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Authors

McDaniel, J Crites, B

Curtis, C

<u>et al.</u>

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Design Automation for Flow-based Microfluidic Biochips

Jeffrey McDaniel, Brian Crites, Christopher Curtis, and Philip Brisk-Member, IEEE

Abstract— Flow-based microfluidic biochips are presently designed, verified, and physically laid out manually. Software automation, similar to that employed for integrated circuits in the semiconductor industry, will raise productivity and reduce the cost of using biochips in scientific experiments.

I. SYSTEM OVERVIEW

The integrated microvalve is the building block for flow-based biochips. Similar in principle to transistors in the semiconductor industry, microvalves can be combined to form components (e.g., mixers, memories, etc.); fully functional integrated biochips can then be designed as a collection of interconnected components. At present, this design process is carried out by hand using software (e.g., AutoCAD) which is tedious, time-consuming, and prone to error. To reduce design time, we propose that future biochip designers should use domain-specific languages to specify their systems, and rely on Microfluidic Design Automation (MDA) software to synthesize and physically lay out the devices. This approach is analogous to Electronic Design Automation (EDA) in the semiconductor industry.

Fig. 1 depicts an typical design flow for flow-based microfluidic biochips [1]. The application (a biochemical assay) is specified using BioCoder [2], a domain-specific language for automated biology. The software automatically synthesizes a biochip architecture that can execute the assay. The architecture is converted to MHDL, a human-readable microfluidic hardware design language, enabling manual refinement [3]; alternatively, MHDL can be used to design general-purpose biochips that are not assay-specific. The software includes modules that can simulate and verify the ability of the MDHL-specified chip to execute the assay. When the designer is satisfied with the architecture, the software physically lays out the different layers of the chip. The output is an AutoCAD DXF (or other vector graphics) file that can be transferred to a foundry for fabrication.

II. EXAMPLE

Fig. 2 depicts a variant of the UC Berkeley Mars Organic Analyzer (MOA), which was designed and physically laid out using our software. The original MOA was designed and laid out manually by device experts who have a deep understanding of the underlying technology [4]. MDA offers productivity benefits to designers, and, moreover, opens the possibility for non-experts to design biochips using domain specific language specifications as entry points.

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J. McDaniel, B. Crites, C. Curtis, and P. Brisk are with the, University of California, Riverside, Riverside, CA 92521 USA. (Corresponding author phone: 951-827-2030; e-mail: philip@cs.ucr.edu).

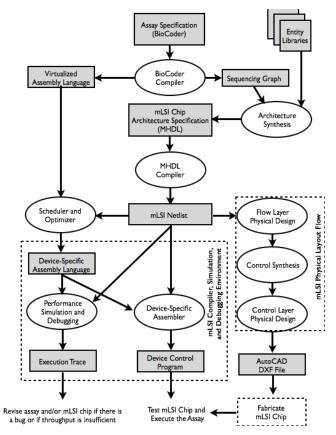


Figure 1. Overview of the MDA software under development [1, 3].

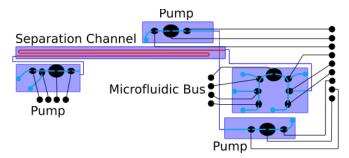


Figure 2. Picture of the Mars Organic Analyzer [4], laid out by software.

REFERENCES

- J. McDaniel, C. Curtis, and P. Brisk, "Automatic synthesis of microfluidic large scale integration chips from a domain-specific language," in Proc. BioCAS, 2013.
- [2] V. Ananthanarayanan and W. Thies, "Biocoder: a programming language for standardizing and automating biology protocols. *Journal* of Biological Engineering 4(13), 2010.
- [3] J. McDaniel, et al., "Design and verification tools for continuous fluid flow-based microfluidic devices," in Proc. ASPDAC 2013.
- [4] A. M. Skelley, et al. "Development and evaluation of a microdevice for amino acid biomarker detection and analysis on Mars," *Proceedings of the National Academy of Sciences of the United States* of America 102(4):1041-1046, 2005.