

INTRODUCTION

Atrial fibrillation (AF) is a common cardiac arrhythmia caused by abnormal bioelectricity originating in some parts of tissues in the left atrium [1]. AF can be treated by destroying those tissues or creating scar tissue to prevent the bioelectricity from spreading. Recently, radiofrequency ablation (RFA) has been used to burn the tissues, and electrical conduction testing is used to determine the ablated region [2]. Electro-anatomical mapping can improve RFA therapy success rates. This method needs to visualize the ablated region directly during the operation. MRI and CT had been proposed for this testing, but these methods are expensive, space-consuming and do not provide real-time monitoring [3,4]. Therefore, we apply another visualization approach called **auto-fluorescence hyperspectral imaging (aHSI)** [5] (Fig.1).

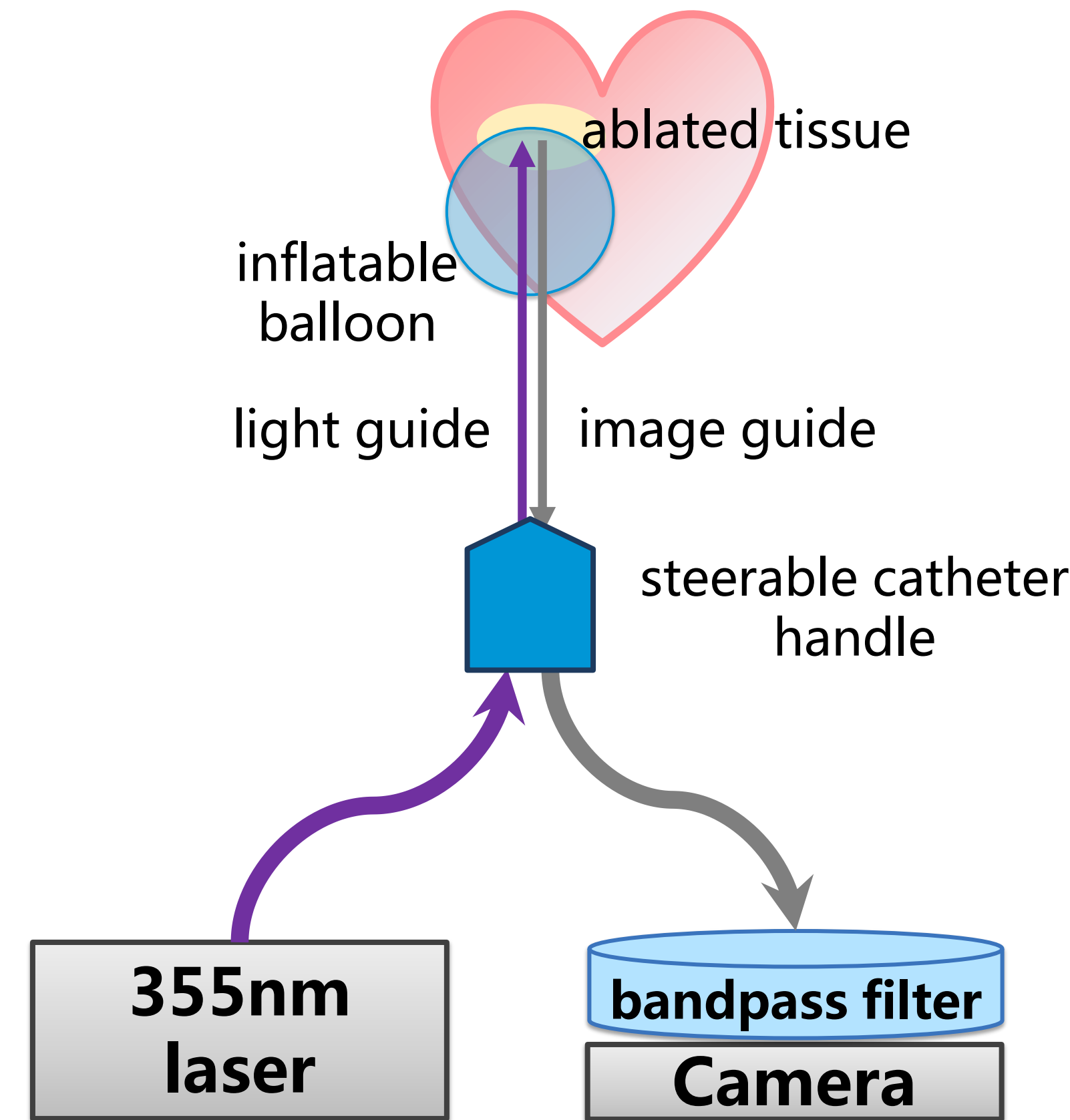


Fig.1. aHSI system

DATA

The auto-fluorescence is retrieved through a fiber-optic guide and forms images at the camera in different wave-lengths from **420nm to 720nm (interval is 10nm)**. We acquire the images simultaneously; each presents a certain wave-length of auto-fluorescence for that region. These images can construct a **data-cube**. Images are ordered by their wave-length increasingly on the spectral (Z) dimension. Each pixel on the X-Y plane thus has an associated spectrum V_{ij} (Fig.2).

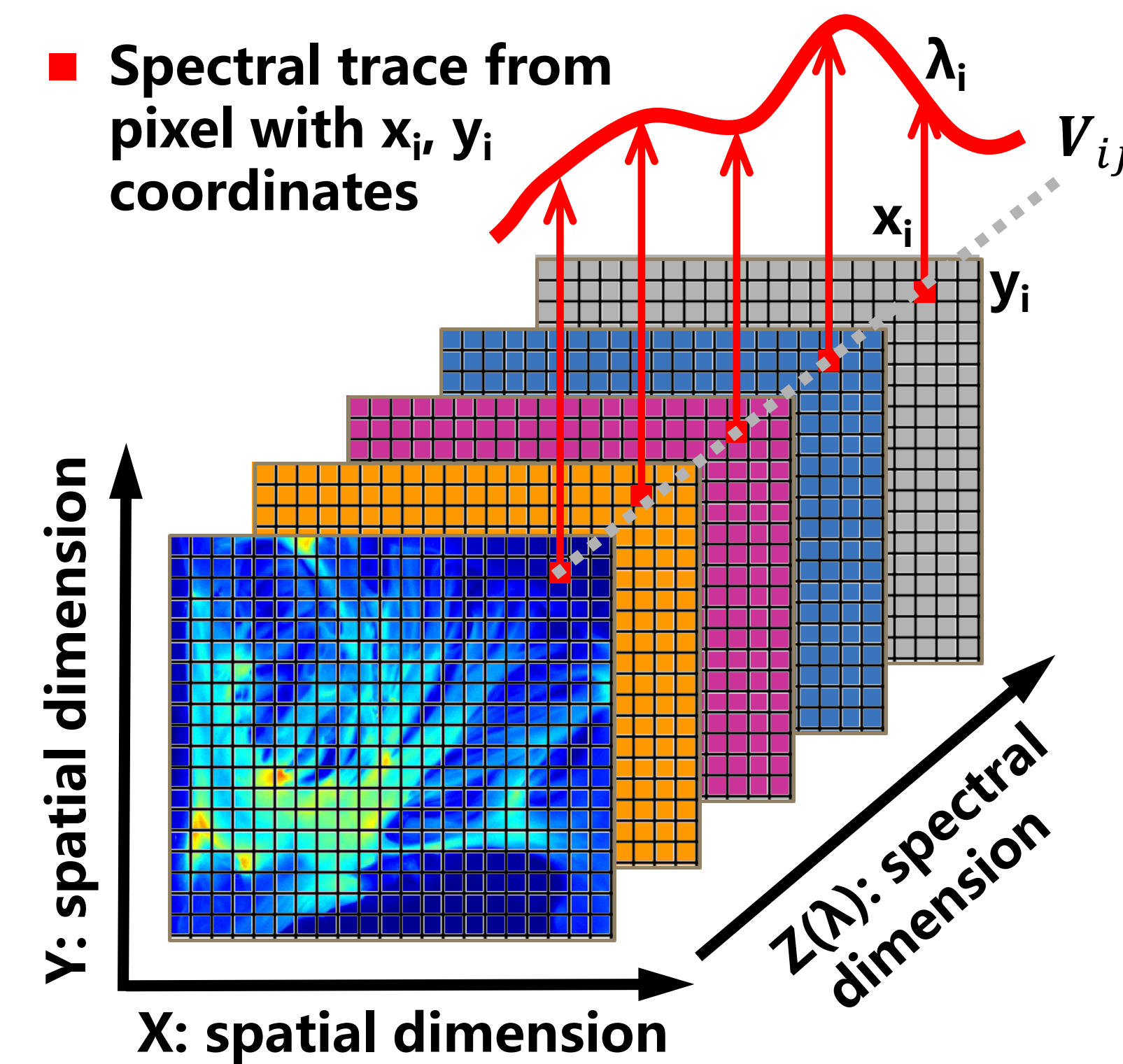
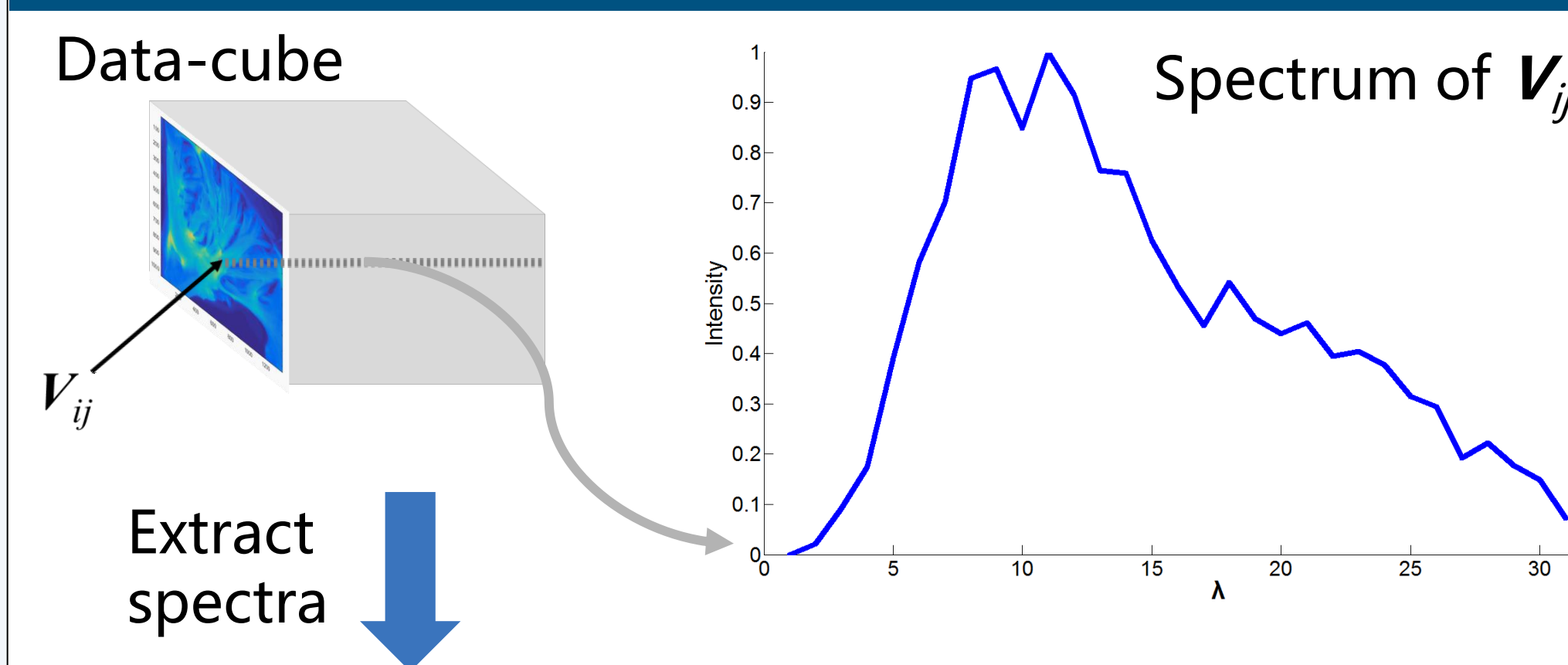


Fig.2. Data-cube of HSI images

QUESTIONS

(1) To **detect the lesion areas** from auto-fluorescence images. (2) To **decrease the number of auto-fluorescence images** without influencing the accuracy of lesion detection through bandpass filter. This will not only speed-up the processing, but also make the output images more robust to noise. That is because the total light energy that the catheter can deliver is limited. Thus, the energy should be concentrated on the most useful wavelength bands.

METHODS



Use k-means to group the spectra. Every pixel has been assigned a label from {1,2,3,...,k}.

Fig.3. Spectral clustering

We cluster these samples into k groups by **k-means clustering** and assign labels to each group. Then, we put these labels back onto the X-Y plane by keeping their original locations, and assign a different color to each label so that we can see the lesion (special) areas (Fig.6b).

Given a input set $\{x_i\}$ has n d -dimensional real vectors, **k-means clustering** partitions the n vectors into k ($k \leq n$) sets $S = \{s_1, s_2, \dots, s_k\}$ and minimizes the within-cluster sum of squares:

$$\arg \min_S \sum_{j=1}^k \sum_{x \in s_j} \|x - \mu_j\|^2$$

μ_j is the mean of vectors in s_j .

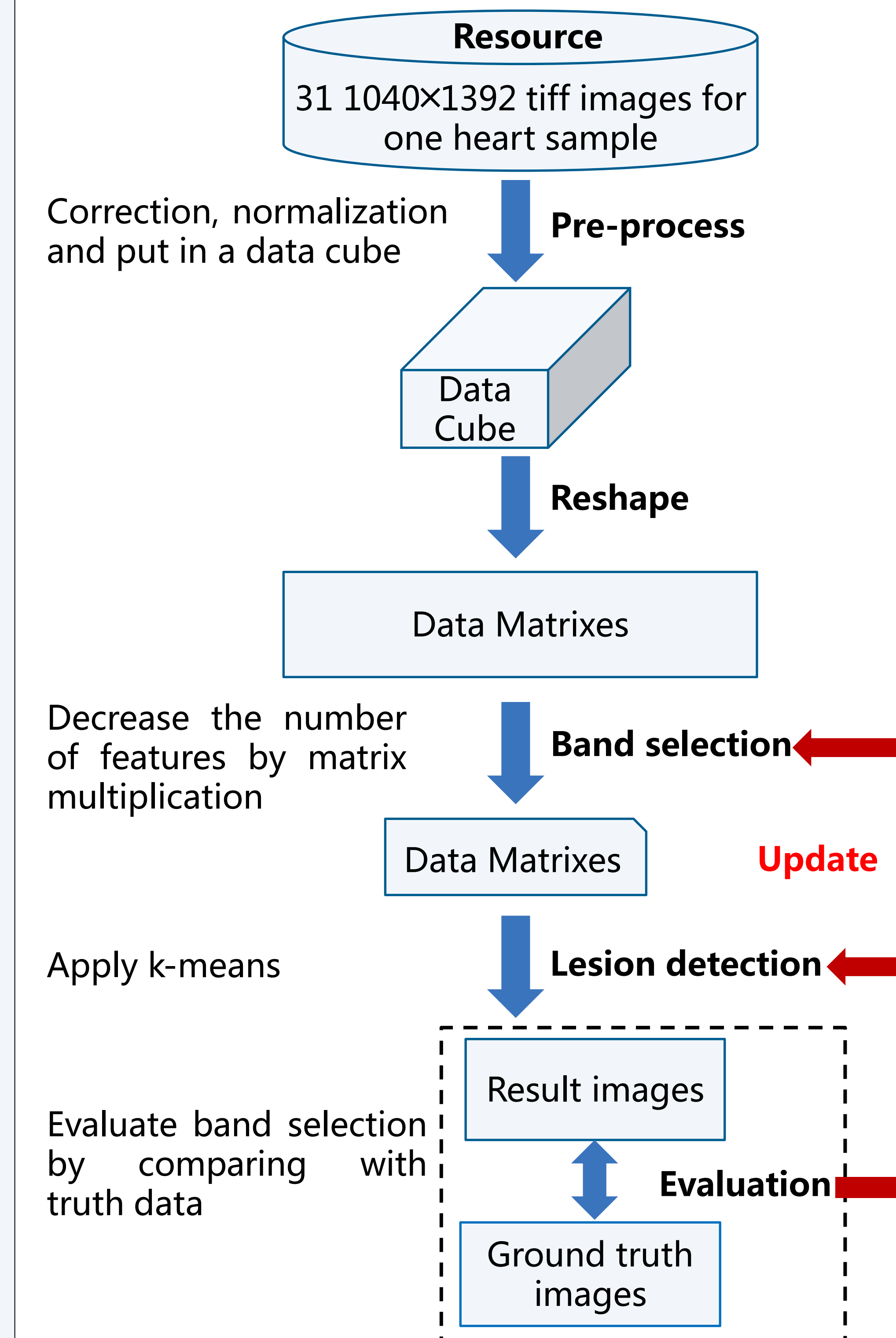


Fig.4. The general process

To decrease the number of features, we break the 31 features (in each vector) into contiguous groups. In each group, we calculate the **sum** (Fig.5) of values as a new feature value. The next step is using k-means to **detect lesion areas** through these selected features. By comparing the detected lesion areas with ground truth lesion areas pixel by pixel, we can get the **accuracy** of detected result.

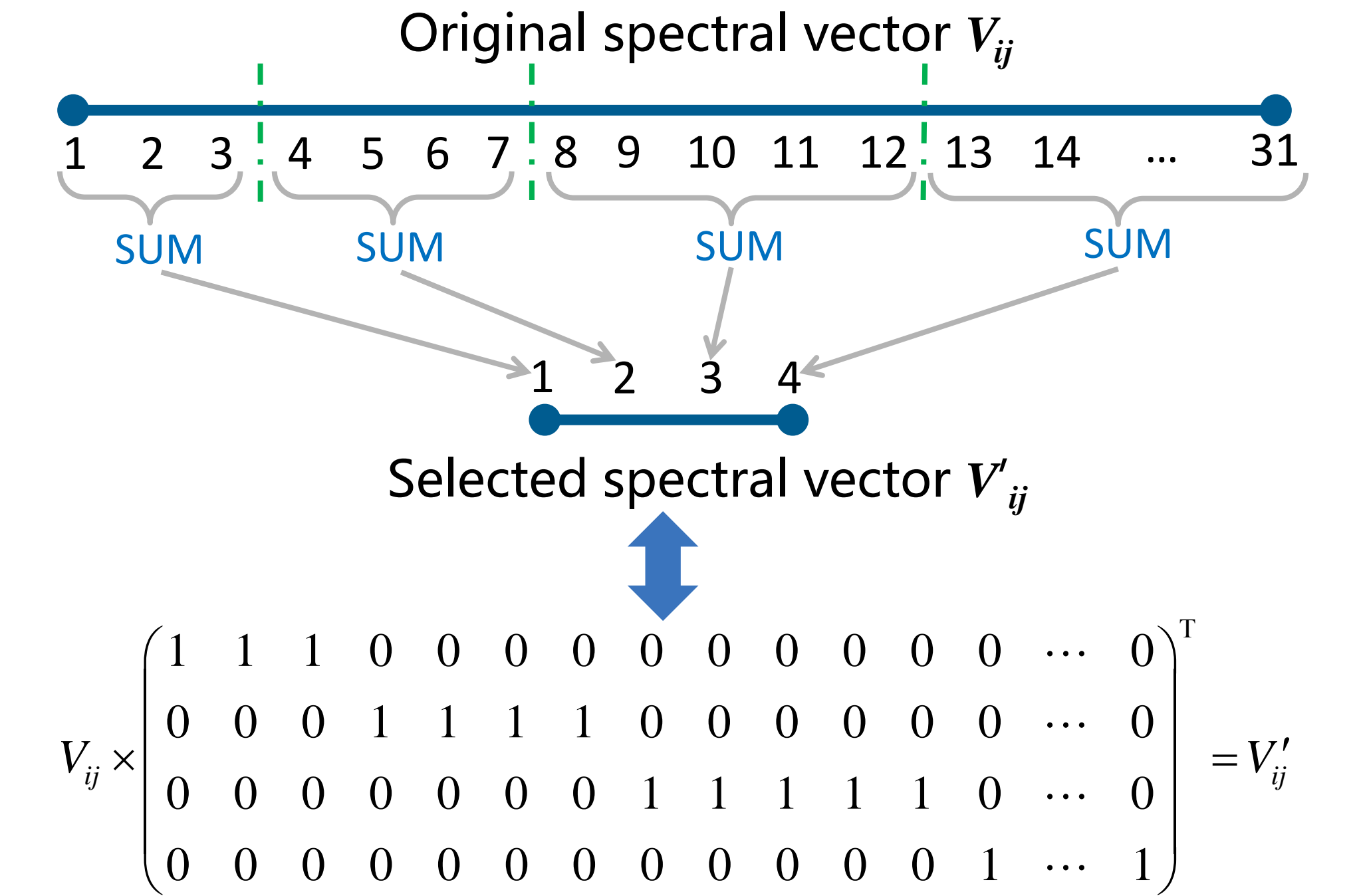


Fig.5. One kind of 4-bands selection

RESULTS

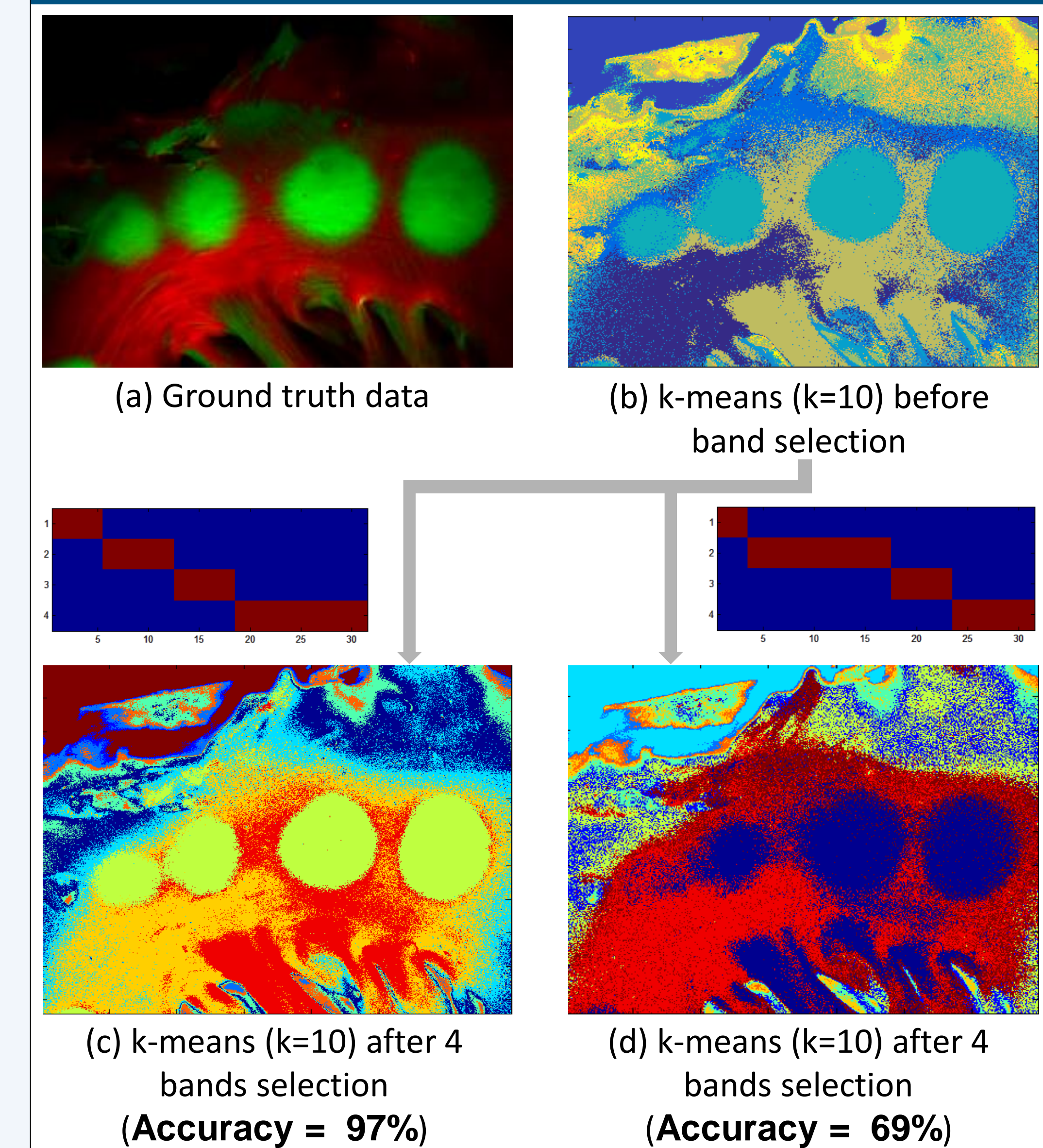


Fig.6. Band selection results

ACKNOWLEDGMENT & REFERENCES

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