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Reconstruction of Overlapped Protein Spots Using RBF Networks

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Introduction

All proteins from the sample under investigation during process of two-dimensional electrophoresis (2DE) simultaneously are separated according to their molecular mass and isoelectric point, facilitating afterwards to identify each of them individually. Knowledge about all proteins existed in the sample is crucial for the development of modern diagnostics and prognostics systems, intelligent and personalized drugs, etc. Frequently several different proteins have very close values of molecular mass and isoelectric point and often appear as single protein spot in the gel image (Fig. 1.a). Thus detection and quantification of proteins in 2DE gel images is important, but at the same time complicated task.

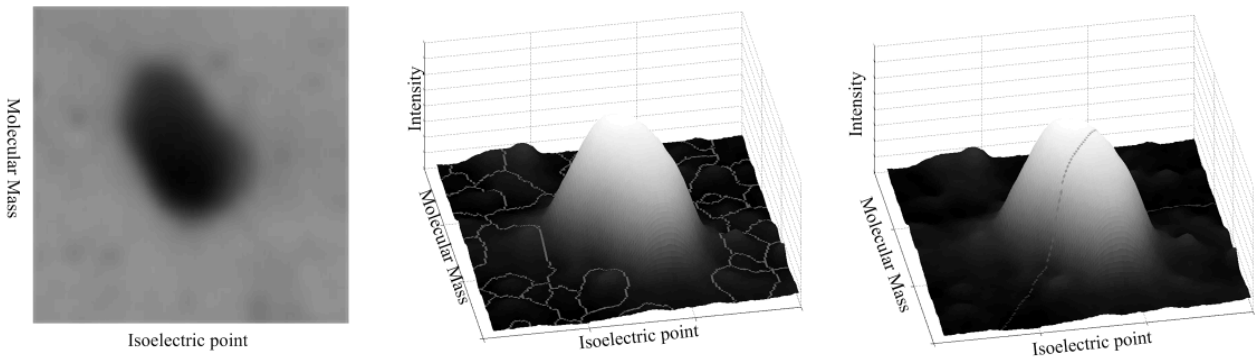
Overlapped protein spots are hardly detectable and separable by the human eye and dedicated 2DE gel image analysis software (Fig. 1.b). Intensities of overlapped protein spots sum together washing up boundaries of individual spots. Even if intensity values are high enough, the real centers of the protein spots differs from the peak intensities, observed in the 2DE gel images. Such artifacts have great influence on precision of automatic 2DE gel image analysis systems and require additional user intervention to achieve proper segmentation and identification of the proteins in the scanned gel image.

In this paper the solution of effective protein spot segmentation in two-dimensional electrophoresis gel images is proposed. It is based on the reconstruction of protein spots that are overlapping by the use of modified Radial Basis Function (RBF) network (Fig. 1.c). The Anisotropic Gaussian Function with a tilt is proposed for individual protein spot shape model and as the basis function for modified RBF network. By experimentation modified RBF network is proven to be superior to watershed transformation and shape modeling based approaches.

We start with introductory presentation of RBF network, then present structure of modified RBF network and comment its training. Afterwards we present results of three experimental studies on: segmentation of overlapped protein spots; capabilities of overlapped spots separation; and computational load. Finally we comment results of modified RBF network use for reconstruction of overlapped protein spots in 2DE gel images and discuss possible further ways of improvement.

Radial basis function networks

Radial basis functions are widely used for scattered data interpolation tasks. RBF is one of the possible choices of transfer functions for linear neural networks. One of the main features of the linear network with radial basis functions is in the way such systems act to an input. Increasing the distance between input and centre of RBF, the response of the system smoothly decreases.



(a) image with two protein spots (b) after watershed transform (c) after modified RBF network

Fig. 1. Segmentation of original 2DE gel image fragment

Output signal of radial basis function that actually corresponds to hidden layer of RBF network [1] can be expressed by:

$$z_h(\mathbf{x}) = \Phi\left(\left\|\mathbf{x} - \mathbf{c}_h\right\|, \mathbf{r}_h\right), \quad (1)$$

here h – index of the basis function; $\Phi(\bullet)$ – general radial basis function; $\mathbf{x}$ – input signal; $\mathbf{c}_h$ – RBF center; $\mathbf{r}_h$ – RBF radius; $\|\bullet\|$ – Euclidean norm.

Radial basis functions are nonlinear and can be formed by the use of various functions, which possess similar properties. Some commonly used functions are:

Gaussian $\Phi^{\mathrm{G}}(x) = \exp\left(\left\|(x-c)^2 / r^2\right\|\right)$;

Multiquadric $\Phi^{\mathrm{M}}(x) = \left[\|x-c\|^2 + r^2\right]^{1/2}$;

Inverse multiquadric $\Phi^{\mathrm{I}}(x) = \left[\|x-c\|^2 + r^2\right]^{-1/2}$;

Logistic $\Phi^{\mathrm{L}}(x) = \left[1 + \exp\left(\|x-c\|/r\right)\right]^{-1}$;

Cauchy $\Phi^{\mathrm{C}}(x) = \left[r\left(\|x-c\|^2 + r^2\right)\right]^{-1}$.

Gaussian basis function receding from the centre decreases monotonically. Using this function, the model of the surface of 2DE gel image, reconstructed by the RBF network, can be viewed as a mix of normal density functions. In 2DE gel images, where geometric distortions are not big, protein spots often appear similar to scaled normal distribution. Thus the Gaussian basis function is chosen for the following experimentation.

RBF networks have similar to Multilayer Perceptrons feed-forward structure that consists of three layers: input, hidden and output. The hidden layer of the network has radial basis activation functions, as was already discussed, while the output layer has linear activation functions. In general the output of RBF network [2] is expressed by:

$$y_o = w_{0,o} + \sum_{h=1}^{N} w_{h,o} z_h(\mathbf{x}), \quad (2)$$

here o – index of the output; $w_{0,o}$ – offset (bias) of output signal; $w_{h,o}$ – weights of output layer; $\mathbf{x}$ – input signal; N – the total number of RBFs in the network.

The input vector $\mathbf{x}$ of the network is shifted in $\Re^n$ space according to parameters, stored in the network. For each of shifted vectors, the Euclidean norm is computed and the centers are defined for each radial basis function in the network (for each unit of network's hidden layer).

Let us briefly comment training of RBF network. During training following parameters are determined:

- number of RBFs;
- centers of RBFs;
- radiuses of RBFs;
- weights and offsets of output layer.

The number of radial basis functions can be determined using Orthogonal Least Squares or Constructive Learning algorithms [3, 4]. In both cases reduction of errors is measured and if necessary additional basis functions are added.

There are several approaches for determination of centers of radial basis functions. The simplest way to define center is to use one centre for each data point. This approach is suitable for small datasets and in cases when sufficient memory is available.

The large data sets have to be modeled with computationally acceptable number of centers. Thus the subset must be selected in the input data set. There are several approaches for subset selection and centre estimation from training dataset:

- random point selection;
- semi random (selecting each *r*th data point);
- even spread of centres over dataset;
- pre-processing of data using clustering algorithms or Support Vector Machines.

The performance of approximation to data with random point selection method highly depends on the way random centers are sampled. It is important to have some prior knowledge about distribution of centers in order to choose the right method for sampling. Semi random and center selection by even spread algorithms are more suitable for data sets with even distribution of objects to be modeled.

Most popular clustering algorithm for centre detection of RBF is hybrid learning algorithm, which uses self organizing approach. Data are clustered into *k* regions and the centers are determined evaluating the Euclidean centre for each cluster. This approach is known as *k*-means clustering algorithm [5]. *k*-means clustering is an iterative algorithm that minimizes the sum of distances from each object to centroid of a cluster over all clusters and is more suitable for large amount of data.

The supervised learning also can be used to train the centers of RBFs. Usually the gradient descent algorithm is employed and received network is called Generalized Radial Basis Function Network.

The way how output layer weights are determined depends on the complexity of the problem. When only output layer weights are unknown, the problem is linear and weights can be computed using Least Squares algorithm. When centers, output layer weights and shape parameters are unknown, only nonlinear optimization techniques – deterministic or stochastic – can be used as the problem solution has many local minima. Deterministically it can be solved using: first or second order gradient, Orthogonal Least Squares, Linear Programming based algorithms or Support Vector Machines. Stochastic approaches include: genetic algorithms, massive random search and Simulated Annealing.

The modeling of protein spots using RBF networks is complicated because all of the network parameters have to be estimated. The solution can be found only using nonlinear optimization techniques.

Structure of modified RBF network

The main aim of the protein spot reconstruction, presented in this paper is to model separate and overlapped protein spots in the 2DE gel image using adopted RBF network. The complexity of estimation of RBF network's parameters depends on the selected radial basis function –

protein spot model (in our case). Selection of the spot model [7] has to be made taking into account process of two-dimensional electrophoresis and gel scanning influence to acquired spots shapes.

During the 2DE process all proteins from the sample under investigation simultaneously are separated according to their molecular mass and isoelectric point, facilitating afterwards to identify each of them individually. The proteins are separated during two successive procedures that are done in orthogonal directions, thus protein spot shape inherently have two different dispersion values. This feature can be successfully modeled by the use of Anisotropic Gaussian Function (AGF) based shape model [7].

During the 2DE process proteins are moving affected by various ingredients and the protein spot shape may appear with dispersions not parallel with image axis. Also during gel acquisition after 2DE process, various geometric distortions may appear in the scanned image.

The factors discussed above stipulate the use of the modified RBF network. The basis function in the modified RBF network is no longer radial as it forms an ellipsis instead. Also the widths for the basis functions in modified RBF network are no longer single variables and are represented as covariance matrixes $\mathbf{\Sigma}$.

A radial basis function assumes that all variables have the same relevance and the same dimensions. In our approach it is useful to linearly transform input variables $\mathbf{x}$ to $\mathbf{Sx}$ and compute weighted norm instead of Euclidean. The weighted norm can be defined as:

$$\left\|\mathbf{x}-\mathbf{c}\right\|_{\mathbf{S}}^2=\left(\mathbf{x}-\mathbf{c}\right)^T\mathbf{S}^T\mathbf{S}\left(\mathbf{x}-\mathbf{c}\right), \qquad (3)$$

here $\mathbf{c}$ – the centre of the spot shape.

Mathematically basis functions in a modified RBF network are radial in new metric, as defined in equation (3). For Anisotropic Gaussian Function, the matrix $\mathbf{S}^T\mathbf{S}$ is equal to inverse covariance matrix $\mathbf{\Sigma}^{-1}$ and diagonal elements of the matrix correspond to $1/\sigma^2$. Thus the Anisotropic Gaussian Function with a tilt (AGF+) can be expressed as follows:

$$z^{\mathrm{M}}\left(\mathbf{x}\right)=\frac{1}{\sqrt{\left(2\pi\right)^2\det(\mathbf{\Sigma})}}\exp\left(-\frac{1}{2}\left(\mathbf{x}-\mathbf{c}\right)^T\mathbf{\Sigma}^{-1}\left(\mathbf{x}-\mathbf{c}\right)\right). \qquad (4)$$

In Fig. 2 the structure of modified RBF network for 2DE gel image segmentation as it is defined by (2) and (4) is shown. Network has two inputs that are used to define pixels' coordinates in the image. Given specific coordinates, pixel's intensity value is calculated at the single output of RBF network. The number of hidden units (basis functions) is varying and it depends on the number of protein spots in the 2DE gel image under segmentation. Thus for each protein spot center and covariation matrix of AGF+ should be computed. The covariance matrix consists of four parameters that define dispersions in two orthogonal directions and tilt coordinates of the spot shape.

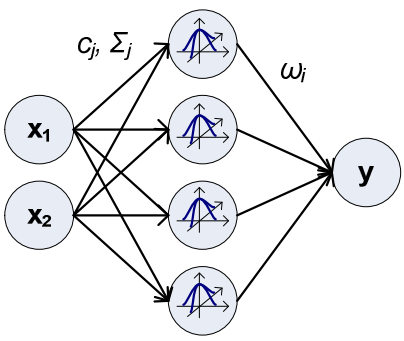


Fig. 2. Modified RBF network for image segmentation

Training of modified RBF network

The training of modified RBF network refers to estimation of four parameter groups:

- centers of AGF+;
- covariance matrixes of AGF+;
- output weights;
- offset parameter.

Taking into account 2DE gel image size (the amount of data to be modeled) for the estimation of AGF+ centers the *k*-means clustering algorithm is used. The input data is divided in *k* clusters and the centre is computed in each of them. The centre is the point in the cluster, to which the sum of distances from each point in that cluster is minimized.

The covariance matrix for each AGF+ is computed using Expectation Maximization algorithm. The protein spots in the 2DE gel image are treated as sets of points, distributed around the estimated clusters centers. Aim of the use of Expectation Maximization algorithm is to model the distribution of image points using AGF+ protein shape model [7].

Expectation Maximization algorithm is composed of expectation and maximization steps. First, the local lower-bound to the posterior distribution is constructed and then it is optimized estimating parameters of the spot shape models (centers of the spots, covariance matrices and weights).

Offset parameter added to algorithm is important since it assumes the influence of background in the image. The selection of the offset parameter can be made finding the minimal intensity value in the scanned gel or in each of *k* clusters. Relying on background intensity variation, the relative value of intensity must be added to offset parameter, to avoid influence of background to estimated protein spot shape.

Results of experimental investigations

There are two main problems that emerge when protein spots in 2DE gel image overlap. The first one is a faulty segmentation of gel image region. The second problem is incorrect protein detection. Both of them can lead to incorrect protein quantification.

The peak values (centers) of the protein spots when proteins overlap often differs from the real values because of influence of neighborhood spot intensities that sum with each other and form the new shape (see Fig. 3). Modeling the region of overlapped spots, it is possible to identify the real coordinates of the spot centers in the gel image and asses true values of protein isoelectric point and molecular

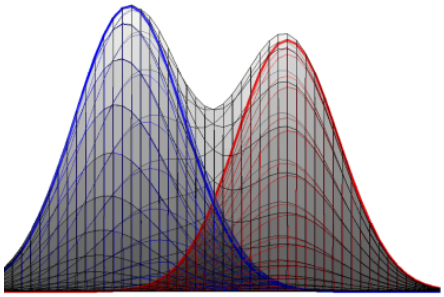


Fig. 3. Linear combination of two spot intensity shapes

mass. This is important issue when automatic protein regimentation and grouping is needed to compare with the values, stored in the database.

Three different experimental studies were done in order to test capabilities of here proposed 2DE gel image segmentation based on protein spot reconstruction by modified RBF network.

Study on segmentation of overlapped protein spots. The set of 32 overlapped spot pairs taken from real 2DE gel images were tested for the possibility to segment them using three approaches based on:

A1. *watershed transformation* [9];

A2. *protein shape modeling* [8];

A3. *reconstruction by modified RBF network.*

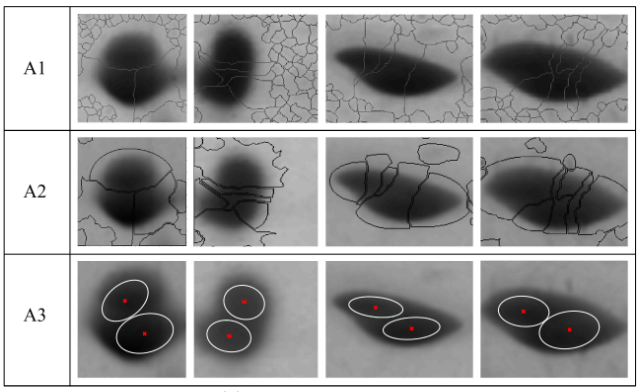
The watershed transformation based segmentation algorithm filters the input image with smoothing filter to eliminate small local minima caused by the noise and other artifacts in the image [9]. Such filtering of the input gel image permits to reduce the over-segmentation effect. Thus the influence of the background irregularity causes detection of non-existent small spots while over-sized filter stipulated the overpass of protein spots mostly when spots overlap (A1 image rows in Fig. 4).

The improved protein spot shape modeling based segmentation algorithm uses watershed transformation to divide gel image into segments, too [8]. Then the area of each segment is measured and comparatively small segments are eliminated from further analysis. For the each of remaining segment, the Anisotropic Gaussian Function based protein spot model [7] is fitted. Depending upon user specified threshold value for the model fit error, badly fitted segments are merged together and final image segmentation is received (A2 image rows in Fig. 4).

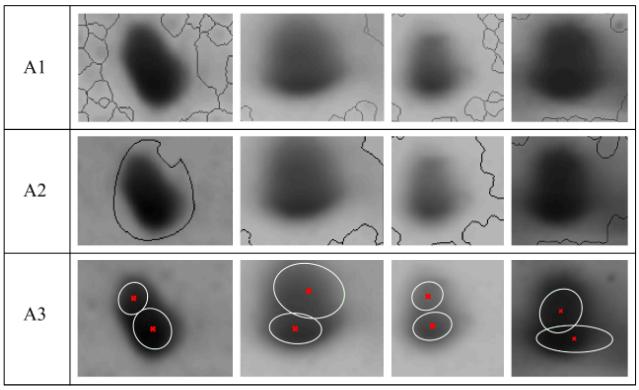
From all 32 test images, eight overlapped spot pairs were not separated by first two segmentation algorithms A1 and A2. These worst results are presented in Fig. 5. Contrary, proposed method based on protein spot reconstruction by modified RBF network performed well and succeeded to separate all overlapped spots in all 32 images (see A3 image rows in Fig. 4 for the same 8 difficult spot pairs).

Study on capabilities of overlapped spots separation. This set of experiments was done by the use of synthetic spots. The main aim was to evaluate the capabilities of separation of overlapped synthetic spots upon the three factors:

- distance between two spots, d;
- dispersion of the spots, σ;
- amplitude ratio of overlapped spots, r.



(a) oversegmentation



(b) spot overpass

Fig. 4. Comparison of the segmentation results

The distance between two synthetic spots was varied in $[2I; 42I]$ using $2I$ step size. The dispersion of the spots was varied in $[6I; 10I]$ using $0.2I$ step size. Also amplitude ratio of the overlapped spots was varied in $[0.2I; 1I]$ with $0.1I$ step size. That gives 3,200 different cases: 20 (d var.) × 20 (σ var.) × 8(r var.). All factors – d, σ and r – are dependent on I being a spot intensity. For the convenience we set I equal to 1.

This time the separation of overlapped synthetic spots was tested by the use of same two approaches based on:

A1. *watershed transformation* [9];

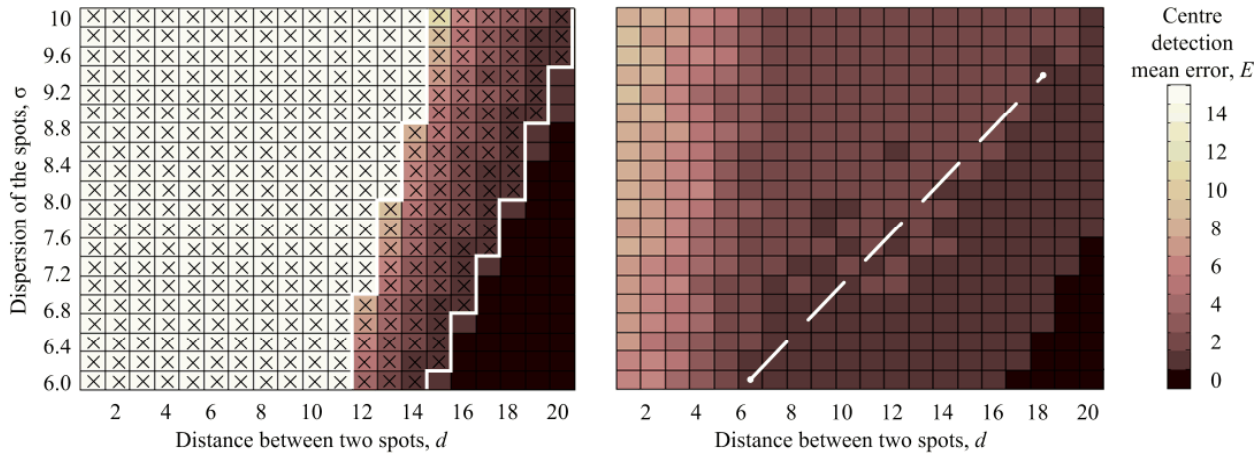
A3. *reconstruction by modified RBF network.*

While segmenting the synthetic image with watershed transformation, the centre of the spot was computed estimating the peak value in each of the segment. In the case of proposed RBF reconstruction based segmentation algorithm the centre of the each reconstructed spot was estimated using *k*-means clustering and corrected by the Expectation Maximization algorithm.

The error of the overlapped spot detection e was computed using the Euclidean distance of the real and estimated centers of the spots. Then the mean error for a set of experiments varying only size ratio of overlapped spots was calculated, i.e.:

$$E = \frac{1}{16}\sum_{i=1}^{8} e_i = \frac{1}{8}\sum_{i=1}^{8}\frac{1}{2}\left(\left\|c_{1i} - \bar{c}_{1i}\right\| + \left\|c_{2i} - \bar{c}_{2i}\right\|\right), \qquad (5)$$

here $\bar{c}_{1i}$ and $\bar{c}_{2i}$ are real centers of two spots; c_{1i} and c_{2i} are estimated centers of two spots; $\|\bullet\|$ – Euclidean norm.



(a) watershed transformation algorithm – A1 (b) reconstruction by modified RBF network – A3

Fig. 5. Results of overlapped spots separation: '×' – failure to separate spots; gray level – mean error of spot center detection

Results on centers of overlapped protein spots detection mean errors are presented in Fig. 5. By the gray level mean error is showed, while by '×' marks failures to separate spots are indicated. First of all becomes evident, that proposed reconstruction by modified RBF network succeeds to separate overlapped spots in all 3,200 cases, while watershed transform based algorithm performs considerably worse – only 13 % of all cases are segmented for all considered amplitude ratios of overlapped spots.

Let us analyze (a) part of Fig. 5 more thoroughly. By white line two main boundaries are indicated. Basing on the boundary from the left we can conclude that watershed transformation algorithm completely fails (for all spots amplitude ratio values in $[0.2;1]$) to separate overlapped spots that are closer than $d=12$ and have dispersion not bigger than 6. Increasing analyzed spots dispersion (up to 10), will cause the algorithm to fail completely when spots will be even more separated ($d=15$). The right boundary let us to conclude, that watershed transformation algorithm completely succeeds (for all considered spots amplitude ratio values and with detection mean error less than 2) to separate overlapped spots within distance $d>15$ when spots dispersion are not bigger than 6. Increasing analyzed spots dispersion (up to 10), will cause the algorithm to succeed completely only if spots will be more separated ($d=21$). In the between of left and right boundaries, watershed transformation based algorithm capability to separate overlapped spots depends on the value of spots amplitude ratio and even if it is adequate, the algorithm separates spots with center detection mean error greater than 1.

While comparing results presented in (a) and (b) parts of Fig. 5, let us select center detection mean error, E equal to 1. With this biggest error value watershed transformation algorithm completely succeeds to separate overlapped spots (see results on the right from the right boundary in (a) part). Within variation limits of selected factors d, σ and r, proposed reconstruction by modified RBF network approach exhibits $E\le 1$ in cases at the right of approximate boundary shown as white dashed line in Fig. 5.b. That let us to conclude that proposed approach in comparison to watershed transformation algorithm gives the same $E\le 1$ when distance between spots is approximately two times shorter (15/7) and spots dispersion is 6. Increasing analyzed spots dispersion will reduce the advantages of proposed reconstruction by modified RBF network approach over the watershed transformation. They will be approximately the same when spots dispersion will reach 10.

Study on computational load. The set of experiments was done in order to evaluate computation time of two overlapped 2DE gel image protein spots reconstruction by:

A3. modified RBF networks with AGF+;

A4. modified RBF networks with AGF;

A5. usual RBF network with Gaussian functions.

During experimentation, reconstruction was stopped if the number of iterations of EM algorithm was reaching 150 or the level of the error change approached 0.001.

Results presented in Fig. 6 confirm that computational load for all networks increases proportionally with the number of RBFs. Comparing the total number of parameters that must be optimized in the networks is evident that smallest RBF network is in A5 case, then follows RBF network in A4 case (extra parameters for anisotropy), and the biggest RBF network is in A3 case (extra parameters for anisotropy and tilt). Nevertheless presented results indicate that computational load of proposed A3 approach differs from the other two only slightly. When the number of RBFs is 7 and more usual RBF network (A5) has highest computational load.

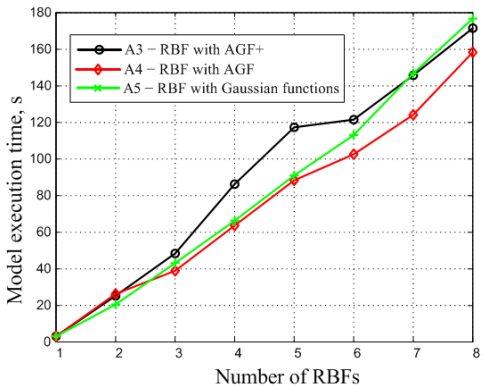


Fig. 6. Computational load while segmenting two 2DE gel spots

Conclusions

Effective protein spot segmentation in two-dimensional electrophoresis gel images approach is proposed. It is based on the reconstruction of protein spots that are overlapping by the use of modified RBF network that employs Anisotropic Gaussian Functions with a tilt. Performed experimental studies show that:

1. For segmentation of natural two-dimensional electrophoresis gel images modified RBF network is superior to watershed transformation and shape modeling based approaches.

2. The proposed modified RBF network in comparison to watershed transformation separates overlapped synthetic spots with the same accuracy in up to two times shorter distance between spots.

3. Computational load of usual RBF and modified RBF networks differs insignificantly.

Automatic determination of offset value and number of hidden units in modified RBF network for the use in automatics two-dimensional electrophoresis gel images segmentation are the pending problems.

References

1. **Carr J. C., Beaton R. K., Cherrie J. B., et al.** Reconstruction and representation of 3D objects with radial basis functions // Proceedings of the 28th annual conference on Computer graphics and interactive techniques. – New York: ACM Press, 2001. – P. 67–76.
2. **Jain L. C.** Recent Advances in Artificial Neural Networks: Design and Applications // ENGnetBASE. – CRC Press LCC. – 2000.
3. **Chen S., Cowan C. F. N, Grant P. M.** Orthogonal least squares learning algorithm for radial basis functions networks // IEEE Transactions on Neural Networks. – 1991. – No. 2(2). – P. 302–309.
4. **Campbell C.** Constructive Learning Techniques for Designing Neural Network Systems // In (ed CT Leondes) Neural Network Systems Technologies and Applications. – San Diego: Academic Press, 1997.
5. **Hartigan J. A., Wong M. A.** A K-Means Clustering Algorithm // Applied Statistics. – 1979. – No. 28. – P. 100–108.
6. **Dempster A., Laird N., Rubin D.** Maximum likelihood from incomplete data via the EM algorithm // Journal of the Royal Statistical Society, Series B. – 1977. – No. 39(1). – P. 1–38.
7. **Matuzevičius D., Serackis A., Navakauskas D.** Mathematical Models of Oversaturated Protein Spots // Electronics and Electrical Engineering. – Kaunas: Technologija, 2007. – No. 1(73). – P. 63–68.
8. **Matuzevičius D., Serackis A., Navakauskas D.** Improved Segmentation of 2D Electrophoresis Gel images by the Use of Bell Shape Function // Biomedicininė inžinerija. Tarptautinės konferencijos pranešimų medžiaga. Kaunas: Technologija, 2006. – P. 150–153.
9. **Matuzevičius D., Navakauskas D.** Investigation of Segmentation Methods for Proteomics // Electronics and Electrical Engineering, 2005. – No. 7(63). – P. 74–78.

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A. Serackis, D. Navakauskas. Reconstruction of Overlapped Protein Spots Using RBF Networks // Electronics and Electrical Engineering. – Kaunas: Technologija, 2008. – No. 1(81). – P. 83–88

Detection and quantification of proteins in two-dimensional electrophoresis gel images is complicated but the same time important task for the development of modern diagnostics and prognostics systems. In this paper the solution of effective protein spot segmentation in two-dimensional electrophoresis gel images is proposed. It is based on the reconstruction of protein spots that are overlapping by the use of modified RBF network. The Anisotropic Gaussian Function with a tilt is proposed for individual protein spot shape model and as the basis function for modified RBF network. By experimentation modified RBF network is proven to be superior to watershed transformation and shape modeling based approaches. The modified RBF network in comparison to watershed transformation separates overlapped spots with the same accuracy in up to two times shorter distance between spots. At the same time computational load of usual and modified RBF networks differs insignificantly. Ill. 6, bibl. 9 (in English; summaries in English, Russian and Lithuanian).

А. Серацкис, Д. Навакаускас. Реконструкция слитых пятен двумерного электрофореза белков с применением сети радиально симметричных скрытых нейронов // Электроника и электротехника. – Каунас: Технология, 2008. – № 1(81). – С. 83–88.

Разделение и оценка белков в изображениях двумерного электрофореза – важный, но сложный этап проектирования современных систем диагностики и прогноза. В настоящей статье представлен эффективный метод сегментации пятен белков. Основой метода является модифицированная сеть радиально симметричных скрытых нейронов. Как базовые функции в представленной сети предлагается использовать анизотропную модель Гаусса с наклоном. В результате экспериментов доказано что модифицированная нейронная сеть лучше выделяет слитые пятна белков по сравнению с методами преобразования водораздела и моделирования пятен белков современными моделями. Сравнив с методом преобразования водораздела доказано, что представленный метод разделяет слитые пятна, расположенные ближе друг другу до двух раз. Также доказано, что отличия времени обучения обычной и модифицированной сети радиально симметричных скрытых нейронов несущественны. Ил. 6, библ. 9 (на английском языке; рефераты на английском, русском и литовском яз.).

A. Serackis, D. Navakauskas. Susiliejusių baltymų dėmių rekonstrukcija taikant spindulio tipo bazės tinklus // Elektronika ir elektrotechnika. – Kaunas: Technologija, 2008. – Nr. 1(81). – P. 83–88.

Baltymų, esančių dvimatės elektroforezės gelių vaizduose, aptikimas ir įvertinimas yra sudėtingas, tačiau labai svarbus uždavinys kuriant šiuolaikines diagnostikos ir prognostikos sistemas. Šiame straipsnyje pasiūlytas efektyvus baltymų dėmių segmentavimo būdas. Jis remiasi susiliejusių baltymų dėmių rekonstrukcija tam taikant modifikuotą spindulio tipo bazės tinklą. Siūloma šiame tinkle taikyti anizotropines Gauso funkcijas su pasvirimu. Eksperimentiškai parodyta, kad modifikuotas spindulio tipo bazės tinklas geriau nei vandenskyros transformacija ar baltymo dėmių modeliavimas atskiria susiliejusias baltymų dėmes. Palyginus siūlomą metodą su vandenskyros transformacija, nustatyta, kad esant tam pačiam dėmių centrų nustatymo tikslumui, siūlomas metodas gali atskirti iki dviejų kartų arčiau esančias baltymų dėmes. Kartu parodyta, kad modifikuoto ir originalaus spindulio tipo bazės tinklų mokymo trukmės mažai skiriasi. Il. 6, bibl. 9 (anglų kalba; santraukos anglų, rusų ir lietuvių k.).