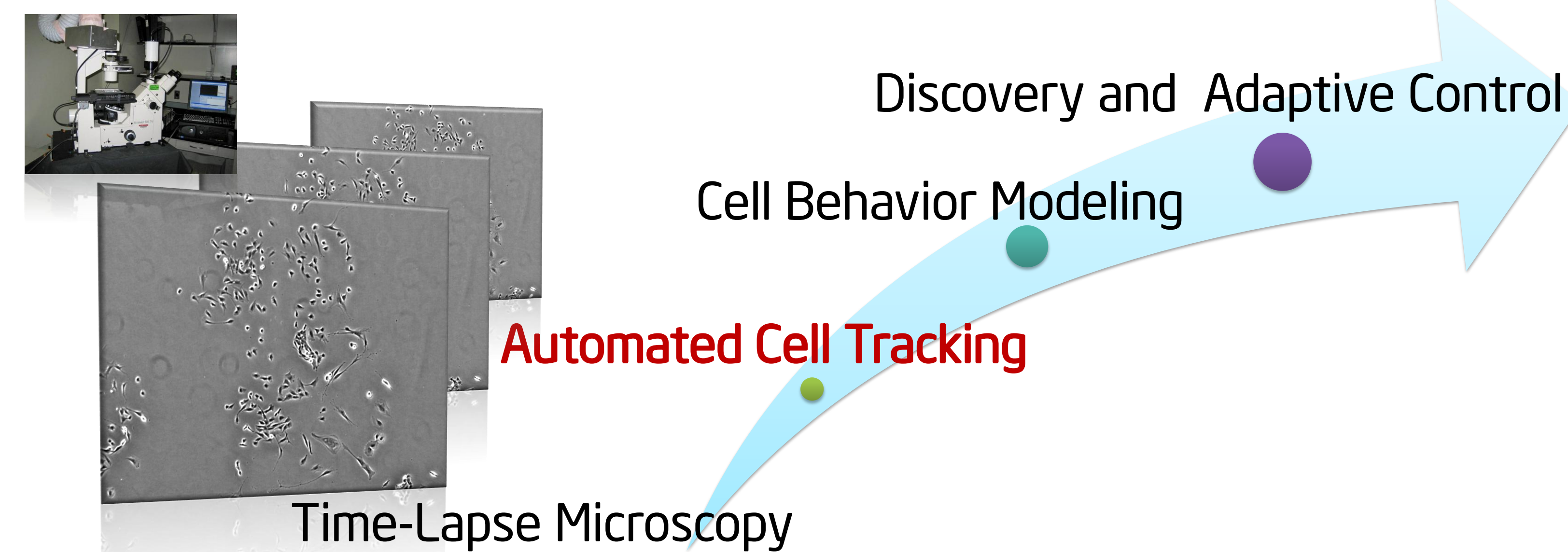


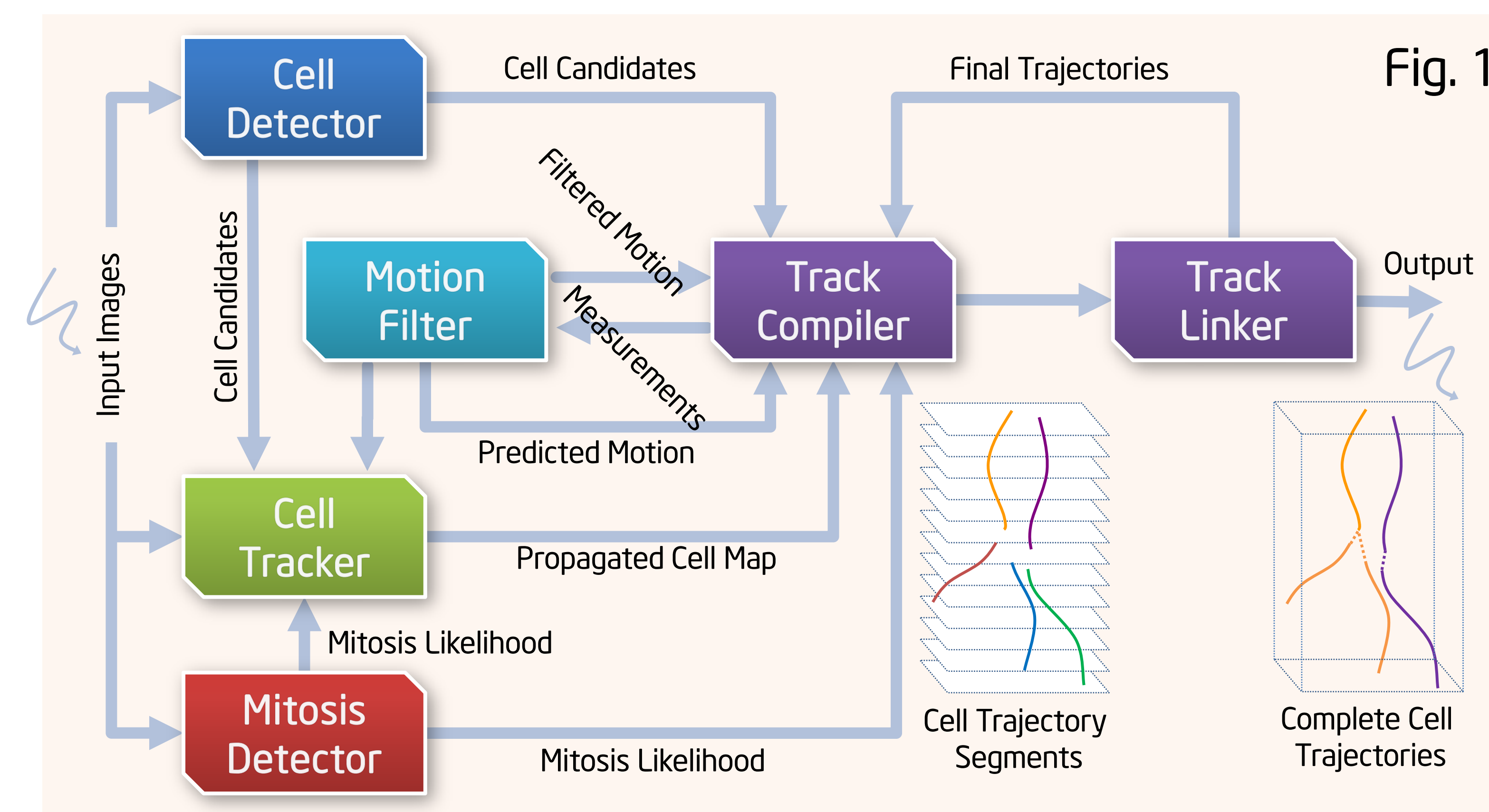
Automated Visual-Tracking of Stem Cell Populations in Time-Lapse Microscopy Video

1. Introduction



- **High-throughput** spatiotemporal measurements of cell behaviors, including migration, mitosis, apoptosis, differentiation, and lineage facilitate rapid advancements of biological discovery and its translation into new clinical therapies.
- **Significant challenges** to be addressed: massive amount of image data, low signal-to-noise ratio, high and varying cell numbers, topological complexities of cell shapes, and cell divisions/deaths.
- We present a vision-based cell tracking system that can simultaneously follow up to **thousands** of individual cells within a population in an image sequence acquired with **time-lapse phase contrast microscopy** or **differential interference contrast (DIC) microscopy**.

2. Overview of Cell Tracking System

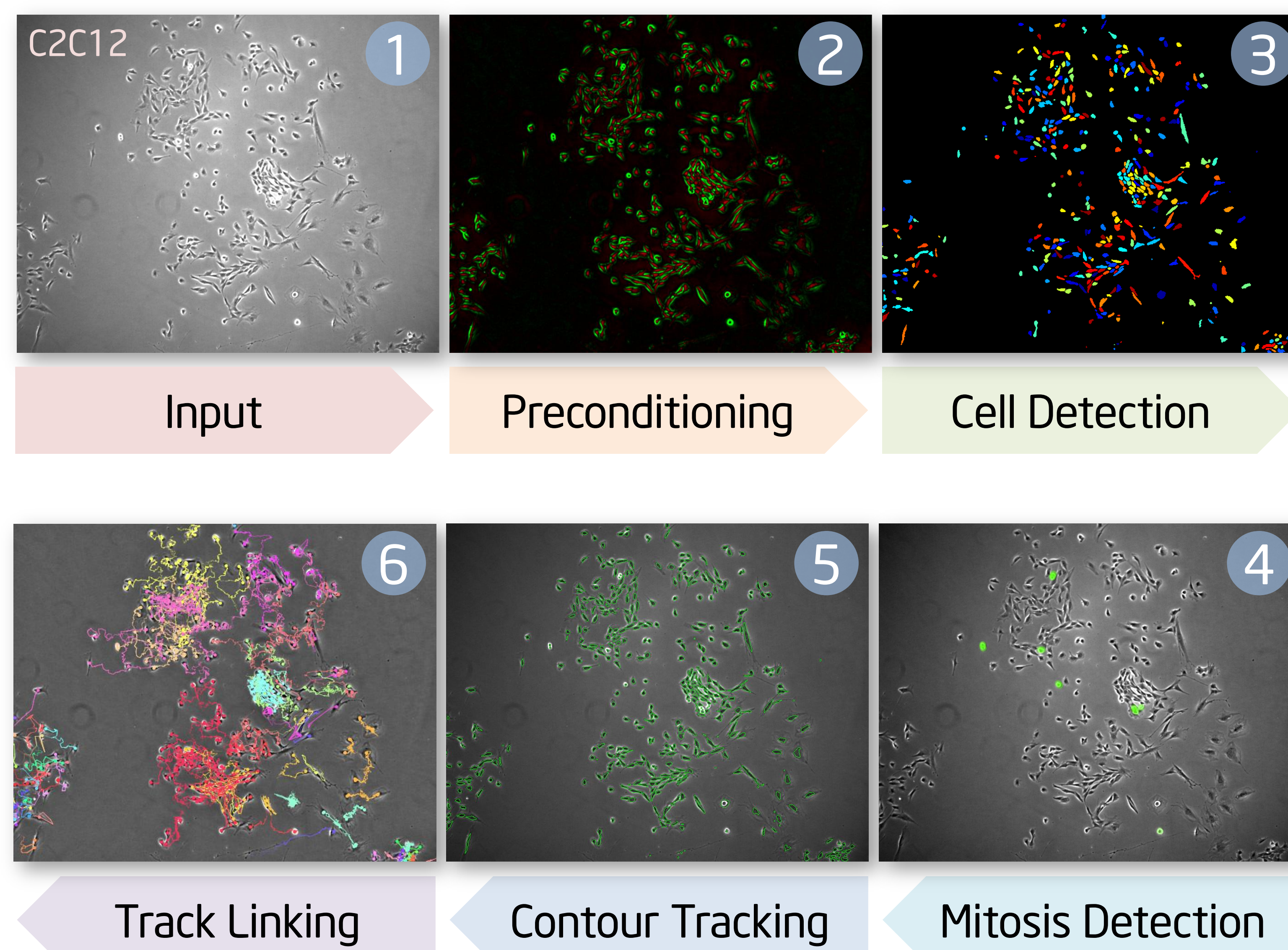


- Multi-modular design enables fully-automated cell detection and tracking
- Integrates the power of three tracking mechanisms:
 - Active contour tracking
 - Bayesian probabilistic tracking
 - Spatiotemporal feature-based tracking

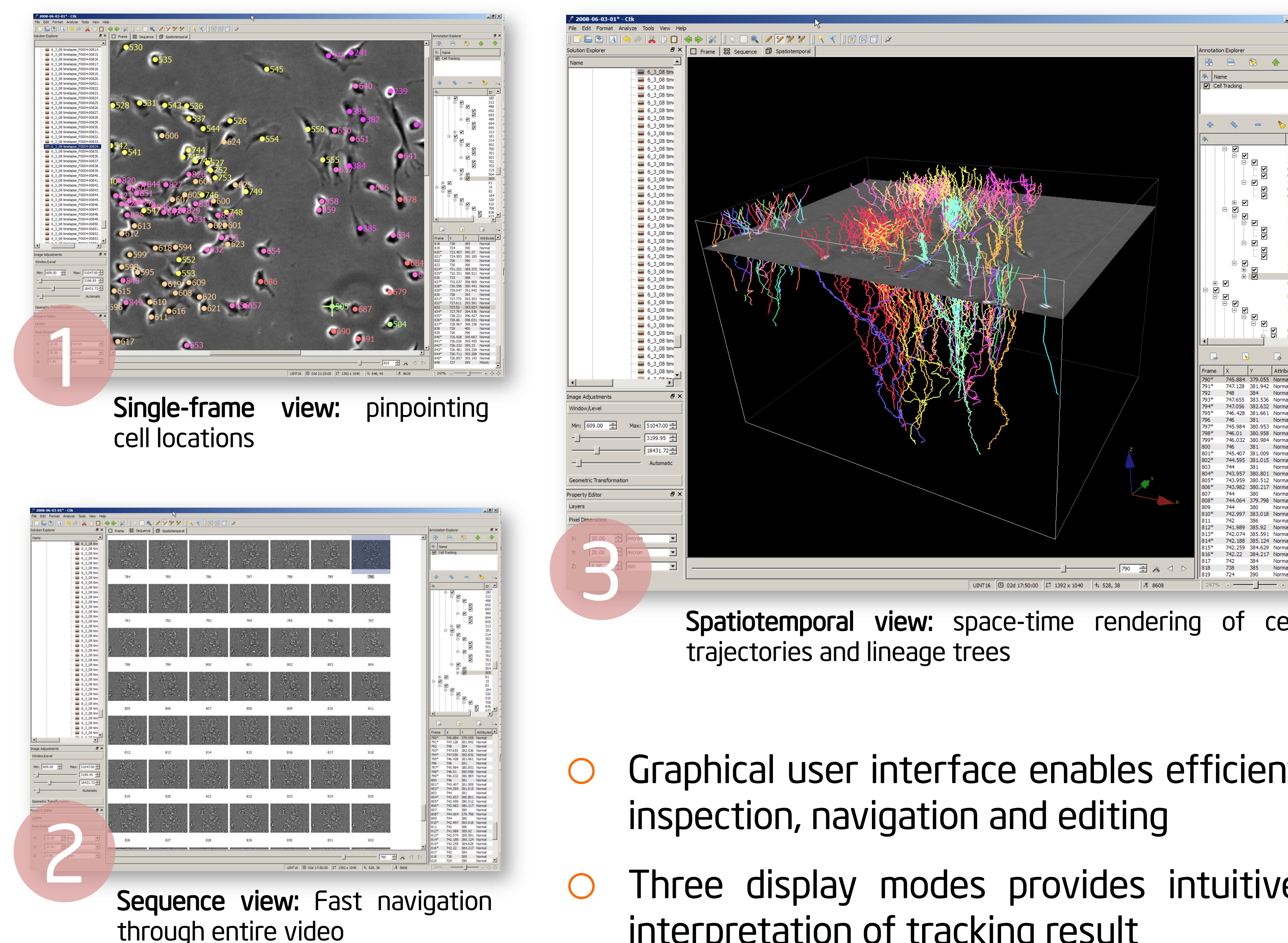
3. System Modules

- **Image preconditioner** (omitted in Fig. 1): enhances/transforms the input images into a form that is more suitable for subsequent image analysis.
- **Cell detector**: detects and labels candidate cell regions in the input images utilizing region, edge, and shape information.
- **Cell tracker**: tracks candidate cell regions and their identities across frames, and in the meantime, detects cellular divisions and deaths. It consists of the following two sub-modules:
 - **Model propagator**: propagates cell regions and identities through time using a fast active contour algorithm.
 - **Event detector**: detects cellular mitosis and apoptosis events using feature-based classification.
- **Motion filter**: performs prediction and filtering of the cell motion dynamics using a biologically relevant interacting multiple-models filter.
- **Track arbitrator**: manages the whole tracking task. It consists of two sub-modules:
 - **Track compiler**: generates intermediate result called track segments by fusing the output from the above modules;
 - **Track linker**: utilizes spatiotemporal context to establish complete cell trajectories and lineages.

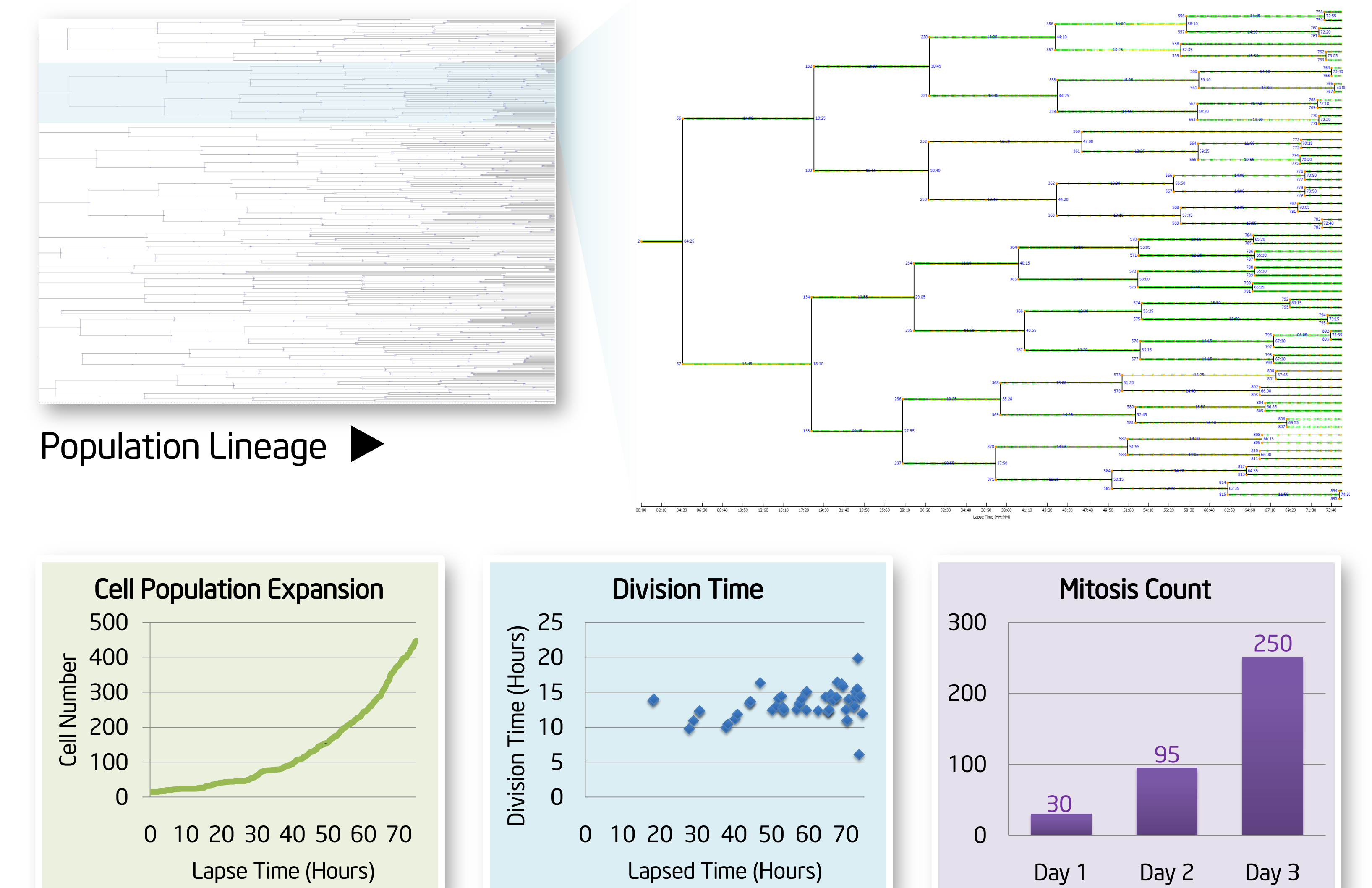
4. Key Processing Steps



5. Graphical User Interface



6. Quantification & Reporting



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