Virtual Blot for quantification at a glance

Introduction

Virtual Blot turns raw Western blot images into an intuitive and accurate visualization that enables effortless absolute protein quantification.

The Virtual Blot technology, integrated in the Fusion Absolute imaging system, provides an augmented representation of a Western blot image. It converts the 2D blot into a Virtual Blot, where each lane and band is reconstructed according to the weight and volume density of protein it contains. This reconstruction is based on the measured signal intensities, while fully preserving the integrity and traceability of the original data.

By correlating the image information with quantitative data extracted from signal analysis, the Virtual Blot™ offers a clear and structured display of protein distribution across the blot. Researchers can directly visualize the concentration gradients, saturation zones, and quantities of protein in each lane.

Advantages

Virtual Blot offers multiple advantages for researchers seeking high accuracy and time efficiency in their protein quantification workflows:

- **Quantification at a glance:** Virtual Blot provides a direct and intuitive visualization of protein amounts, enabling researchers to assess quantities and distributions instantly without additional processing.
- **Enhanced clarity and structure:** Bands and lanes are displayed in a refined, noise-free layout that makes signal patterns easier to interpret and compare across samples.
- **Saturation awareness:** The visualization highlights saturation regions and quantification is based on validated pixel values rather than on apparent band height.
- **Time-saving automation:** Manual band selection is no longer required. Automated lanes and bands detection significantly reduces analysis time.

Methods

Virtual Blot relies on artificial intelligence algorithms developed through deep learning, a subfield of machine learning based on convolutional neural networks (CNNs). Convolutional operations are mathematical functions that extract relevant image features such as contrast, edges, and texture. These features are then used to perform instance segmentation, the process by which each pixel of an image is classified according to its content (ie. background, lane, or protein band).

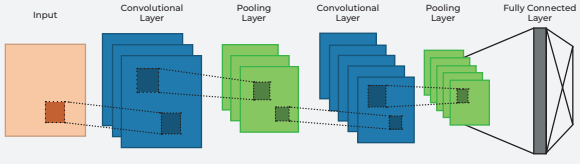

Figure 1. Convolutional neural networks (CNNs) functioning

Our model has been trained using a large dataset of Western blot images, each associated with labeled masks identifying the corresponding structures. This supervised learning approach allows the neural network to learn the characteristic visual and quantitative patterns of protein bands. During training, the model iteratively compares its predictions with the assigned labels and adjusts its internal parameters to minimize error.

Once trained, our model can accurately segment new blot images, automatically identifying lanes and bands with high precision. The resulting segmentation is then combined with the signal intensity data to compute absolute quantities. The final Virtual Blot reconstruction is obtained through data fusion, where each identified region is rendered proportionally to its calculated protein amount, ensuring both visual coherence and quantitative accuracy.

Output

Within the Fusion software interface, the Virtual Blot appears in the upper-left section of the analysis dashboard and serves as the central visual reference for data interpretation. Selecting a lane within the Virtual Blot automatically updates the quantitative table and intensity profile, providing an immediate correlation between visual and numerical information.

In addition to the Virtual Blot visualization, the software includes several advanced analytical tools designed to refine and complement data interpretation. The lane and band profile viewer allows detailed examination of signal distribution and background correction through a dedicated noise subtraction algorithm. The quantity of reference feature enables smart normalization, using a defined reference band or standard protein to ensure reliable comparisons between samples. Finally, the marker management tool allows users to assign known molecular weights or quantities to marker bands. A regression curve is automatically generated, providing a consistent quantitative reference across the gel for precise molecular weight or concentration estimation.

Together, these features transform the image into a fully quantitative dataset, giving users a precise, visual, and traceable understanding of their Western blot results.

Summary

Vilber's Virtual Blot technology introduces a new paradigm in Western blot analysis by turning conventional 2D blot images into quantitative, data-driven representations. Built on deep learning–based segmentation and intensity mapping, it ensures absolute quantification and visual clarity while maintaining full data integrity. Researchers gain immediate access to reliable, interpretable, and publication-ready results effortlessly.

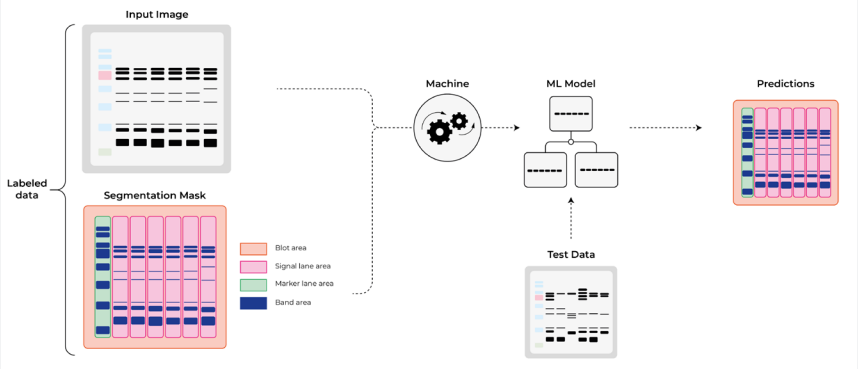

Figure 2. Supervised Learning method used to train our model