Embryo Quality Assessment from Image Sequences
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Abstract—Analysis of long image sequences can provide information for embryo quality assessment. Previous methods use morphological features from a short sequence of images from day-1, day-3 or day-5 embryos. Efficiency remains poor due to uncertainty of short-span features and inter-observer variability. In this research, we propose a method for assessing the quality of mouse embryos by analyzing feature consistency over long time-series up to blastocyst stage. Two features viz. nuclei counts and nuclear volumes are computed automatically from 4D time-series. An adaptive threshold technique is proposed for extracting nuclear volumes using locally mean intensity difference as texture feature. Cellular damages were mimicked by frequent light excitation on embryo samples. An investigation with ten embryo images reveal a promising achievement of the technique presented in terms of normalized cross correlation.

I. PROPOSED METHOD

Transferring single healthy embryo is very important for successful in vitro fertilization (IVF). Currently, this decision is made by manually justifying morphological features from 2D images. A few automated methods do exist but they exploit features from short 2D image sequences in the cleavage or blastocyst stage. Selection efficiency is poor [1] due to uncertainty of short-sequence features. Analysis of long time-series up to blastocyst stage is an option. In this research, we propose an automated method for embryo quality assessment based on analyzing feature consistency of 4D time-series. Nuclei count and nuclear mean volume are used as features.

Counting of cell nuclei is done by automated extraction of centroids from 4D time-series [2-3]. Nuclear volumes are extracted using a locally adaptive threshold technique, which integrates a texture feature, called mean absolute intensity difference (MAD) with a global threshold. Since MAD varies with space, we can compute local threshold \( t_i \) using

\[
t_i(x,y,z) = 1 - \left( \frac{\text{MAD}(x,y,z)}{\text{Max}(t_{\text{pre}}) - \text{Min}(t_{\text{pre}})} \right)^n \times t_{\text{oth}},
\]

where \( t_{\text{oth}} \) is the global threshold [4]. Exponent \( n \) is chosen to be 5 in our study. Binary output is post-processed to remove holes using morphological operations.

II. RESULTS AND REMARKS

Ten (10) embryos are analyzed. First five, captured at 15 minute interval, constructs healthy group. The rest five, captured at 225 seconds, constructs unhealthy group. Embryo volume consists of 103×103×51 voxels with 0.8×0.8×2.0 \( \mu \text{m} \) resolution. Figure 1 (left) shows consistent and rhythmic development of nuclear counts and volumes, keeping pace with cell division cycles as expected from Group-1 embryos (blue lines). In contrast, consistency gets broken in Group-2 members (red lines), implying their unhealthy conditions.

Quantitative evaluation of embryo quality is performed using normalized cross-correlation (NCC). Each-pair of time-series of the intra- and inter-group features is considered as leave-one-out fashion. Graphs in Fig. 1 (right) show highly positive correlations among Group-1 and highly negative between group correlations for all possible combinations of nuclear volumes and counts features. However, slightly oscillating inter-group correlations are found for count-count and volume-count time-series. Results suggest that our method can be used for discriminating healthy embryos from unhealthy counterpart. Future studies will be performed for overall improvement of the features and method.

REFERENCES


