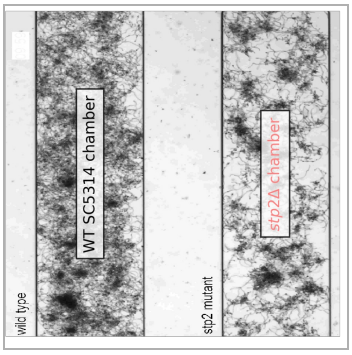

Bioflux Analyses V.2

VERSION 2
FEB 06, 2020

WORKS FOR ME 1

COMMENTS 0

DOI
dx.doi.org/10.17504/protocols.io.bb7qirmw

Tobias Weise[1], Bettina Boettcher[2], Slavena Vylkova[2]

[1]BioControl Jena GmbH, Jena, Germany; [2]Septomics Research Center, Friedrich Schiller University and Leibniz Institute for Natural Product Research and Infection Biology – Hans Knöll Institute, Jena, Germany

Tobias Weise
BioControl Jena GmbH

ABSTRACT

Biofilm formation under shear flow conditions was monitored using the Bioflux1000 device (Fluxion Biosciences, Inc.). In short, Candida albicans overnight cultures were washed in pre-warmed RPMI medium. Cells were seeded for 2-5 sec from the outlet well into the channels of Bioflux1000 flow chambers, which were primed before with warm medium. The cells were allowed to adhere to the channels for 90 min without any flow, followed by removal of non-adherent cells by flowing fresh, pre-warmed RPMI medium for 5 sec. Shear flow was set for time series experiments over 24 h biofilm formation and images were captured every 20 min. Two channels were investigated in parallel having a 10 × magnification to allow a direct comparison between a mutant and a reference (wild type) strain. Image capturing and stacks to movies was performed using the MetaMorph® Software (Molecular Devices).

Source material provided as AVI files was converted into single TIFF images as well as data frames containing meta data annotations. The individual image contains two growth chambers (wild type and mutant) separated by four edge lines. Images were rotated automatically to vertical alignment in order to carry out an automated chamber detection and analysis. The mean pixel intensity (i. e. grey scale value; reflecting cell density) of the individual chamber was calculated and added into the respective data frame.

An ODE model reflecting the logistic growth as well as the lag phase was fitted to the individual experiments. Fitting was carried out by minimising a cost function (unweighted least-squares-based) using the *Nelder-Mead* algorithm. Growth rate time series generated from the fitted model were used to compare wild type and mutant regarding the maximum observed growth rates at their respective time points.

All computations were performed using the programming language python (version 3.6.9) and the additional packages numpy (version 1.16.2), opencv-python (version 4.1.1.26), pandas (version 0.25.0), scipy (version 1.3.1) and scikit-image (version 0.15.0).

ATTACHMENTS

Bioflux_Analyses_samples.zip

DOI

dx.doi.org/10.17504/protocols.io.bb7qirmw

COLLECTION CITATION

Tobias Weise, Bettina Boettcher, Slavena Vylkova 2020. Bioflux Analyses. **protocols.io** https://dx.doi.org/10.17504/protocols.io.bb7qirmw

MANUSCRIPT CITATION please remember to cite the following publication along with this collection

This work was supported by the German Ministry for Education and Science in the program Unternehmen Region (BMBF 03Z2JN11).

KEYWORDS

Candida Albicans, Biofilm, Biofilm Formation, Growth Rate, Image Preprocessing, Edge Detection, ODE Model, Parameter Estimation

CREATED

Feb 05, 2020

LAST MODIFIED

Feb 06, 2020

COLLECTION INTEGER ID

32720

ATTACHMENTS

Bioflux_Analyses_samples.zip

FILES

Protocol

NAME

Bioflux Analyses: Image Preprocessing

VERSION 2

CREATED BY

Tobias WeiseBioControl Jena GmbH

OPEN →

Protocol

NAME

Bioflux Analyses: Modelling

VERSION 2

CREATED BY

Tobias WeiseBioControl Jena GmbH

OPEN →

Citation: Tobias Weise, Bettina Boettcher, Slavena Vylkova Bioflux Analyses https://dx.doi.org/10.17504/protocols.io.bb7qirmw