

Software for Genomic/Epigenomic Research Based on Capillary Electrophoresis

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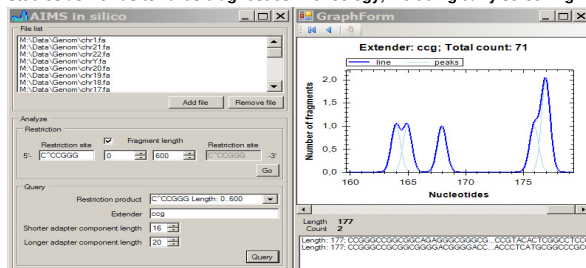
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AIMS *in silico*

A suggestion tool for AIMS experimental design and results analysis

Amplification of intermethylated sites (AIMS) is a powerful tool for differential methylation screening of genomes. Its applications have nevertheless been limited until recently for the absence of appropriate computer software for the analysis of AIMS results. *AIMS in silico* computer suggestion tool is capable of predicting possible experimental outcomes. It assists in designing AIMS experiments depending on the research goals and available instrumentation, and in analyzing experimental results from the point of view of genomic locations of the DNA fragments under study.

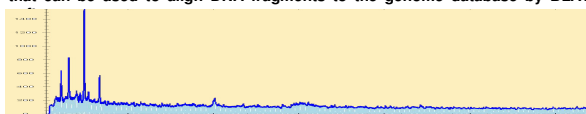
AIMS in silico computer software is intended to standardize AIMS applications and to turn it into one of the principal approaches towards cancer methylomes studies as well as towards diagnostics in oncology, including early screening.



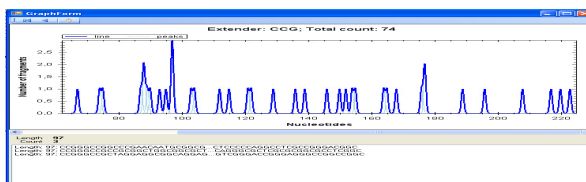
This computer program interactive interface invites a user to input the files containing sequences to be analyzed and to select the preliminary experimental conditions, such as restriction endonuclease recognition and cleavage sites, lengths of the adaptor's shorter and longer components, and/or nucleotide sequences of specific extenders of the universal primer. There is an option to limit the lengths of the resulting AIMS fragments, in dependence upon the technique used for their physical separation.

The output information includes total number of the PCR products obtainable with AIMS with the preset conditions, distribution of the products by their lengths, and 25-base individual sequences flanking each of them. Graphically information is presented as a virtual capillary electropherogram. The peaks are clickable, calling forth their individual information in a separate window.

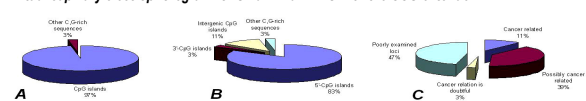
Flanking 3'- and 5'- nucleotide sequences suggested by *AIMS in silico* computer program for each PCR product represent unique genomic descriptors that can be used to align DNA fragments to the genome database by BLAT



Virtual capillary electropherogram for *Smal*-*XmaI* AIMS with non-extended primers



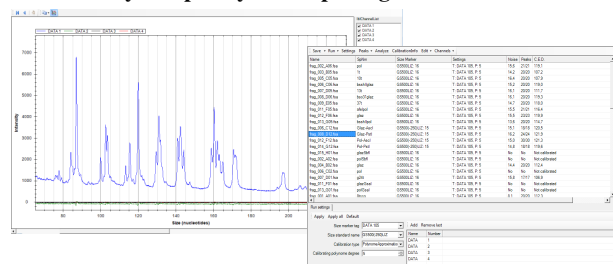
Virtual capillary electropherogram for *Smal*-*XmaI* AIMS with the CCG extender



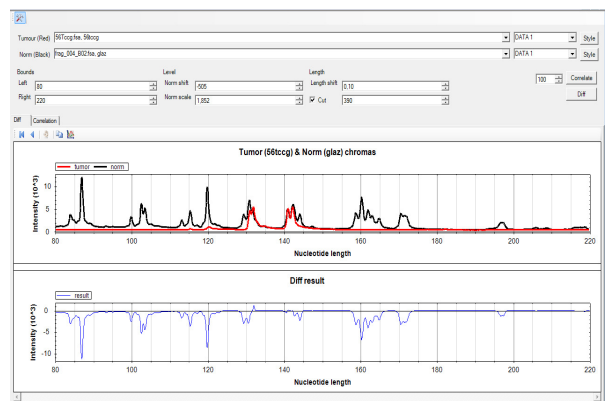
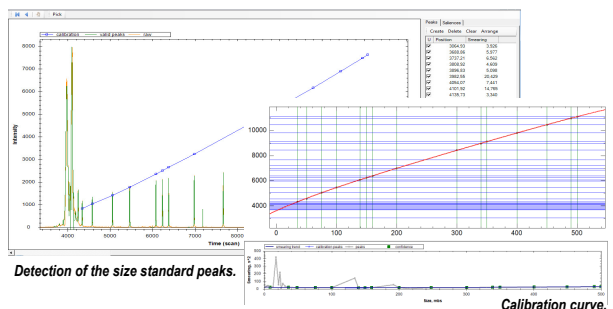
The composition of the predicted genomic representation obtainable with the CCG-extender-AIMS. A – fractions of CpG islands and other sequences; B – positions of the CpG islands in relation to the coding sequences; C – Estimated cancer relation of the genes associated with the predicted CpG islands.

PeakPick

View & analyse capillary electropherograms



PeakPick is a light and easy to use program suitable for viewing and analyzing capillary electropherograms. It is especially recommended for use with complex fingerprint-like results where the adjacent peaks tend to influence each other distorting the landscape.



Differentiation of fingerprint-like capillary electropherograms. Upper plot: correlated and normalized electropherograms (red and black). Lower plot: differentiation (blue).

Availability: *AIMS in silico* & *PeakPick* are computer programs downloadable from the web site of the Epigenetics laboratory:

<http://abif.freeflux.net/projects/ais>

<http://abif.freeflux.net/projects/peakpick>