

The GELINSPECTOR: A Friend and Helper for Systems Biologists

A quantitative evaluation of Western blots is now possible

Systems biologists from the German Cancer Research Center (Deutsches Krebsforschungszentrum, DKFZ) have developed a method that enables exact quantitative data to be obtained from Western blots. Western blots are used to detect proteins. Until now, however, this biochemical procedure only allowed one to determine the relative concentration of the protein in question. Using Western blots, the research group of Ursula Klingmueller has succeeded not only in detecting various signal transduction proteins but also in establishing the amount of these proteins in the cells. Working with colleagues from the University of Freiburg, the scientists have developed the computer program GELINSPECTOR. This software facilitates the quantitative analysis of the blots.

A cell contains a mixture of many different proteins. In a Western blot, these proteins are first separated according to their size and charge in a special gel (electrophoresis gel). The protein of interest is then detected using suitable antibodies. The quantity of a protein can be determined using a Western blot if the corresponding antibody is coupled to a light-emitting enzyme. From the light intensity, which is recorded with a camera, one can determine the protein concentration. The same procedure can be applied with Northern blots (RNA detection) and Southern blots (DNA detection).

The method of Klingmueller and colleagues also enables one to measure how the concentration of molecules changes over time. The scientists discovered that the data become more accurate when the samples in a time-dependent measurement are placed onto the electrophoresis gel not in chronological but in random order. The software GELINSPECTOR arranges the data in the correct order in the computer. Klingmueller and colleagues also found that the quality of the data improves if they are standardized. For this purpose they use, for example, proteins of the cytoskeleton, because these always occur in the same concentration in cells and do not undergo chemical changes. This standardization can also be performed automatically by the program GELINSPECTOR; it requires only the data on the light intensity from the camera.

Exact quantitative data are the foundation for systems biology. This relatively young branch of research attempts to understand complex metabolic pathways and signal transduction chains with the help of mathematical models. Once a model has been constructed, systems biologists can predict on the computer how the system will react when important parameters are changed. One can estimate, for example, the effects and side effects of medication. In addition, such models make an important contribution to our understanding of processes taking place in the cell. The networking of metabolic pathways and signal transduction are too complex there to be successfully tackled with conventional methods.

M. Schilling et al.: „Computational processing and error reduction strategies for standardized quantitative data in biological networks“, FEBS Journal, 272 (2005), 6400-6411

The task of the Deutsches Krebsforschungszentrum in Heidelberg (German Cancer Research Center, DKFZ) is to systematically investigate the mechanisms of cancer development and to identify cancer risk factors. The results of this basic research are expected to lead to new approaches in the prevention, diagnosis and treatment of cancer. The Center is financed to 90 percent by the Federal Ministry of Education and Research and to 10 percent by the State of Baden-Wuerttemberg. It is a member of the Helmholtz Association of National Research Centers (Helmholtz-Gemeinschaft Deutscher Forschungszentren e.V.).

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