



AddFCSEventIndex Documentation

Description: Adds indexes to events in a Flow Cytometry Standard (FCS) data file.

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Summary

The module takes an input FCS data file and adds an index to each event as a new parameters. The index may be used identify events in different analytical processing steps, e.g., to facilitate back-gating independently of the flow cytometry analysis tools used.

For more information about the FCS file standard and its parameters, see [this page at the International Society for Advancement of Cytometry](#).

References

Spidlen J, Moore W, Parks D, Goldberg M, Bray C, Bierre P, Gorombey P, Hyun B, Hubbard M, Lange S, Lefebvre R, Leif R, Novo D, Ostruszka L, Treister A, Wood J, Murphy RF, Roederer M, Sudar D, Zigon R, Brinkman RR. Data file standard for flow cytometry, version FCS 3.1. *Cytometry A*. 2010;77:97-100.

Parameters

Name	Description
Input data file	An FCS data file to which you want to add indexes.
Start index	The index number for the first event in the data set; the default is 1. The index will be incremented by 1 for each of the events in the data set.
Index parameter short name	The short name (\$PnN keyword) of the parameter to get the index; the default is "Index."
Index parameter long name	The long name (\$PnS keyword) of the parameter to get the index; the default is blank.

GenePattern

Output fcs file name	The output file name. The default uses the input file name as the base.
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Output Files

1. Output FCS data file

A single FCS data file containing the events from the input data file with an additional index parameter. The index is assigned to events in the order in which they are stored in the FCS file. The first event gets the number specified in the *Start index* parameter.

Platform Dependencies

Module type:	Flow Cytometry
CPU type:	any
OS:	any
Language:	Java (1.5 minimum)

GenePattern Module Version Notes

Date	Version	Description
6/29/2012	v. 2	AddFCSEventIndex version 2 added fix for parsing empty keyword values