

Intelligent Karyotyping Workflow



METAPHASE FINDING

- Fully automated capture of metaphase chromosomes with Metafer.
- Unattended high-volume imaging of up to 800 slides.
- Manual image capture with oneclick for additional details.
- Support of human and non-human chromosomes and most common banding techniques.



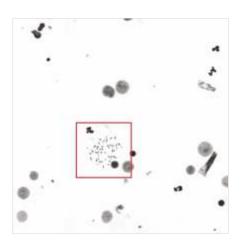
CHROMOSOME SEPARATION

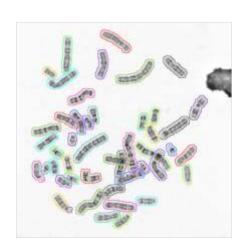
- Separation in Ikaros is based on Deep Neural Networks (DNNs), an advance in artificial intelligence.
- DNN-based proposal for the individual chromosomes as separate objects to help users separate clusters faster.
- Colored contour lines and brush tool for easy manual separation.

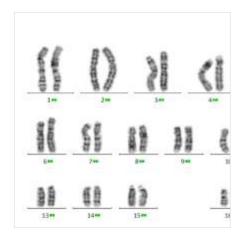


KARYOGRAM ASSIGNMENT

- Ikaros also uses Deep Neural Networks (DNNs) for karyogram assignment.
- Karyogram proposals ready for expert review. Colored squares indicate software-calculated chromosome assignment probabilites.
- Manual shifting, swapping, rotating, etc. for quick manual operations.

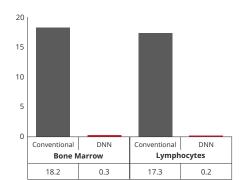








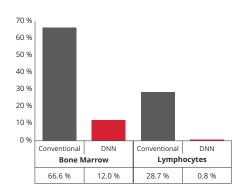
CHROMOSOME SEPARATION Number of Manual Operations



KARYO

KARYOGRAM ASSIGNMENT

Error Rates per Metaphase



EUROPE

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Italy, Milan info@metasystems-italy.com

AMERICAS

USA, Medford

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ASIA

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China, Taizhou info@metasystems-china.com

India, Bangalore info@metasystems-india.com

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We experienced a time gain of up to 50% in the karyotype analysis of bone marrow metaphases. This enormous gain in efficiency allows us to keep pace with the ever-increasing workload in times of shortage of personnel resources.

Prof. Claudia Haferlach

MD from MLL (Münchner Leukämielabor GmbH, Germany) www.mll.com

Diagrams above:

Mean number of manual operations by the user for 10 metaphase cells either derived from bone marrow or lymphocytes analyzed with the conventional (grey) and the DNN-based algorithm (red) in Ikaros.

Mean error rates for chromosome assignment per metaphase in Ikaros using the conventional (grey) and the DNN-based algorithm (red) for ~ 100,000 bone marrow and ~ 150,000 lymphocyte metaphases.

The new DNN-based algorithms showed significant improvements in the proposed chromosome separation and assignment.

The described functions refer to the following software versions: **Ikaros** 6.3 | **Metafer** 4.3

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The presented solutions are application-specific adaptations of the lkaros and Metafer software. It is possible that further adaptations to specific specimen conditions are necessary.



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