#### Datasheet of the IKTA3/086 project

# I. Development of data analysis software for processing "multiplex microbead assay" data

Project start: November 1, 2000, duration: 14 months.

Amount of support: KHUF 14 500, total project cost: KHUF 29 000.

Project leader: Lustyik György Dr.

Soft Flow Hungary Kutató Fejlesztő Kft.

H-7628 Pécs, Kedves u. 24.

<mailto:lustyik@softflow.hu>, phone: +36 (72) 240-064

Project URL: <http://www.softflow.hu>

#### **II.** Consortium members (number of members = 1, the first member is the project co-ordinator)

no	name	support	total cost
1	Soft Flow Hungary Ltd.	KHUF 14 500	KHUF 29 000

#### III. Public presentations

Presentation #1 (28-január-2001): HTML (72 KB)

Presentation #2 (28-november-2001): PPT (2316 KB)

The presentations are accessible through a special webpage summarizing the project presentations.

### IV. Goals of the project

A multi-platform software package that supports biomedical research and clinical applications is being developed. The software is a quantitative fluorescence cytometry (QFCM) application designed according to the guidelines of the European Working Group on Clinical Cell Analysis, National Committee on Clinical Laboratory Standards, USA and the International Federation of Clinical Chemistry. The program package supports the analysis and processing of research and clinical data acquired with the so-called Suspension Array Technology (SAT) or Multiplexed Microbead Assay (MMA) technology. The software package provides sophisticated off-line analysis tools for data acquired with various instruments using microbeads of different sources. The software has built-in tools to design an assay setup for both clinical and research projects, standardized data evaluation modules, quality control for both the instrument performance and the assay protocol, and flexible reporting forms. - The software package builds a communication channel between the manufacturers of the MMA kits and the users of these products. In addition, the software provides adequate tools for those users who develop their own, individually designed microbead assay kits and/or experimental protocols. The users of the software are laboratory personal that is familiar with various forms of the ELISA type techniques, therefore the software adapted as much as possible from the terminology and human interface solutions of the existing ELISA software packages. The program supports any language and the use of any non-English character sets. - Regarding the specific application of the software we focus on four overlapping subprojects: (a) Technological development of biological microbead procedures using cells or microorganisms as substitutes for polymeric microspheres to lower the cost of SAT compared to the cost of methods using microbeads manufactured by polymer chemistry. (b) Development of a test to detect gene translocations and rearrangements frequently responsible for malignant transformations. A method based on measuring bead-based hybridization of specific 5' and 3' nucleotide sequences in the vicinity of chromosomal translocation breakpoints would allow large scale screening of leukemias and various types of cancers by the measurement of 5'/3' sequence ratio. (c) Development of a DNA binding protein profiling assay providing easy, reproducible and high throughput technology to determine the expression pattern of transcription factors (TFs) binding to single stranded hexamere oligonucleotide sequences anchored to the solid phase surface of microspheres. (d) Development of artificial neural network software applications to analyze and classify the "fingerprint patterns" produced by the SAT measurements. - The substitution of cells and bacteria (biological microbeads) for the polymer microspheres in SAT is a cheaper

solution than the application of the polymer beads. Potential users are all clinical and research laboratories performing qualitative SAT. The gene rearrangement test using the 5'/3' ratioing has an almost immediate clinical application for large throughput screening of DNA samples of cancer tissues and cells. The development of a non-parametric data analysis algorithm based on the artificial neural network technology provides the ability to classify the "empirical fingerprint pattern" formed by both the SAT data points and the biological microchip readings.

# V. Project results (in case of finished projects)

The project is not finished.

### VI. Data on consortium members (number of members = 1)

1. Soft Flow Hungary Ltd. (co-ordinator)

URL: <http://www.softflow.hu>

Support for the co-ordinator: KHUF 14 500, and its total cost: KHUF 29 000.

Contract number: OMFB-02596/2000.

Team leader: Lustyik György Dr.

Soft Flow Hungary Kutató Fejlesztő Kft.

H-7628 Pécs, Kedves u. 24

<mailto:lustyik@softflow.hu>, phone: +36 (72) 240-064