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MATHEMATISCH-
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Bachelor Thesis

Investigation of *Finegoldia magna* ATCC 29328 in the nasal environment

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1 Background and Motivation

Finegoldia magna is a gram-positive, facultative, opportunistic human pathogen [2]. It was formerly known as *Peptostreoptococcus magnus* until it became a separate genus. Infection with *F. magna* can lead to various symptoms, including several kinds of abscesses, with reported locations in the breast [2], brain [1], or implanted joints [3]. In rare cases, the infection may proceed to necrotizing fasciitis [4, 5] or chronic infections such as osteomyelitis [6]. While the bacterium is known to have the potential for resistance against some antimicrobial drugs, widespread resistance against multiple antibiotics is not yet commonly reported [7].

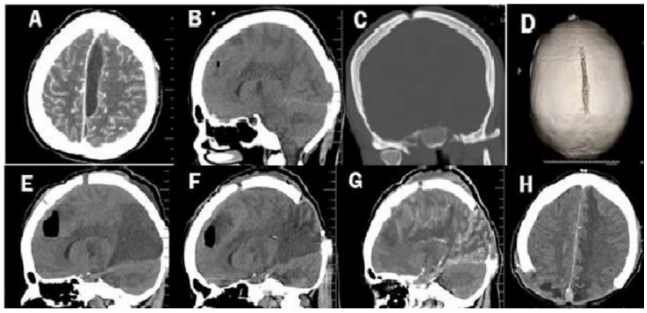

Figure 1 | Abscess in the brain, before surgery (A-D) and after several operations (E-H), caused through infection with *F. magna* [1].

After a recent revision of the metabolic model, new insights into some substances and reactions were gained. It was suggested that *F. magna* could cause inflammation by interactinng *F. magna* adherence factors (FAF) and L proteins with human neutrophils [8].

2 Aim and Approach

In order to gain a better knowledge of metabolic processes, the first automated metabolic models were made with methods of the Path2Models project [9]. The most current metabolic models of the organism were curated semi-automatically via assembly of gut organisms through reconstruction and analysis (AGORA) [10]. In light of discoveries and the current lack of manual curation, this project aims to refine the existing metabolic model and use the complemented model to simulate growth in the human nasal environment. In the case of *F. magna*, an *in silico* model can also serve as an approach to find suitable minimal conditions required to facilitate cultivation in laboratory conditions. This will be done by using findings from literature and automated tools such as CarveMe [11] to reconstruct and expand the current model. The concluding quality assessment will be done via metabolic model testing (MEMOTE) [12].

3 Requirements

(1) Fundamental understanding of biochemistry (2) interest in systems biology, particularly in constraint-based modeling (3) python programming using COBRApy [13] and libSBML [14] (4) interest in learning the usage of third-party tools (e.g., CarveMe, MEMOTE).

References

[1] M.Akif Sönmez, Yeşim Çağlar, Mustafa Karademir, and Olcay eser. Finegoldia magna causing brain abscess with subdural empyema: Case report. *Journal of Spine & Neurosurgeryy*, 05, 09 2016. doi:10.4172/2325-9701.1000245.

[2] Fernando Cobo, Javier Rodríguez-Granger, Antonio Sampedro, and José María Navarro-Marí. Breast abscess due to finegoldia magna in a non-puerperal women. *Anaerobe*, 47:183–184, 2017. ISSN 1075-9964. doi:https://doi.org/10.1016/j.anaerobe.2017.06.001. URL `https://www.sciencedirect.com/science/article/pii/S1075996417301191`.

[3] Bo Söderquist, Sanna Björklund, Bengt Hellmark, Anders Jensen, Holger Brüggemann, and Robin Patel. Finegoldia magna isolated from orthopedic joint implant-associated infections. *Journal of Clinical Microbiology*, 55(11):3283–3291, 2017. doi:10.1128/JCM.00866-17. URL `https://journals.asm.org/doi/abs/10.1128/JCM.00866-17`.

[4] Margherita Scapaticci, Sabina Marchetto, Andrea Nardi, Maira Zoppelletto, and Andrea Bartolini. A case of necrotizing fasciitis caused by finegoldia magna in a patient with type 2 diabetes mellitus. *Le infezioni in medicina : rivista periodica di eziologia, epidemiologia, diagnostica, clinica e terapia delle patologie infettive*, 26:359–363, 12 2018.

[5] Ardit Begaj, Ross C McLean, and Pudhupalayam Bhaskar. Finegoldia magna: a rare cause of necrotising fasciitis. *BMJ Case Reports CP*, 13(5), 2020. doi:10.1136/bcr-2020-235115. URL `https://casereports.bmj.com/content/13/5/e235115`.

[6] Kamron Salavitabar, Amar Vyas, Maria Barry, Maria Masih, and Sandeep Gandhi. Chronic osteomyelitis caused by finegoldia magna. *Consultant*, Apr 2021. doi:10.25270/con.2021.06.00014.

[7] A. C. M. Veloo, G. W. Welling, and J. E. Degener. Antimicrobial susceptibility of clinically relevant gram-positive anaerobic cocci collected over a three-year period in the netherlands. *Antimicrobial Agents and Chemotherapy*, 55(3):1199–1203, 2011. doi:10.1128/aac.01771-09.

[8] Ariane Neumann, Lars Björck, and Inga-Maria Frick. Finegoldia magna, an anaerobic gram-positive bacterium of the normal human microbiota, induces inflammation by activating neutrophils. *Frontiers in Microbiology*, 11:65, 2020. ISSN 1664-302X. doi:10.3389/fmicb.2020.00065. URL `https://www.frontiersin.org/article/10.3389/fmicb.2020.00065`.

[9] Finja Büchel, Nicolas Rodriguez, Neil Swainston, Clemens Wrzodek, Tobias Czauderna, Roland Keller, Florian Mittag, Michael Schubert, Mihai Glont, Martin Golebiewski, Martijn van Iersel, Sarah M. Keating *et al.* Path2Models: large-scale generation of computational models from biochemical pathway maps. *BMC Systems Biology*, 7(1):116, November 2013. doi:10.1186/1752-0509-7-116. URL `https://www.biomedcentral.com/1752-0509/7/116`.

[10] Stefanía Magnúsdóttir, Almut Heinken, Laura Kutt, Dmitry A Ravcheev, Eugen Bauer, Alberto Noronha, Kacy Greenhalgh, Christian Jäger, Joanna Baginska, Paul Wilmes, and et al. Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota. *Nature Biotechnology*, 35(1):81–89, 2016. doi:10.1038/nbt.3703.

[11] Daniel Machado, Sergej Andrejev, Melanie Tramontano, and Kiran Raosaheb Patil. Fast automated reconstruction of genome-scale metabolic models for microbial species and communities. *Nucleic Acids Research*, 46(15):7542–7553, 06 2018. ISSN 0305-1048. doi:10.1093/nar/gky537. URL `https://doi.org/10.1093/nar/gky537`.

[12] Christian Lieven, Moritz E. Beber, Brett G. Olivier, Frank T. Bergmann, Meric Ataman, Parizad Babaei, Jennifer A. Bartell, Lars M. Blank, Siddharth Chauhan, Kevin Correia, Christian Diener, Andreas Dräger *et al.* MEMOTE for standardized genome-scale metabolic model testing. *Nature Biotechnology*, March 2020. ISSN 1546-1696. doi:10.1038/s41587-020-0446-y. URL `https://doi.org/10.1038/s41587-020-0446-y`.

[13] Ali Ebrahim, Joshua A. Lerman, Bernhard Ø Palsson, and Daniel R. Hyduke. COBRApy: COnstraints-Based Reconstruction and Analysis for Python. *BMC Systems Biology*, 7:74, August 2013. doi:10.1186/1752-0509-7-74. URL `http://www.biomedcentral.com/1752-0509/7/74`.

[14] Benjamin J. Bornstein, Sarah M. Keating, Akiya Jouraku, and Michael Hucka. LibSBML: an API Library for SBML. *Bioinformatics*, 24(6):880–881, March 2008. doi:10.1093/bioinformatics/btn051. URL `https://doi.org/10.1093/bioinformatics/btn051`.