Nonparametric Color Clustering in Chrominance Plane by Parzen Window

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Abstract

Image segmentation is a first step to vision system and used for many applications such as pattern recognition, image classification, understanding, or picture coding. In the previous work, we reported unsupervised image segmentation by our ***k-means Bayesian*** *classifier and applied it to automatic scene color interchange. Although* ***Bayesian*** *decision rule is a robust tool based on the minimum error criterion, it needs to preset any appropriate class centers before starting the classifier. Since the location of initial seed points much influences segmentation accuracy, the better color clustering is a key to success for image segmentation.*

This paper presents a novel approach to a ***non-parametric*** *color clustering by introducing* ***Parzen window*** *and discusses how to estimate the probability density function and how to preset the reliable seed points. The paper proposes a* ***Particle*** *model as an alternative and fast algorithm for* ***Parzen window*** *model. Experimental results applied to unsupervised image segmentation are demonstrated.*

Introduction

Color Image segmentation plays an important role in many applications. Color clustering is a low-level task in the first stage of pattern classification and a basis for image segmentation that aims at partitioning the pixel data into homogeneous regions. Among a great number of clustering algorithms, perhaps ***k-means*** algorithm is most popular and widely used. It's an iterative method for finding the optimum centroid in cluster as a local minimum solution based on Lloyd's algorithm [1]. Although a study on efficient ***k-means*** [2] to find the better candidate centers is lasting, nonparametric clustering algorithm is necessary for unsupervised image segmentation. For example, ***mean shift*** model [3] is based on local maxima of the probability density function in the joint color-spatial domain. The detection of saddle points to estimate the density on the clustering boundary is newly introduced to this model [4].

Since color clustering has a drawback in nonuse of spatial information, ***JSEG*** [5] introduced an excellent post-processing of region growing and region merging to avoid over segmentations. However ***JSEG*** doesn't use color clustering algorithm but simple color quantization process to make-up the class-map in the first stage. In the previous work [6], we introduced ***Bayesian*** classifier and improved the model by a combination with ***JSEG*** [7], but the results depended heavily on the initial "*seed*" points in the first stage of color clustering. We placed the initial seed points at the center of gravity in a sampled box with the higher population density of pixel colors and improved the performance of *"k-means"*. In our model, ***k-means*** works as a pre-processor to move these initial seed points into the more reliable centers, then to drive the main ***Bayesian*** classifier. Our ***k-means+Bayesian*** model [8] worked better, but nevertheless the optimum selection of initial seed points is left for more improvement to reflect the image color distribution.

This paper focuses the "*nonparametric*" color clustering algorithm on the placement of initial seeds points from a different point of view and discusses how to estimate the probabilistic density function and find the mountain peaks of naïve distribution.

The paper introduces the following ideas.

- 2-D "***Parzen window***" estimates the probability density of image color distribution and searches the initial seed points in "***chrominance plane***" because the colored object is mainly characterized by "*hue*" and "*chroma*" features.
- 3-D "***Parzen window***" is equivalently formed by synthesizing the three 2-D probability density planes in "*a*-b*", "a*-L*"* and "*b*-L**" in CIELAB space.
- A binary "***Particle***" model is proposed for the faster search of probability density peaks as a substitute for *Parzen window*.
- "***Spatial filter***" is applied following the *Parzen window* to find the local maxima in the probability density distribution.
- The extracted seed candidates with the coordinates close to each other are merged to avoid over-segmentation.
- The obtained initial seed points are fed to the next ***k-means*** process and corrected.
- Finally, the corrected seed points by ***k-means*** drive the main ***Bayesian*** classifier.

Fig.1 shows the overview of proposed basic 2-D model.

Chrominance Density by Parzen Window

Non-parametric Color Density Estimation

Supposing that N pixel samples in 2-dimensional a^*-b^* chrominance plane of CIELAB space

$$\boldsymbol{X}_i = \left[a_i^*, b_i^*\right]^t ; i = 1 \sim N \tag{1}$$

are distributed according to the probabilistic density function $p(\boldsymbol{X})$, the probability P that a vector $\boldsymbol{X}$ will fall in a region R is given by

$$P = \int_R p(\boldsymbol{X}) d\boldsymbol{X} \tag{2}$$

Assuming k training samples are included in the region R, the probability taking k *out of* n for binomial density is given by

$$P_k = \binom{n}{k} P^k (1-P)^{n-k} \tag{3}$$

The expected value for k is given by binomial theorem as

$$E[k] = \sum_{k=1}^{n} k P_k = nP, \quad P = \frac{k}{n} \tag{4}$$

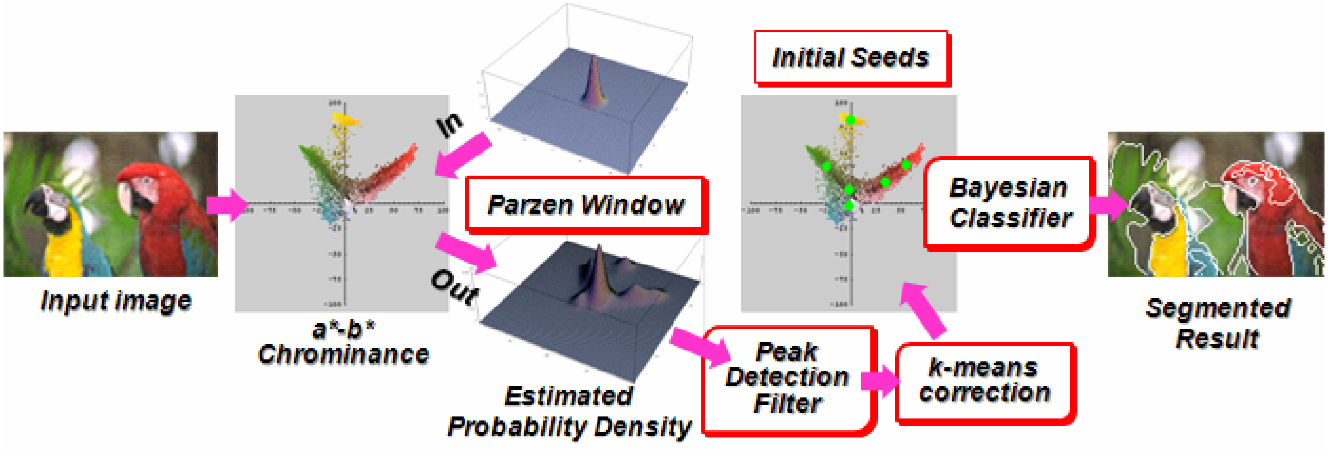


***Figure 1.** Overview of proposed model (Basic 2-D model)*

When $p(\boldsymbol{X})$ is continuous and region R has a small volume V,

$$\int_R p(\boldsymbol{X})d\boldsymbol{X} \cong p(\boldsymbol{X})V, \text{ then } p(\boldsymbol{X}) \cong k/nV \tag{5}$$

Parzen Window

Assuming that the region R_n is a d-dimensional hyper cube with the side length of h_n, its volume is $V_n = h_n{}^d$.

Here we use a Gaussian function as Parzen window [9]

$$\varphi(u,v) = \frac{1}{\sqrt{2\pi}} exp\left[-0.5\left(u^2+v^2\right)\right] \tag{6}$$

The number of samples falling in the hyper cube centered at $\boldsymbol{X} = [a^*, b^*]^t$ is given by

$$k_n = \sum_{i=1}^{n} \varphi_n\left(\frac{\boldsymbol{X}-\boldsymbol{X}_i}{h_n}\right) \tag{7}$$

Thus, the probability density function is estimated as

$$\begin{aligned} p(a^*,b^*) &= \frac{1}{n}\sum_{i=1}^{n}\frac{1}{V_n}\varphi_n\left(\frac{\boldsymbol{X}-\boldsymbol{X}_i}{h_n}\right) \\ &= \frac{1}{n}\sum_{i=1}^{n}\frac{1}{\sqrt{2\pi h_n}} exp\left[-\frac{1}{2}\left\{\left(\frac{a^*-a_i{}^*}{h_n}\right)+\left(\frac{b^*-b_i{}^*}{h_n}\right)\right\}\right] \end{aligned} \tag{8}$$

In practice, h_n is decided depending on the trained sample number n, like as $h_n = h_1/\sqrt{n}$. The selection of window size h_1 and sample number n can be problematic.

Detection of Maximum Probability Density in Chromatic Mountain

Searching for Mountain Peaks by Spatial Filter

The maximum points on the ridges of estimated probability density function will be the promising candidates for the initial seeds. The mountain peaks are detected by a local spatial filter.

Most simply, the estimated $p(a^*,b^*)$ in Eq. (8) is scanned by 3 × 3 mask operator and the maximum peaks are detected at the position that the center cell in the mask has the largest value than any other surrounding 8 neighbors.

The seed points are given by the CIELAB address $\boldsymbol{\mu}_k$ of the detected maxima as

$$Seed = \{\boldsymbol{\mu}_k\} = arg \overset{max}{\boldsymbol{X}_k}\{p(a^*,b^*)\} \tag{9}$$

Fig.2 illustrates the shape of Gaussian Parzen window function $\varphi_n(\boldsymbol{X}/h_n)$ for two different values of h_n and the estimated probability density function for a sample image "*parrot*". The narrower window width h_n gives the higher resolution but causes noisy estimation, while the wider h_n gives a smoothed density function but loses the details.

The sample shows 8 mountain peaks detected for the image "*parrot*" in CIELAB a^*-b^* chrominance plane. The "*red-marked"* points are the detected peaks by ***Parzen** window*

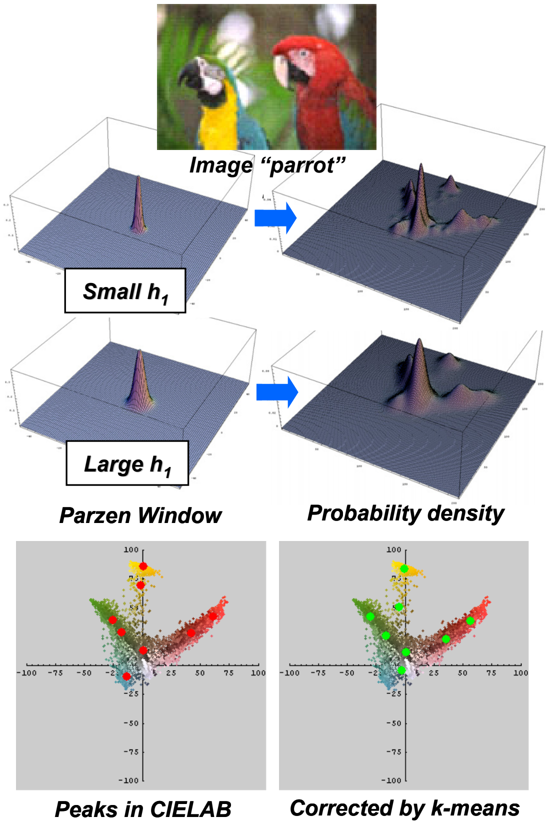


***Figure2.** Detection of maximum probability density by Parzen window*

and these initial seeds positions are moved into the more reliable cluster centers by ***k-means*** as shown in the "*green-marked*" points.

Elimination of Multiple Peaks

The peaks with close addresses are occasionally detected due to a small fluctuation around uncertain mixed color clusters. Since these multiple peaks may cause *over segmentation*, they are unified or thinned out. The multiple peaks located within $\Delta E^*_{ab}=d_{min}$ is unified to the representative single address.

Correction of Seed Points by k-means

In order to place the seed candidates $\boldsymbol{\mu}_{seed}(j)$ at the right position, ***k-means*** clustering is applied to move the selected $\boldsymbol{\mu}_{seed}(j)$ into the more plausible address.

k-means algorithm partitions N data points into j=1~J disjoint subsets $\boldsymbol{S}_j$ containing N_j data points so as to minimize the following sum-of-squares criterion,

$$E_j = min\sum_{j=!}^{J}\sum_{i\subseteq S_j}\left|\boldsymbol{X}_i-\boldsymbol{\mu}_j\right|^2 \qquad (10)$$

Where $\boldsymbol{\mu}_j$ is the geometric centroid of the data points in $\boldsymbol{S}_j$. First the initial seed points $\boldsymbol{\mu}_{seed}(j)$ are assigned to j=1~J classes, then the centroid is recomputed after clustering and the seed points are renewed. The renewal is continued until no further change occurs in the centroid by iteration.

Although ***k-means*** is used as unsupervised classifier, here we applied this technique to relocate the initial seeds to the more reliable gravity centers to be fed to Bayesian classifier.

Extension to 3D Parzen window

Although the colored objects with distinct "*hue*" and "*chroma*" may be well separated in 2-D chrominance plane, the ***3-D Parzen window*** is desirable for finding the better initial seeds points in 3-D CIELAB space with "*lightness*" features. However it's hard to estimate the true 3-D probabilistic density function by 3-D Parzen window directly. Here we tried to synthesize the detected seeds in the three planes of "*a*-b**", "*a*-L**" and "*b*-L**" by each 2-D Parzen window into 3-D *CIELAB* space.

The 2-D seeds are given by

$$Seed(a^*,b^*)=\{\boldsymbol{\mu}_k\}_{ab}=arg\max_{\boldsymbol{X}_k}\{p(a^*,b^*)\} \qquad (11)$$

$$Seed(a^*,L^*)=\{\boldsymbol{\mu}_k\}_{aL}=arg\max_{\boldsymbol{X}_k}\{p(a^*,L^*)\} \qquad (12)$$

$$Seed(b^*,L^*)=\{\boldsymbol{\mu}_k\}_{bL}=arg\max_{\boldsymbol{X}_k}\{p(b^*,L^*)\} \qquad (13)$$

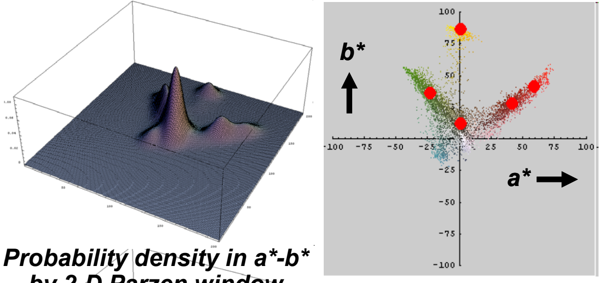
The 3-D seeds are synthesized by coupling the chrominance $Seed(a^*,b^*)$ with $Seed(a^*,L^*)$ and $Seed(b^*,L^*)$ that have the nearly close addresses to a^* and b^* of $\{\boldsymbol{\mu}_k\}_{ab}$ as follows.

$$\begin{aligned}Seed(L^*,a^*,b^*)&=\{\boldsymbol{\mu}_k\}_{Lab}\\&\cong[\{\boldsymbol{\mu}_k\}_{ab}\cap\{\boldsymbol{\mu}_k\}_{aL}]\cup[\{\boldsymbol{\mu}_k\}_{ab}\cap\{\boldsymbol{\mu}_k\}_{bL}]\end{aligned} \qquad (14)$$

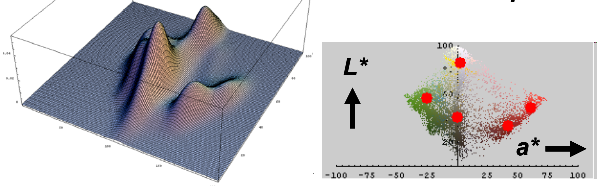
Here the operation $[\{\boldsymbol{\mu}_k\}_{ab}\cap\{\boldsymbol{\mu}_k\}_{aL}]$ means to combine the address $\{\boldsymbol{\mu}_k\}_{ab}$ with L^* of $\{\boldsymbol{\mu}_k\}_{aL}$ nearly matched to a^* of $\{\boldsymbol{\mu}_k\}_{ab}$ and the operator adds $[\{\boldsymbol{\mu}_k\}_{ab}\cap\{\boldsymbol{\mu}_k\}_{bL}]$ to it.

Thus the set of 3-D initial seeds $Seed(L^*,a^*,b^*)$ is obtained.

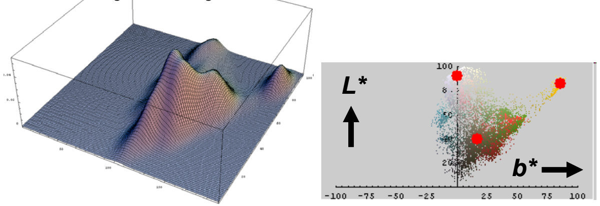
Fig.3 shows a synthesized example of 3-D initial seeds for the image "*parrot*".



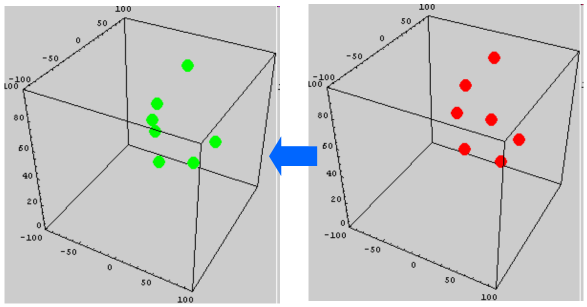
Probability density in a*-b* by 2-D Parzen window ***Peaks in a*-b* plane***



Probability density in a*-L* ***Peaks in a*-L* plane***



Probability density in b*-L* ***Peaks in b*-L* plane***



Corrected by k-means ***Synthesized seeds***

Figure3. *Initial seeds points by extended 3-D Parzen window model*

Binary Particle Model

Parzen window proved to be a useful tool for unsupervised image segmentation based on "*non- parametric*" color clustering. However, it takes too much computation time.

The key point in the proposal is to use ***Parzen window*** for searching the peaks on the mountain ridges in 2-D density distribution of chrominance. Since the probability $p(a^*, b^*)$ in Eq. (8) should be calculated for all of the (a^*, b^*) coordinates and all of the pixel color values $\boldsymbol{X}_i=\left[a_i^*,b_i^*\right]^t; i=1\sim N$, it takes too much time. Hence the simpler and faster algorithm is requested in practical application. An easy alternative idea to find the density peaks of chrominance is to scan a^*-b^* plane by a local spatial filter as follows.

The color distribution of pixel X_i is converted into a kind of "***particle image***" $g(a^*,b^*)$ by placing a ***bi-level dot*** at the address (a^*,b^*).

The bi-level B/W image $g(a^*,b^*)$ is convolved with a Gaussian filter. As a result, the smoothed density distribution image $q(a^*,b^*)$ is obtained.

$$g(a^*,b^*) = \begin{cases} 1, & \text{if } \ (a^*,b^*) = (a_i^*,b_i^*) \\ 0, & \text{otherwise} \end{cases} \tag{15}$$

$$q(a^*,b^*) = G_S(a^*,b^*) \otimes g(a^*,b^*) \ ; \otimes = \text{convolution} \tag{16}$$

$$G_S(a^*,b^*) = K \exp\left[-\frac{\left(a^{*2} + b^{*2}\right)}{\sigma_S{}^2} \right] \tag{17}$$

$$\text{where, } \iint G_S(a^*,b^*) da^* \, db^* = 1$$

Since the filtered output image $q(a^*,b^*)$ is thought to be reflecting the probabilistic density of chrominance for the given image, the same subsequent process as ***Parzen window*** model is applied for peak detection. Of course, the density profile of ***particle image*** is not equal to the probability density function, but it is shown that the mountain peaks approximately reflect the similar cluster centers to ***Parzen window*** model.

Fig. 4 shows a result by the simplified ***Particle*** model. The ***Particle*** model shows a different 3-D mountain view in the filtered density profile of bi-level ***particle image*** from that by ***Parzen window*** model. The initial seed points after ***k-means*** correction are placed at subtle different positions but are nearly close to the ***Parzen*** model and resulted in the good segmentation for the tested images.

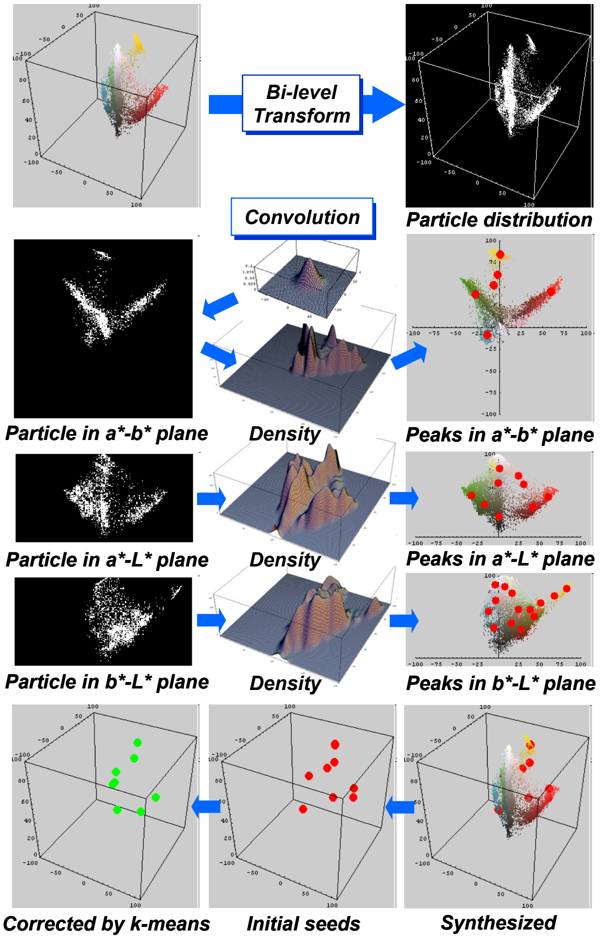


Figure4. *3-D Particle model and initial seeds synthesized from 2-D planes*

Bayesian Classifier

According to the ***Bayesian*** decision rule, the maximum likelihood is obtained when the following quadratic discrimination function is minimized for *j*.

$$d_j(Bayes) = -\log P(j) + \tfrac{1}{2} \log\left|\boldsymbol{C}_X(j)\right| + \tfrac{1}{2}\left(\boldsymbol{X} - \boldsymbol{\mu}_j\right)^t \boldsymbol{C}_X(j)^{-1}\left(\boldsymbol{X} - \boldsymbol{\mu}_j\right) \tag{18}$$

Where *P(j)* denotes the occurrence probability of class *j* and $\boldsymbol{C}_X(j)$ is the covariance matrix for ***X***.
Thus a color vector ***X*** is classified into class *j=c*, if

$$\min_{j=1\sim J}\left\{d_j(Bayes)\right\} = c \tag{19}$$

Bayesian classifier is expected to work better when coupled with ***k-means*** clustering for setting the initial seed points. Here we call the coupled model as ***k-means Bayesian.***

Experimental Results

Comparison in 2D/3D Parzen and Particle model

The proposed ***Particle*** model worked similarly to the ***Parzen window*** model. Fig.5 shows a result for JIS SCID II standard test image "*flower*". The obtained initial seeds positions look to be much the same for both of ***Parzen*** and ***Particle*** models. The simplified 2-D ***Particle*** model resulted in close to or better segmentations than 3-D model for this sample, because the colored objects are mostly characterized by the clusters in *chrominance* plane. This result showed the better segmentation in the details than our previous 3-D model [8].

Performance of [*k-means + Bayesian*] *Classifier*

K-means is a popular clustering method but needs any initial seeds for *non-parametric* segmentation. Although the proposed model is useful for feeding the initial seeds to ***k-means***, we reported that ***k-means*** coupled with ***Bayesian*** classifier works better than ***k-means*** only [8].

Fig.6 demonstrates the performance of *non-parametric* [***k-means*** + ***Bayesian***] classifier. The initial seeds by proposed models are firstly fed to the normal ***k-means*** and its output drives the second main ***Bayesian*** classifier. As clearly shown in the segmented image "*parrot*", ***k-means*** coupled with ***Bayesian*** exhibited the better performance than the normal ***k-means*** for both of ***Parzen*** and ***Particle*** models.

Comparison with JSEG

JSEG [ ] is known as an excellent algorithm to separate the textural images by two steps processing of color quantization and spatial segmentation. The color textures are very well segmented by its region growing and region merging processes.

Since the proposed algorithm lacks these spatial processes, it has a weakness in the segmentation of textural images. As a counter measure to make insensitive to the textural regions, a pre-processing Gaussian spatial filter was operated to the *L*a*b** components in the proposed model.

Fig.7 shows a segmented sample in comparison with *JSEG*. In general, *JSEG* is excellent in the extraction of global boundaries from the complicated textural regions superior to our algorithm, while the proposed method has the better performance for the detailed segmentations of individual colored

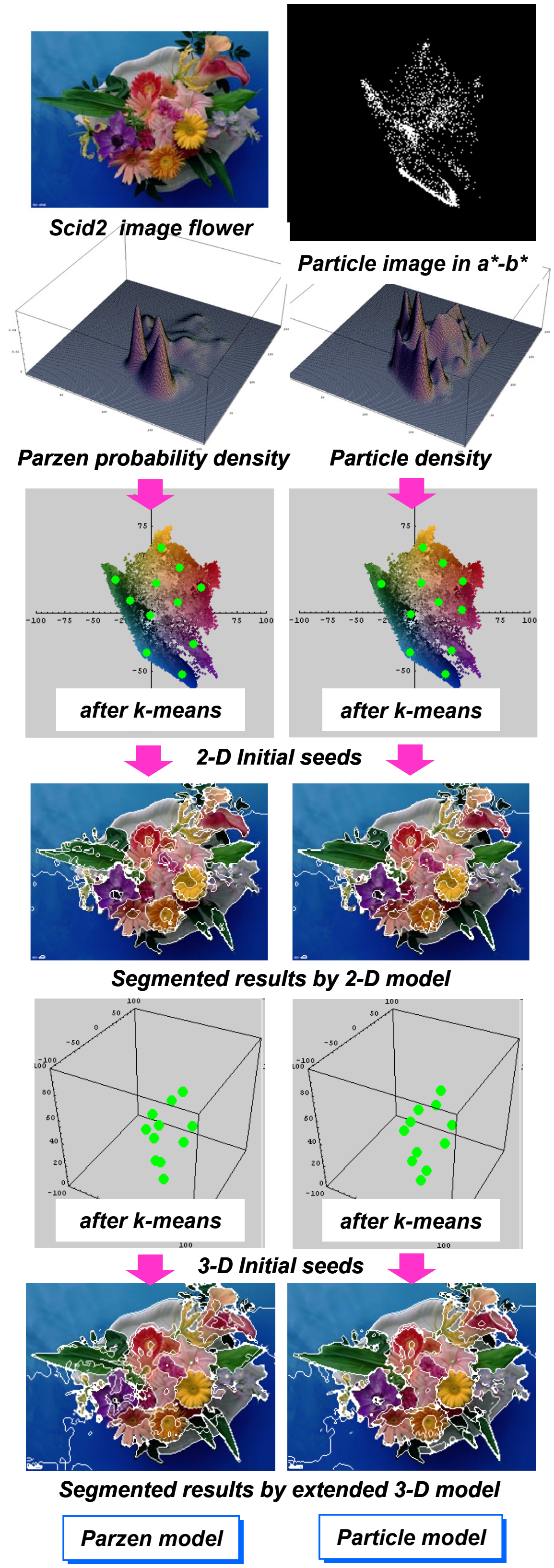


Figure5. *Comparison in 2D/3D Parzen vs. Particle model*

object. In the *"baboon"* sample, it may be difficult to make the subjective judgment which is better. On the other hand, in the *"flower garden"* sample, *JSEG* is superior to our method in the

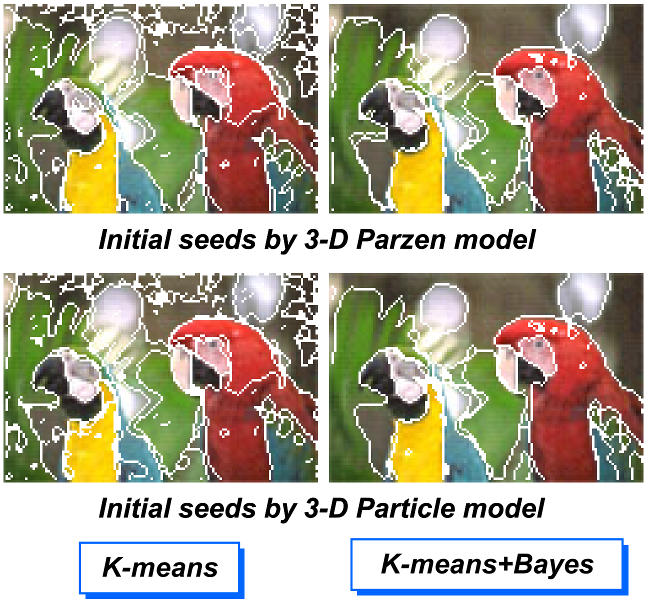
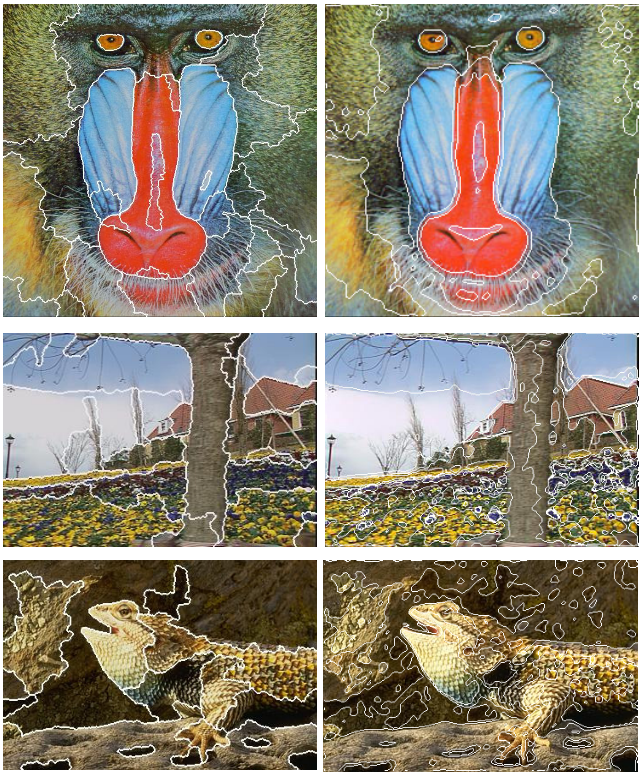


Figure6. [*k-means+Bayesian*] *classifier in comparison with normal k-means*



JSEG

[K-means + Bayesian]
initial seeds by 3D particle model

Figure7. *Segmentation of textural images in comparison with JSEG*

global merging of the textural regions but worse in the boundary sharpness of each object rather than our method. The similar feature is observed in the 3rd sample image "*Lizard*".

Conclusions

The paper presented a novel approach to the *non-parametric* color clustering algorithm by introducing *Parzen window* method to feed the initial seeds points appropriate to the unsupervised image segmentation.

Though the proposed algorithm is still in progress, some of the experimental results claim that

- Initial seed points for nonparametric clustering are rationally searched by *Parzen window* estimation of probabilistic density function.
- The maxima of ***Parzen*** probability density function in 2-D chrominance plane can catch the reliable candidates for clustering centers of colored objects.
- 2-D ***Parzen*** *window* is extended to 3-D model by synthesizing the detected peaks in three planes of *a*-b**, *a:-L**, and *b*-L**.
- ***Particle*** distribution model is introduced as a substitute for the probabilistic density distributions by ***Parzen*** *window* and applied successfully to find the initial seeds positions located at the mountain peaks in a simple and fast way.
- 2-D ***Particle*** model is extended to 3-D model in the same way as ***Parzen*** *window* model.

Further investigation and experiments on the optimum selection of parameters are left behind for the future works; how to find the optimum size of ***Parzen*** *window*, the sampling granularity and resolution of spatial filter depending on the size and the color gamut of the given image, and so on.
That same thing can be said of ***Particle*** model.

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