Fisher Waves – draft paper

Intro:

- Generalized FK equation plays a huge role in mathematical biology, ecology etc.
- It predicts travelling waves
- travelling waves have been observed in experimental systems but it remains unclear whether their behaviour, in particular the profile, is such as predicted by the FK equation
- potentially many factors contribute: food, waste, growth dynamics (Poissonian vs quasi-synchronous divisions) etc., all these neglected by the FK equation

Goal:

- we want to see if the FK equation can be used as the minimal model of an experimental system of growing and migrating bacteria

Methods

- experimental design
- media, strains used
- method for determining g(n) from growth curves
- calibration (diffusion of methylene blue, swimming/tumbling/diffusion constants of bacteria)

Results

- travelling waves observed for different media and strains, show the profiles, and videos (SI)
- relate their speed to the growth rate and effective (active) diffusion constant of bacteria
- show discrete model with continuous biomass (ODEs, $dn_i/dt = \cdots$.) with growth function g(n)
- show the profiles do not agree with logistic etc simple functions for g(n)
- g(n) determined from WM growth curves fed into the model
- show it now reproduces the profiles very well
- show that if diffusion can be neglected, the profile is just the rescaled growth curve
- show the stochastic model, discuss how it affects the profile/speed
- do experiments with varying carrying capacity to verify that
- show that a more accurate model with explicit nutrients, spatial distribution of bacteria etc. does not work better than the simple model

Commented [WB1]: Done, but re-do for MOPS and M9 because profiles are too noisy (old technique, now I can do it better)

Commented [WB2]: To do, hopefully it will work!

Commented [WB3]: To do

Conclusion:

- generalized FK equation correctly predicts features of travelling population waves

Fisher Waves – summary of experiments

Media used

- LB [lab Notebook/Fisher Waves]
- M9, three carbon sources (LB/Glycerol/Glucose x 0.1%/0.05%) [lab Notebook/Fisher Waves]
- MOPS x (Gly/Glu both 0.1%) x (no/M2103+M2104) [lab Notebook/Fisher Waves 3]

Strains:

- Mg1655
- HCB437 – smooth swimmer from Jana (no tumbling) [1] [lab Notebook/Fisher Waves]
- RJA002 = MG1655 + YFP on the chromosome

Growth curves in isolated wells:

- M9 x (glucose/glycerol) x (0.1%, 0.2%, 0.4%) x (Mg1655/RJA002) x (no CAA/CAA) [lab notebook/tests of the new plate reader ClarioStar] ["C:\\Moje Dokumenty\\bio\\Fisher_waves\\TRno7.CSV"] – bad data, with cutoff at OD=1, initial phase missing?

Best curves from

- M9, various media and strains [lab Notebook/Fisher Waves]
- LB and MOPS x (Gly/Glu) x(poor/rich), for MG1655, HCB437, RJA002, MG1655+p702+CFP, and MG1655_NalAcid_resistant [lab Notebook/Fisher Waves 3]
- Many additional LB curves from antibiotic gradient experiments

Comments:

- Protocol for M9 used transparent film. This has now changed, hence redo these experiments
- Use new protocol as for antibiotic gradients
- 10^9 bacteria dry weigth is about 0.0003g, 0.05%glu has 0.0005g/ml --> amount of food should slightly limit the carrying capacity at this concentration. But it would be better to go to even lower concentrations of Glu/Gly/LB.
- run different media on the same plate for the same strain. this way variations in plate preparations (evaporation etc.) won't be significant for determining the speed
- always add growth tests (isolated wells)
- Do not use [lab Notebook/Fisher Waves 2] because for some reasons it did not work well.

Research questions:

- v=2*sqrt(D*g(0)) ?

- does K matter?

- profile at the front? Can theory predict it?

- chemotaxis important?

- swimming important?

TO DO:

- do not forget to add 10ml 0.132 M K2HP04 for 1000ml of MOPS medium. When preparing the medium use 60C water with 0.15% agarose, do not add agarose later!
- Perhaps measure again growth rates of all these strains in LB and different MOPS media?
- Dilute inoculum enough to not to contribute food to experiments on non-LB media
- fluorescence measurement slow - don't do it if unnecessary!
- test how sensitive is the PR to YFP compared to OD. Do that in M9+agarose when repeating growth curves with more diluted (and resuspended in PBS) MG1655 to get rid of initial OD=0.1 and waste products
- use YFP-labelled bacteria to measure low concentrations in M9/MOPS, use both protocols (YFP/OD). Probably better do this in ClarioStar
- use very low nutrient & YFP bacteria to go into the stochastic regime?
- Alternative method to determine speeds/profiles at low K: replica-plate into a new 384-well plate with separated wells and plenty of nutrients, and measure OD(t) in each well

[1] Wolfe, A. J., Conley, M. P., Kramer, T. J. & Berg, H. C. Reconstitution of signaling in bacterial chemotaxis. *J. Bacteriol.* **169,** 1878–1885 (1987).