

Dr Sara Jabbari BA, PhD

Birmingham Fellow

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Contact details

Telephone **+44 (0) 121 414 6196** (tel:+44 121 414 6196)

Email s.jabbari@bham.ac.uk (mailto:s.jabbari@bham.ac.uk)

University of Birmingham
Edgbaston
Birmingham
B15 2TT
UK



About

Sara Jabbari is a Birmingham Fellow in mathematical biology. Specialising in the modelling of gene regulation networks using both numerical and analytical approaches, her work spans a range of biological applications, from drug development to bioenergy to understanding bacterial behaviour. Her MRC fellowship has afforded her the opportunity to gain experimental training in order to generate the complementary data required to adopt a truly interdisciplinary approach to mathematical modelling in biology.

Qualifications

- PhD Mathematical Biology, University of Nottingham, 2007
- BA Mathematics, Durham University, 2003

Biography

Sara Jabbari graduated from Durham University in 2003, incorporating a year of study at the Université Louis Pasteur in Strasbourg, France. She went on to complete a PhD in mathematical modelling of cell-cell bacterial communication under the supervision of Prof. John R. King at the University of Nottingham.

Following a post-doc position on an international interdisciplinary systems biology project examining biofuel production by bacteria, in 2011 Sara was awarded a Biomedical Informatics Fellowship from the MRC. This has provided her with invaluable laboratory experience for carrying out and designing interdisciplinary projects. Sara was appointed a Birmingham Fellow in 2012 to explore mathematical modelling of medically significant microorganisms. In addition to her role in the School of Mathematics, she is a member of the Centre for Systems Biology at Birmingham.

Research

Research themes

- Mathematical modelling, particularly applied to biological systems, e.g. gene regulation networks.
- The use of asymptotic methods to analyse and simplify mathematical models.

Research activity

Mathematical modelling of:

- Cell-cell bacterial communication (quorum sensing)
- Biofuel production
- Sporulation
- Virus dynamics
- Bacterial toxin production
- The emergence of antimicrobial resistance
- Novel treatments for bacterial infections

Publications

- Ternent L., Dyson R.J., Krachler A.-M., Jabbari S. (2015) Bacterial fitness shapes the population dynamics of antibiotic-resistant and -susceptible bacteria in a model of combined antibiotic and anti-virulence treatment. In press, **J. Theor. Biol.**
- Jabbari S., Cartman S.T., King J.R. (2014), Mathematical modelling reveals properties of TcdC required for it to be a negative regulator of toxin production in *Clostridium difficile*. **J. Math. Biol.** 70:773-804.
- Fletcher S.J., Iqbal M., Jabbari S., Stekel D., Rappoport J.Z. (2014), Computational modelling of occludin trafficking, demonstrating continuous endocytosis, degradation, recycling and biosynthetic secretory trafficking. **PLoS ONE** 9: e111176.
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- Thorn G.J., King J.R., Jabbari S. (2013), pH-induced gene regulation of solvent production by *Clostridium acetobutylicum* in continuous culture: parameter estimation and sporulation modelling. **Bull. Math. Biol.**241:149-66.
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- Brown R.J.P., Hudson N., Wilson G., Rehman S.U., Jabbari, S., Hu K., Tarr A.W., Borrow P., Joyce M., Lewis J., Zhu L.F., Law M., Kneteman N., Tyrrell D.L., McKeating J.A., Ball J.K. (2012), Hepatitis C virus envelope glycoprotein fitness defines virus population composition following transmission to a new host. **J. Virol.**, 86: 11956-11966.
- Haus S., Jabbari S., Millat T., Janssen H., Fischer R.J., Bahl H., King J.R., Wolkenhauer O. (2011) A systems biology approach to investigate the effect of pH-induced gene regulation on solvent production by *Clostridium acetobutylicum* in continuous culture. **BMC Syst. Biol.**, 5:10.
- Jabbari S., Heap J.T., King J.R. (2011) Mathematical modelling of the sporulation-initiation network in *Bacillus subtilis* revealing the dual role of the putative quorum-sensing signal molecule PhrA. **Bull. Math. Biol.**, 73:181-211.
- Jabbari S., King J.R., Williams P. (2010) A mathematical investigation of the effects of inhibitor therapy on three putative phosphorylation cascades governing the two-component system of the agr operon. **Math. Biosci.**, 225: 115-131.
- Jabbari S., King J.R., Koerber A.J., Williams P. (2010) Mathematical modelling of the agr operon in *Staphylococcus aureus*. **J. Math. Biol.**, 61:17-54.

