

Reporting Summary

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Statistics

For all statistical analyses, confirm that the following items are present in the figure legend, table legend, main text, or Methods section.

n/a Confirmed

- ☐ ☒ The exact sample size (n) for each experimental group/condition, given as a discrete number and unit of measurement
- ☐ ☒ A statement on whether measurements were taken from distinct samples or whether the same sample was measured repeatedly
- ☐ ☒ The statistical test(s) used AND whether they are one- or two-sided
Only common tests should be described solely by name; describe more complex techniques in the Methods section.
- ☒ ☐ A description of all covariates tested
- ☐ ☒ A description of any assumptions or corrections, such as tests of normality and adjustment for multiple comparisons
- ☐ ☒ A full description of the statistical parameters including central tendency (e.g. means) or other basic estimates (e.g. regression coefficient) AND variation (e.g. standard deviation) or associated estimates of uncertainty (e.g. confidence intervals)
- ☐ ☒ For null hypothesis testing, the test statistic (e.g. F , t , r) with confidence intervals, effect sizes, degrees of freedom and P value noted
Give P values as exact values whenever suitable.
- ☒ ☐ For Bayesian analysis, information on the choice of priors and Markov chain Monte Carlo settings
- ☒ ☐ For hierarchical and complex designs, identification of the appropriate level for tests and full reporting of outcomes
- ☒ ☐ Estimates of effect sizes (e.g. Cohen's d , Pearson's r), indicating how they were calculated

Our web collection on [statistics for biologists](#) contains articles on many of the points above.

Software and code

Policy information about [availability of computer code](#)

Data collection	ImageJ (v1.49), BD FACSDivaTM Software (v8.0.1), Microsoft Excel, Kaleidagraph (v4.1), ZEN v3.0 (black edition), Matlab R2020a
Data analysis	Data on swimming velocity and flagella rotation were analyzed with custom-written plugins of ImageJ. Additional information is provided in the Supplementary Note 1. The Image analysis plugins have been published previously and are available at https://gitlab.gwdg.de/remy.colin/FourierImageAnalysis For flow cytometry data analysis, the population of interest was first selected during measurements using BD FACSDivaTM Software v8.0.1 (see Methods). The events for only this population were exported as raw FCS files and processed with the flowCore package in R v4.2.2. Summary statistics was collected using "Batch analysis" function of BD FACSDivaTM Software v8.0.1 and processed with basic R functions as well. Swimming parameters (swimming fraction and swimming velocity of swimmers) were extracted from the output txt files generated by ImageJ, which were further processed in R v4.2.2 using custom-written functions. Flagellar rotation data were processed as indicated in Supplementary note 1 in Kaleidagraph (v4.1) To count flagella number, images were first processed in ZEN v3.0 (blue edition). Flagellar lengths were measured in ImageJ using "segmented line" tool. Both measurements were manually transferred into Excel files and summary statistics was using rstatix package in R v4.2.2 (details are provided in the respective figure legend). Most plots were generated with a custom-written R script (R version 4.2.2) using packages from the tidyverse library.

For manuscripts utilizing custom algorithms or software that are central to the research but not yet described in published literature, software must be made available to editors and reviewers. We strongly encourage code deposition in a community repository (e.g. GitHub). See the Nature Portfolio [guidelines for submitting code & software](#) for further information.

Data

Policy information about [availability of data](#)

All manuscripts must include a [data availability statement](#). This statement should provide the following information, where applicable:

- Accession codes, unique identifiers, or web links for publicly available datasets
- A description of any restrictions on data availability
- For clinical datasets or third party data, please ensure that the statement adheres to our [policy](#)

All data are available in the main text or in Supplementary Information. Source Data are provided with the manuscript. All materials are available from the corresponding author upon request.

Matlab codes for the model are available at <https://gitlab.gwdg.de/remy.colin/RFTMultiflagella>. The plugins for DDM (previously published) and DFFM are available at <https://gitlab.gwdg.de/remy.colin/FourierImageAnalysis>

Research involving human participants, their data, or biological material

Policy information about studies with [human participants or human data](#). See also policy information about [sex, gender \(identity/presentation\), and sexual orientation](#) and [race, ethnicity and racism](#).

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Reporting on race, ethnicity, or other socially relevant groupings

Population characteristics

Recruitment

Ethics oversight

Note that full information on the approval of the study protocol must also be provided in the manuscript.

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Please select the one below that is the best fit for your research. If you are not sure, read the appropriate sections before making your selection.

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Life sciences study design

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We require information from authors about some types of materials, experimental systems and methods used in many studies. Here, indicate whether each material, system or method listed is relevant to your study. If you are not sure if a list item applies to your research, read the appropriate section before selecting a response.

Materials & experimental systems

n/a	Involvement in the study
☐	☒ Antibodies
☒	☐ Eukaryotic cell lines
☒	☐ Palaeontology and archaeology
☒	☐ Animals and other organisms
☒	☐ Clinical data
☒	☐ Dual use research of concern
☒	☐ Plants

Methods

n/a	Involvement in the study
☒	☐ ChIP-seq
☐	☒ Flow cytometry
☒	☐ MRI-based neuroimaging

Antibodies

Antibodies used	anti Flagellin rabbit polyclonal FITC conjugate primary antibody (Antikoerper; AA 2-498-FITC, ABIN2831532, 1.5 mg/ml), IRDye 800CW Donkey Anti-Rabbit IgG secondary antibody (LI-COR Biosciences; P/N: 926-32213, 1 mg/ml). Both antibodies were used at 1:10000 dilution
Validation	For the primary antibody AA 2-498-FITC, validation was done by the manufacturer (https://www.antikoerper-online.de/antibody/1992301/anti-Flagellin+FliC+AA+2-498+antibody+FITC/). Negative control was included in the analysis (Supplementary Fig. 4)

Plants

Seed stocks	no plant material was used
Novel plant genotypes	no plant material was used
Authentication	no plant material was used

Flow Cytometry

Plots

Confirm that:

- ☐ The axis labels state the marker and fluorochrome used (e.g. CD4-FITC).
- ☒ The axis scales are clearly visible. Include numbers along axes only for bottom left plot of group (a 'group' is an analysis of identical markers).
- ☐ All plots are contour plots with outliers or pseudocolor plots.
- ☒ A numerical value for number of cells or percentage (with statistics) is provided.

Methodology

Sample preparation	Mono- and co-cultures of bacteria expressing different fluorescent markers were prepared as described in Methods.
Instrument	BD LSRFortessa SORP cell analyzer (BD Biosciences, Germany)
Software	BD FACSDivaTM Software v8.0.1, flowCore package in R v4.2.2
Cell population abundance	The samples were prepared by diluting the highly abundant cell cultures (see Methods). 30,000 cells (events) were recorded and analyzed in each experimental run
Gating strategy	All gating strategies we used are described in the Methods. Gating was first performed on an FSC-A/SSC-A plot and on an SSC-W over SSC-H plot to exclude doublets. Events in the samples with fluorescence intensities higher than the background signal from the MG1655 WT or Ptac strain without the reporter plasmid were considered 'positive' (illustrated in Supplementary Fig. 8)

- ☒ Tick this box to confirm that a figure exemplifying the gating strategy is provided in the Supplementary Information.