State of the art high throughput microscopy calls for software solutions that can handle huge volumes of heterogeneous image data. These kinds of software solutions have to fulfill an extensive range of requirements (e.g. image analysis, machine learning, statistics, and visualization) and yet still be easy to use for the non expert. There are many monolithic platforms and some highly task oriented platforms that can process and analyze biological image data.

However, in view of the diverse nature of present problems, it is often necessary to integrate several applications. This involves going through many manual, time consuming and error prone steps, which are hard to document and therefore incomprehensible to others. This explains the increasing popularity of integrative workflow systems. KNIME is a user friendly and comprehensive open source data integration, processing, analysis, and exploration platform designed to handle large amounts of heterogeneous data. It therefore satisfies the aforementioned requirements. As an integration platform, KNIME directly combines functionality from several different domains. The KNIME Image Processing Extension is designed to extend KNIME by providing algorithms and datastructures, which enable KNIME users to process and analyze images. Combined with other existing KNIME extensions, non experts can easily compose complex domain comprehensive workflows. Further advantages directly inherited from KNIME include intelligent data caching strategy and fast prototyping of understandable workflows. Not wishing to reinvent the wheel, KNIME Image Processing integrates with ImageJ1, ImageJ2, OMERO, OpenCV and Tess4J, among others.

KNIME Image Processing is already used to solve several segmentation, classification and tracking problems in different areas of science, such as biology, chemistry and physics.