Editorial

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Bio-signal and System Modeling: From Image Processing to System Biology

Modeling is the main core of any signal and system processing and analysis. For example, an image can be seen as a matrix (mathematical/deterministic model) and in this base for a conventional processing such as denoising average operator is used. However, as we know this operator doesn't lead to an optimum result (the produced image is usually blurry). In another point of view, the image can be seen as a random field (statistical model), and so the denoising process is converted to an estimation problem and better denoising results is achieved. Similarly, we can solve the denoising problem by modeling an image using partial differential equation (PDE), atomic representation (e.g., x-let transforms), geometric and graph-based methods, etc.[1-5] The resulted denoising process is completely depended on the proposed model for noise-free image. In this base, we can introduce various methods for modeling of biologic data, including mathematical/statistical models, PDE-based models, transform-based models, and geometric and graph-based models. In this base, new modeling frameworks can also be achieved using a rational combination of these models. For example, energy flow model[6] is a PDE-based model based on using an energy function like Sobolev or total variation norm. We can at first propose an atomic and sparse representation for image and then in the sparse domain employ energy flow model but by using L1 norm.[7] The same thing can be done by using an appropriate statistical model in sparse domain (e.g., a local bivariate mixture model can be used to capture the main statistical properties of sparse coefficients i.e., sparsity, inter- and intra-dependencies[8]).

These methods can also be used to model biological processes given biological data. As an example for biological networks,[9-11] microarrays provide a snapshot of gene expression in a cell and we want to reply to this question: "What are the genes related to a specific cancer and how these genes are correlated. Using a simple mathematical/statistical model, we can compare the mean of the expression level of a gene for healthy and cancerous groups using *t*-test[12] (or similarly compare the variances using *F*-test[13]). However genes are not expressed independently, they regulate each other's activity and we must try to find a model to analyze the interactions between genes. In the statistical modeling framework Bayesian networks can be employed for this reason or similarly interactions between genes can be evaluated using a differential equation model or graph-based models (and again an appropriate combination of them).[14]

The main message of this editorial is that instead of rushing to apply various methods for analysis a huge pool of biological data (from pixels of a medical image to expression levels of genes in a biological network), we must be patient that initially find the best model describing the main interactions between data.

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REFERENCES

1. Chan T, Shen J. Image Processing and Analysis: Variational, PDE, Wavelet, and Stochastic Methods. SIAM; 2005.
2. Sapiro G. Geometric Partial Differential Equations and Image Analysis. Cambridge: Cambridge University Press; 2001.
3. Finn J. An Introduction to Bayesian Networks. New york, NY, USA: UCL Press; 1996.
4. S. Bornholdt, H. G. Handbook of Graphs and Networks: From the Genome to the Internet. New York, NY, USA: Wiley; 2003.
5. West DB. Introduction to Graph Theory. 2nd ed. United States: Prentice Hall; 2001.
6. Peyer G. Advanced Signal, Image and Surface Processing, Available from: http://www.ceremade.dauphine.fr. [Last accessed on 2013 Jan 15].
7. Wright SJ, Nowak RD, Figueiredo MA. Sparse reconstruction by separable approximation. IEEE Trans Signal Process 2009;57:2479-93.
8. Rabbani H, Nezafat R, Gazor S. Wavelet-domain medical image denoising using bivariate laplacian mixture model. IEEE Trans Biomed Eng 2009;56:2826-37.
9. Dorogovtsev SN, Mendes JF. Evolution of Networks: From Biological Nets to the Internet and WWW. Oxford: Oxford University Press; 2003.
10. Kandel A, Bunke H. Mark Last: Applied Graph Theory in Computer Vision and Pattern Recognition. New York: Springer; 2007.
11. Junker BH, Schreiber F. Analysis of Biological Networks. Wiley; 2008.
12. Tusher VG, Tibshirani R, Chu G. Significance analysis of microarrays applied to the ionizing radiation response. Proc Natl Acad Sci U S A 2001;98:5116-21.
13. Prieto C, Rivas MJ, Sánchez JM, López-Fidalgo J, De Las Rivas J. Algorithm to find gene expression profiles of deregulation and identify families of disease-altered genes. Bioinformatics 2006;22:1103-10.
14. Karlebach G, Shamir R. Modelling and analysis of gene regulatory networks. Nat Rev Mol Cell Biol 2008;9:770-80.

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