OSIRIS: A valuable tool for assessing donor cell engraftment after stem cell transplant

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OSIRIS Software
- Open source
- Cross-platform (Windows, Mac)
- Displays - Stacked graph Table
- Quality analysis
- Reanalysis prediction
- Validated as an expert system

Peak analysis
- Osiris mathematically analyzes data in .fsa and .hid files, compares the curves to peak, artifact, and baseline signatures, and assesses sample quality with user criteria.

Artifact recognition
OSIRIS recognizes 150 artifact signatures. Artifact recognition is sensitive and specific.

Using OSIRIS
OSIRIS software is freely available for download on the OSIRIS web page, along with hints for installation:

The OSIRIS User’s Guide is available on the homepage and in the program itself (F1). It includes a tutorial for a quick start using the software. The download also includes a variety of demonstration .fsa and .hid format data generated using different several kits.

Open Source Collaboration
OSIRIS source code is currently available for download from the GitHub source code repository. A number of groups are interested in collaborating on improving OSIRIS. We invite new collaborators to join the OSIRIS community.

For questions or requests, please contact: forensics@ncbi.nlm.nih.gov

For announcements regarding OSIRIS, please subscribe to the forensics-announce list:

Chimerism Analysis

Osis and GeneMapper give similar chimerism analysis results, when the analysis is done using two loci in two PCR replicates of the same sample.

Analysis Comparison

Difference in chimerism estimate of PCR replicates of a single sample analyzed with GeneMapper and with Osiris. Axle distance from the equivalence line shows the degree of disparity between the two programs.

The two graphs suggest that there is significant variability in PCR replicates of the same sample. Variability can be reduced by analyzing multiple loci or PCR replicates.