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The alignment of the segmented sections for each subject was accomplished by a sequential slice-to-slice image-based registration approach. Regions in image pairs were matched by translating and rotating images following a precise registration. First, we converted the RGB image of a section into gray scale and then employed a median filter to remove the noise. Then, we did a rough registration followed by a fine-registration using rigid intensity-based image registrations with different optimizer and metric configuration properties 35 . In MATLAB, we set the `imregconfig` function, which determines the optimizer and the metric configuration, to the multimodal configuration, as images may have varying intensity distributions. The function `imregconfig` was set to its default values for the rough registration, while the growth factor, initial radius, and maximum iterations were updated to 1.02, 2103, and 300, respectively, for the fine-registration. For the image registration, images were downscaled by a factor of four in all directions before any transformations were done in order to increase the registration speed. After the transformation matrix calculation, the images were upscaled again in order to recover the original scales. After all the images were aligned, a window in which only the tissue remained was chosen. The images were chopped to this window and prepared for analysis, see Fig. 3 C. Once we've digitized the radiograph and labeled the anatomical features, we can compute the number of cells that would be expected to be in the sample, including the bone marrow leukemia cells. The calculation is then performed after each section of the sample has been labeled, and then the results are compared to the final labeled scan. This allows us to compute the total number of cells that need to be counted, the number of living cells, and the fraction of leukemia cells in the sample.

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