform peak-picking and alignment as in Section 2.1.2.

```
> cardinal.peaklist <- peakPick(cardinal.norm, pixel = seq(1, ncol(cardinal),  
+   by = 10), method = "simple", SNR = 6)  
> cardinal.peaklist <- peakAlign(cardinal.peaklist, ref = cardinal.norm, method = "diff",  
+   units = "ppm", diff.max = 200)  
> cardinal.peaklist <- peakFilter(cardinal.peaklist, method = "freq", freq.min = ncol(cardinal.peaklist)/10,  
> cardinal.peaks <- reduceDimension(cardinal.norm, ref = cardinal.peaklist, type = "height")
```

Next we perform spatial shrunken centroids clustering on the dataset, with both Gaussian and adaptive weights and a range of parameters for r , k , and s .

```
> set.seed(1)  
> cardinal.sscg <- spatialShrunkenCentroids(cardinal.peaks, r = c(1, 2), k = c(10,  
+   15), s = c(0, 3, 6, 9), method = "gaussian")  
> set.seed(1)  
> cardinal.sscg <- spatialShrunkenCentroids(cardinal.peaks, r = c(1, 2), k = c(10,  
+   15), s = c(0, 3, 6, 9), method = "adaptive")
```

As in Section 2.4.4, we plot the predicted number of classes against the shrinkage parameter s to help determine the most appropriate model parameters for the data. Figure 12d shows this plot for the segmentations with Gaussian weights, and Figure 12e shows this for adaptive weights.

```
> plot(summary(cardinal.sscg))
```

```
> plot(summary(cardinal.sscg))
```


Unsupervised analysis of MS images using Cardinal

For adaptive weights, the predicted number of segments quickly converge at $s = 3$, while the same does not happen for Gaussian weights until $s = 9$. This is likely because adaptive weights are more appropriate for this dataset, in order to fit the thin “DESI-MS” writing below the cardinal.

We plot the segmentation for $r = 1, k = 10, s = 3$, resulting in 8 segments, shown in Figure 12b.

```
> mycol <- c("#5C605C", "#4D2C36", "#A1A1A1", "#999999", "#B02020", "#1B1B1B",
+           "#901010", "#906565")
> image(cardinal.sscg, model = list(r = 1, k = 10, s = 3), key = FALSE, col = mycol)
```

We also plot the segmentation for $r = 2, k = 10, s = 3$, resulting in 8 segments, shown in Figure 12c.

```
> mycol <- c("#1B1B1B", "#A1A1A1", "#906565", "#999999", "#B02020", "#901010",
+           "#5C605C", "#4D2C36")
> image(cardinal.ssca, model = list(r = 2, k = 10, s = 3), key = FALSE, col = mycol)
```

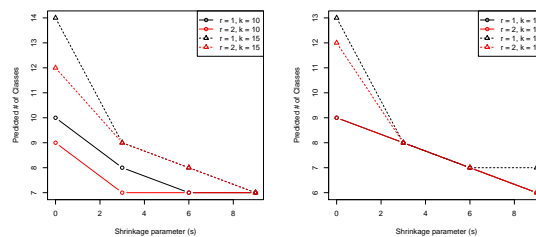
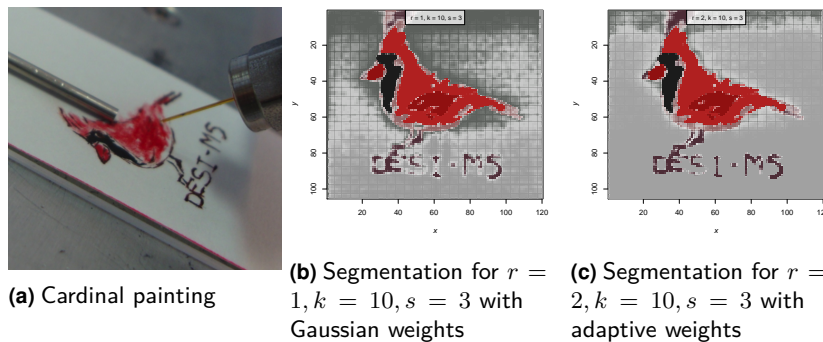


Figure 12: Spatial segmentation of the cardinal painting for both Gaussian and adaptive weights, and the plots for selecting the number of segments

For Gaussian weights, we choose $r = 1$ so that the “DESI-MS” writing is not oversmoothed, and $s = 3$, where the the predicted number of segments are nearly convergent at 8 segments and 9 segments for $k = 10$ and $k = 15$, respectively.

For adaptive weights, we choose $r = 2, s = 3$, since with the adaptive weights we can use a larger smoothing radius without oversmoothing, and the number of segments first converge between both initializations for k at $s = 3$.

Unsupervised analysis of MS images using Cardinal

We note that the segmentation matches up well against the original painting, so the method is performing well.

4 Session info

- R version 3.5.0 (2018-04-23), x86_64-pc-linux-gnu
- Locale: LC_CTYPE=en_US.UTF-8, LC_NUMERIC=C, LC_TIME=en_US.UTF-8, LC_COLLATE=C, LC_MONETARY=en_US.UTF-8, LC_MESSAGES=en_US.UTF-8, LC_PAPER=en_US.UTF-8, LC_NAME=C, LC_ADDRESS=C, LC_TELEPHONE=C, LC_MEASUREMENT=en_US.UTF-8, LC_IDENTIFICATION=C
- Running under: Ubuntu 16.04.4 LTS
- Matrix products: default
- BLAS: /home/biocbuild/bbs-3.7-bioc/R/lib/libRblas.so
- LAPACK: /home/biocbuild/bbs-3.7-bioc/R/lib/libRlapack.so
- Base packages: base, datasets, grDevices, graphics, methods, parallel, stats, utils
- Other packages: Biobase 2.40.0, BiocGenerics 0.26.0, Cardinal 1.12.0, CardinalWorkflows 1.12.0, DBI 0.8, ProtGenerics 1.12.0, biglm 0.9-1, matter 1.6.0
- Loaded via a namespace (and not attached): BiocStyle 2.8.0, MASS 7.3-50, Matrix 1.2-14, Rcpp 0.12.16, backports 1.1.2, compiler 3.5.0, digest 0.6.15, evaluate 0.10.1, grid 3.5.0, htmltools 0.3.6, irlba 2.3.2, knitr 1.20, lattice 0.20-35, magrittr 1.5, rmarkdown 1.9, rprojroot 1.3-2, signal 0.7-6, sp 1.2-7, stats4 3.5.0, stringi 1.1.7, stringr 1.3.0, tools 3.5.0, yaml 2.1.18

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- [3] Theodore Alexandrov and Jan Hendrik Kobarg. Efficient spatial segmentation of large imaging mass spectrometry datasets with spatially aware clustering. *Bioinformatics (Oxford, England)*, 27(13):i230–8, July 2011. URL: <http://www.pubmedcentral.nih.gov/articlerender.fcgi?artid=3117346&tool=pmcentrez&rendertype=abstract>, doi:10.1093/bioinformatics/btr246.
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Unsupervised analysis of MS images using Cardinal

- [5] Robert Tibshirani, Trevor Hastie, Balasubramanian Narasimhan, and Gilbert Chu. Class Prediction by Nearest Shrunken with Applications to DNA Microarrays. *Statistical Science*, 18(1):104–117, 2003.