Fraunhofer
IPA

FRAUNHOFER-INSTITUT FÜR PRODUKTIONSTECHNIK UND AUTOMATISIERUNG IPA

MAGNETO-HYDRODYNAMIC FOCUSING (MHF) FOR POINT OF CARE APPLICATIONS

Christian Reis, Caroline Siegert
Fraunhofer Institute for Manufacturing Engineering and Automation, Project Group for Automation in Medicine and Biotechnology, Theodor-Kutzer-Ufer 1-3, 68167 Mannheim, Germany
Contact: christian.reis@ipa.fraunhofer.de

MOTIVATION

The knowledge of forces acting on magnetizable beads in magnetic fields enables to use them not only as a purification instrument but also for analytical purposes. We wanted to use this to design and build up a Point of Care instrument, which is able to analyze proteins in unpurified samples. Therefore magnetic beads are forced to describe certain trajectories via oscillating magnetic fields. This allows us to move magnetic beads in a hydrodynamic system. This movement creates a dynamic fluorescence signal, which gives an insight about how many molecules are bound to the particle surface. This MHF technology can be combined with several assays, which are already on the market, maximizing signal to noise ratio.

AIMS

- Development of a Point of Care system for protein analysis
- Including optimized magnets with magnetic field design
- Integration of a fluorescence detection system
- Combination of purification and analysis in a one-step process

MATERIALS AND METHODS

The MHF system consists of two optimized permanent magnets and a cuvette with 160 µl total volume (figure 1).

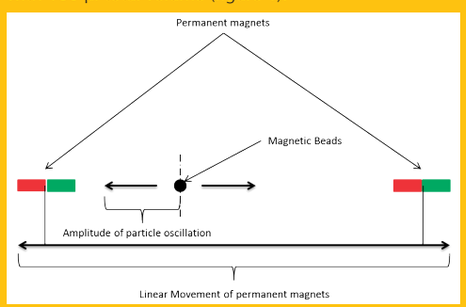


Figure 1: MHF system layout for magnetic bead oscillation.

The optimization of magnetic fields and magnet geometry was performed via ANSYS MAXWELL. The motion equation was derived from magnetic forces and hydrodynamic forces acting on the magnetic beads (figure 2).

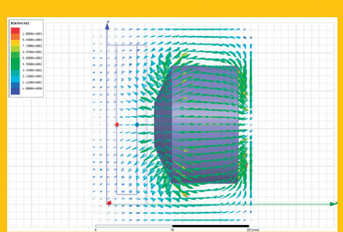
$$F_{magn.} - F_{hydr.} = m_{Part.} a_{Part.}$$

$$m_{Part.} a_{Part.} + 6\pi\eta r v_{Part.} = V_{Part.} M_{Part.(x;t)} \nabla B_{(t)}$$

$$m_{Part.} \frac{d^2 x_{Pp}}{dt^2} - 6\pi\eta r \frac{dx_{Pp}}{dt} = V_{Part.} * M_{Part.(x;t)} * \nabla B_{(t)}$$

Figure 2: Motion equation for particle movement in the MHF system.

The system is also equipped with a fluorescence detection unit to enable fluorescence analysis.
For evaluation of the system a lyophilized protein of interest in human serum was dissolved in PBS. All proteins were dyed using FITC. 1 µg of magnetic beads (Chemicell, 1 µm in diameter, streptavidin labeled) was coated with 0.1 pmol anti-protein of interest monoclonal antibody. A total of 6.5 ng protein of interest with 80 µg serum protein (both FITC labelled) was analyzed in 160 µl total sample volume. The signal was processed using MatLab.
The geometry of the permanent magnet was optimized using B-Field simulations with ANSYS MAXWELL (figure 3 and 4).



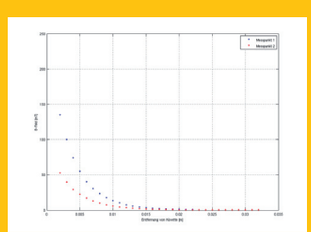


Figure 3 (left) : Simulation of the magnetic field of different permanent magnet geometries (reference points in red and blue).
Figure 4 (right): Linear movement of permanent magnets results in high B-field changes.

RESULTS

Detection of 6.5 ng protein of interest in 160 µl total sample volume was performed with 80 µg labeled serum protein as background (figure 5). The signal portion was ca. 0.008 %. Total protein concentration was 40 ng/ml for our protein of interest.

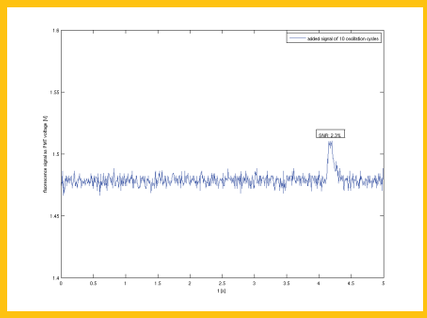


Figure 5: Signal processing with MatLab gives a clear signal for oscillating protein of interest bound to the magnetic beads.