1. Introduction:

**Problem:** Mitosis means the process of cell division. It is a spatio-temporal event with the visual transition from 0 shape to 8 shape.

**Motivation:** automated quantification of cellular mitosis in time-lapse microscopy video is useful for multiple applications, such as tissue engineering, cancer research, and developmental biology.

**Challenges:** cells undergo drastic morphological and appearance changes during mitosis

We propose a **fully-automated detection method** which can accurately locate and count mitosis events in the cell image sequences acquired with **phase contrast microscopy**.

2. Overview:

- Input → Mitosis Candidate Generation → Spatio-temporal Location → Temporal Inference for Refinement → Output

**Advantages:**
- Independent on empirical parameters, ad hoc image processing, or explicit cell tracking;
- Straightforwardly adaptable to different cell types.

3. Methodology:

**A. Mitosis Candidate Generation:** Extraction of mitotic cell candidates & generation of trajectories of mitosis event candidates in the spatio-temporal domain.

- **Image Preconditioning:** Input images are transformed based on physics of phase contrast image formation such that potential mitotic cell candidates are assigned high values.

- **Volumetric Region Grow:** Mitotic cell candidates are linked to generate trajectories of mitosis event candidates based on the intensity similarity in the spatio-temporal domain.

**B. Spatio-temporal Location:** Modeling a mitotic cell classifier with **high recall** for temporal location in each mitosis event candidate.

- **Features:** Area, Convex Area, Eccentricity, Major Axis Length, Minor Axis Length, Orientation, Maximum Intensity, Mean Intensity, Minimum Intensity;
- **Model:** Support Vector Machine with RBF kernel.

**C. Temporal Inference for refinement:** Modeling the transition from 0 shape pattern to 8 shape pattern to eliminate the false positive and refine the location of the first 8 pattern.

- **Features:** Histogram of Oriented Gradient;
- **Model:** Hidden Markov Model

**Baum-Welch estimation method is used for model training; Viterbi algorithm is used to decode the sequence and compute the log probability.**

4. Key Processing Steps:


5. Evaluation:

**A. Data:**
C2C12 Cell imaged with Phase Contrast Microscopy; 10 sequences; 1000 images per sequence.

**B. Performance of SVM classifier for mitosis detection:**
- Little training data: for individual image sequence, we can simply choose the first 100 positive samples and 200 negative samples for training and the average recall and precision are 99% and 75%;
- Generalization: for 5 test image sequences, we can train models with only 10% of positive samples and negative samples from 5 training image sequences and the average recall and precision are 99% and 71%;

**C. Performance of HMM classifier for mitosis detection:**
Average Recall: 97% Average Precision: 90%

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