Insights from modeling metabolism and amoeboid cell motility in the immune system

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Bibliography

[1] N. Prajitha, S. S. Athira, and P. V. Mohanan. “Pyrogens, a polypeptide produces fever by metabolic changes in hypothalamus: Mechanisms and detections”. *Immunology Letters* 204 (2018), 38–46.

[2] Bridgette M. Cumming, Hayden T. Pacl, and Adrie J.C. Steyn. “Relevance of the Warburg effect in tuberculosis for host-directed therapy”. *Frontiers in Cellular and Infection Microbiology* 10 (2020), 506.

[3] Jae Sung Kim, Ye Ram Kim, and Chul Su Yang. “Host-directed therapy in tuberculosis: Targeting host metabolism”. *Frontiers in Immunology* 11 (2020), 1790.

[4] Juho Vuononvirta, Federica M. Marelli-Berg, and Thanushiyan Poobalasingam. “Metabolic regulation of T lymphocyte motility and migration”. *Molecular Aspects of Medicine* 77 (2020), 100888.

[5] Anusha Angajala et al. “Diverse roles of mitochondria in immune responses: Novel insights into immuno-metabolism”. *Frontiers in Immunology* 9 (2018), 1605.

[6] Matthew F. Krummel, Frederic Bartumeus, and Audrey Gérard. “T cell migration, search strategies and mechanisms”. *Nature Reviews Immunology* 16.3 (2016), 193–201.

[7] Hélène D. Moreau et al. “Integrating Physical and Molecular Insights on Immune Cell Migration”. *Trends in Immunology* 39.8 (2018), 632–643.

[8] Alison Gaylo et al. “T cell interstitial migration: Motility cues from the inflamed tissue for micro- and macro-positioning”. *Frontiers in Immunology* 7 (2016), 428.

[9] Nikolay Martyushenko and Eivind Almaas. “ModelExplorer - software for visual inspection and inconsistency correction of genome-scale metabolic reconstructions”. *BMC Bioinformatics* (2019).

[10] Chiara Damiani et al. “Systems metabolomics: from metabolomic snapshots to design principles”. *Current Opinion in Biotechnology* 63 (2020), 190–199.

[11] Eduard Sabidó et al. “Targeted proteomics of the eicosanoid biosynthetic pathway completes an integrated genomics-proteomics-metabolomics picture of cellular metabolism”. *Molecular and Cellular Proteomics* 11.7 (2012), M111.014746–1 –M111.014746–9.

[12] Uwe Sauer. “Metabolic networks in motion: 13C-based flux analysis”. *Molecular systems biology* 2.1 (2006), 62.

[13] Yujue Wang et al. “Utilizing tandem mass spectrometry for metabolic flux analysis”. *Laboratory Investigation* (2020), 1–7.

[14] Nicolas Le Novère et al. "BioModels Database: a free, centralized database of curated, published, quantitative kinetic models of biochemical and cellular systems." *Nucleic acids research* 34.Database issue (2006), D689–D691.

[15] Kieran Smallbone et al. "Towards a genome-scale kinetic model of cellular metabolism". *BMC Systems Biology* (2010).

[16] Charles J. Foster et al. "From Escherichia coli mutant 13C labeling data to a core kinetic model: A kinetic model parameterization pipeline". *PLoS Computational Biology* 15.9 (2019), e1007319.

[17] Kieran Smallbone et al. "Something from nothing - Bridging the gap between constraint-based and kinetic modelling". *FEBS Journal* 274.21 (2007), 5576–5585.

[18] Jeffrey D Orth, Ines Thiele, and Bernhard Ø Palsson. "What is flux balance analysis?" *Nat Biotechnol* 28.3 (2010), 245–248.

[19] Radhakrishnan Mahadevan, Jeremy S. Edwards, and Francis J. Doyle. "Dynamic Flux Balance Analysis of diauxic growth in Escherichia coli". *Biophysical Journal* 83.3 (2002), 1331–1340.

[20] Radhakrishnan Mahadevan and Chrisophe H. Schilling. "The effects of alternate optimal solutions in constraint-based genome-scale metabolic models". *Metabolic Engineering* 5.4 (2003), 264–276.

[21] Shiri Stempler, Keren Yizhak, and Eytan Ruppin. "Integrating transcriptomics with metabolic modeling predicts biomarkers and drug targets for Alzheimer's disease". *PLoS ONE* 9.8 (2014), e105383.

[22] Sabrina Kleessen et al. "Integration of transcriptomics and metabolomics data specifies the metabolic response of Chlamydomonas to rapamycin treatment". *Plant Journal* 81.5 (2015), 822–835.

[23] Keren Yizhak et al. "Integrating quantitative proteomics and metabolomics with a genome-scale metabolic network model". *Bioinformatics* 26.12 (2010), 255–260.

[24] Francesca Patella et al. "Proteomics-based metabolic modeling reveals that fatty acid oxidation (FAO) controls endothelial cell (EC) permeability." *Molecular & cellular proteomics : MCP* 14.3 (2015), 621–634.

[25] Brian J Schmidt et al. "GIM3E: Condition-specific models of cellular metabolism developed from metabolomics and expression data". *Bioinformatics* 29.22 (2013), 2900–2908.

[26] Svetlana Volkova et al. "Metabolic modelling as a framework for metabolomics data integration and analysis". *Metabolites* 10.8 (2020), 303.

[27] Jennifer L. Reed et al. "An expanded genome-scale model of Escherichia coli K-12 (iJR904 GSM/GPR)". *Genome biology* 4.9 (2003), R54.

[28] Jeremy S Edwards and Bernhard O Palsson. “The Escherichia coli MG1655 in silico metabolic genotype: its definition, characteristics, and capabilities.” *Proceedings of the National Academy of Sciences of the United States of America* 97.10 (2000), 5528–33.

[29] Natalie C Duarte, Markus J Herrgård, and Bernhard Ø Palsson. “Reconstruction and validation of Saccharomyces cerevisiae iND750, a fully compartmentalized genome-scale metabolic model.” *Genome research* 14.7 (2004), 1298–309.

[30] Ines Thiele et al. “A community-driven global reconstruction of human metabolism”. *Nature Biotechnology* 31.5 (2013), 419–425.

[31] Martin I Sigurdsson et al. “A detailed genome-wide reconstruction of mouse metabolism based on human Recon 1.” *BMC systems biology* 4 (2010), 140.

[32] Hooman Hefzi et al. “A consensus genome-scale reconstruction of Chinese hamster ovary cell metabolism”. *Cell Systems* 3.5 (2016), 434–443.

[33] Edik M. Blais et al. “Reconciled rat and human metabolic networks for comparative toxicogenomics and biomarker predictions”. *Nature Communications* 8 (2017), 14250.

[34] Michaël Bekaert. “Reconstruction of Danio rerio Metabolic Model Accounting for Subcellular Compartmentalisation”. *PLoS ONE* 7.11 (2012), e49903.

[35] Leonie van Steijn et al. “Predicting Metabolism from Gene Expression in an Improved Whole-Genome Metabolic Network Model of Danio rerio”. *Zebrafish* 16.4 (2019), 348–362.

[36] Eileen Marie Hanna et al. “ReCodLiver0.9: Overcoming challenges in genome-scale metabolic reconstruction of a non-model species”. *Frontiers in Molecular Biosciences* 7 (2020), 345.

[37] Svetlana Kalujnaia, Neil Hazon, and Gordon Cramb. “Myo-inositol phosphate synthase expression in the European eel (*Anguilla anguilla*) and Nile tilapia (*Oreochromis niloticus*): effect of seawater acclimation”. *American Journal of Physiology-Regulatory, Integrative and Comparative Physiology* 311.2 (2016), R287–R298.

[38] Matthew J. Footer et al. “Direct measurement of force generation by actin filament polymerization using an optical trap”. *Proceedings of the National Academy of Sciences of the United States of America* 104.7 (2007), 2181–2186.

[39] Kinneret Keren et al. “Mechanism of shape determination in motile cells”. *Nature* 453.7194 (2008), 475–480.

[40] Tim Lämmermann and Michael Sixt. “Mechanical modes of ‘amoeboid’ cell migration”. *Current Opinion in Cell Biology* 21.5 (2009), 636–644.

[41] Verena Kölsch, Pascale G Charest, and Richard A Firtel. “The regulation of cell motility and chemotaxis by phospholipid signaling.” *Journal of cell science* 121.Pt 5 (2008), 551–559.

[42] Scott A. Weed et al. "Cortactin localization to sites of actin assembly in lamellipodia requires interactions with F-actin and the Arp2/3 complex". *Journal of Cell Biology* 151.1 (2000), 29–40.

[43] Kate M. Byrne et al. "Bistability in the Rac1, PAK, and RhoA Signaling Network Drives Actin Cytoskeleton Dynamics and Cell Motility Switches". *Cell Systems* 2.1 (2016), 38–48.

[44] Sam Walcott and Sean X. Sun. "A mechanical model of actin stress fiber formation and substrate elasticity sensing in adherent cells". *Proceedings of the National Academy of Sciences of the United States of America* 107.17 (2010), 7757–7762.

[45] Albert Einstein. "Über die von der molekularkinetischen Theorie der Wärme geforderte Bewegung von in ruhenden Flüssigkeiten suspendierten Teilchen [AdP 17, 549 (1905)]". *Annalen der Physik* 17 (1905), 549–560.

[46] William Sutherland. "A dynamical theory of diffusion for non-electrolytes and the molecular mass of albumin". *The London, Edinburgh, and Dublin Philosophical Magazine and Journal of Science* 9.54 (1905), 781–785.

[47] Reinhold Fürth. "Die Brownsche Bewegung bei Berücksichtigung einer Persistenz der Bewegungsrichtung. Mit Anwendungen auf die Bewegung lebender Infusorien". *Zeitschrift für Physik* 2.3 (1920), 244–256.

[48] V. Zaburdaev, S. Denisov, and J. Klafter. "Lévy walks". *Reviews of Modern Physics* 87.2 (2015), 483–530.

[49] Catherine Beauchemin, Narendra M. Dixit, and Alan S. Perelson. "Characterizing T Cell Movement within Lymph Nodes in the Absence of Antigen". *The Journal of Immunology* 178.9 (2007), 5505–5512.

[50] Roumen Tsekov and Marga C. Lensen. "Brownian Motion and the Temperament of Living Cells". *Chinese Physics Letters* 30.7 (2013), 070501.

[51] Hui Li et al. "Zigzag Generalized Lévy Walk: the In Vivo Search Strategy of Immunocytes." *Theranostics* 5.11 (2015), 1275–90.

[52] Elizabeth R. Jerison and Stephen R. Quake. "Heterogeneous T cell motility behaviors emerge from a coupling between speed and turning in vivo". *eLife* 9 (2020), e53933.

[53] Mark J Miller et al. "Autonomous T cell trafficking examined in vivo with intravital two-photon microscopy." *Proceedings of the National Academy of Sciences of the United States of America* 100.5 (2003), 2604–9.

[54] Tim Worbs et al. "CCR7 ligands stimulate the intranodal motility of T lymphocytes in vivo". *Journal of Experimental Medicine* 204.3 (2007), 489–495.

[55] Johannes Textor et al. "Defining the quantitative limits of intravital two-photon lymphocyte tracking." *Proceedings of the National Academy of Sciences of the United States of America* 108.30 (2011), 12401–6.

[56] Tajie H. Harris et al. "Generalized Lévy walks and the role of chemokines in migration of effector CD8+ T cells". *Nature* 486.7404 (2012), 545–548.

[57] Gabriel Espinosa-Carrasco et al. “Integrin $\beta1$ optimizes diabetogenic T cell migration and function in the pancreas”. *Frontiers in Immunology* 9.MAY (2018), 1156.

[58] Athanasius F.M. Marée et al. “Polarization and movement of keratocytes: A multiscale modelling approach”. *Bulletin of Mathematical Biology* 68.5 (2006), 1169–1211.

[59] Athanasius F.M. Marée, Verônica A. Grieneisen, and Leah Edelstein-Keshet. “How cells integrate complex stimuli: The effect of feedback from phosphoinositides and cell shape on cell polarization and motility”. *PLoS Computational Biology* 8.3 (2012), e1002402.

[60] Erin M. Craig et al. “Model for adhesion clutch explains biphasic relationship between actin flow and traction at the cell leading edge”. *Physical Biology* 12.3 (2015), 035002.

[61] Erin L. Barnhart et al. “Adhesion-Dependent Wave Generation in Crawling Cells”. *Current Biology* 27.1 (2017), 27–38.

[62] Elisabeth G. Rens and Leah Edelstein-Keshet. “From energy to cellular forces in the Cellular Potts Model: An algorithmic approach”. *PLoS Computational Biology* 15.12 (2019), e1007459.

[63] Gaudenz Danuser, Jun Allard, and Alex Mogilner. “Mathematical modeling of eukaryotic cell migration: Insights beyond experiments”. *Annual Review of Cell and Developmental Biology* 29 (2013), 501–528.

[64] Louis S. Prahl and David J. Odde. “Modeling cell migration mechanics”. In: *Advances in Experimental Medicine and Biology*. Vol. 1092. 2018, 159–187.

[65] Falko Ziebert and Igor S. Aranson. “Effects of Adhesion Dynamics and Substrate Compliance on the Shape and Motility of Crawling Cells”. *PLoS ONE* 8.5 (2013), e64511.

[66] Danying Shao, Herbert Levine, and Wouter Jan Rappel. “Coupling actin flow, adhesion, and morphology in a computational cell motility model”. *Proceedings of the National Academy of Sciences of the United States of America* 109.18 (2012), 6851–6856.

[67] Jakob Löber, Falko Ziebert, and Igor S. Aranson. “Modeling crawling cell movement on soft engineered substrates”. *Soft Matter* 10.9 (2014), 1365–1373.

[68] François Graner and James A. Glazier. “Simulation of biological cell sorting using a two-dimensional extended Potts model”. *Physical Review Letters* 69.13 (1992), 2013–2016.

[69] Koo Chul Lee. “Rejection-free Monte Carlo technique”. *Journal of Physics A: Mathematical and General* 28.17 (1995), 4835–4842.

[70] Noriyuki Bob Ouchi et al. “Improving the realism of the cellular Potts model in simulations of biological cells”. *Physica A: Statistical Mechanics and its Applications* 329.3-4 (2003), 451–458.

[71] Nicholas J. Savill and Paulien Hogeweg. "Modelling Morphogenesis: From Single Cells to Crawling Slugs". *Journal of Theoretical Biology* 184.3 (1997), 229–235.

[72] Joost B. Beltman et al. "Lymph node topology dictates T cell migration behavior". *Journal of Experimental Medicine* 204.4 (2007), 771–780.

[73] Ioana Niculescu, Johannes Textor, and Rob J. de Boer. "Crawling and Gliding: A Computational Model for Shape-Driven Cell Migration". *PLoS Computational Biology* 11.10 (2015), e1004280.

[74] Joeri A J Wondergem et al. "Chemotaxis and topotaxis add vectorially for amoeboid cell migration". *bioRxiv* (2019).

[75] Koen Schakenraad et al. "Topotaxis of active Brownian particles". *Physical Review E* 101.3 (2020), 1–11.

[76] Asha Seth, Derek L. Stemple, and Inês Barroso. "The emerging use of zebrafish to model metabolic disease". *Disease Models & Mechanisms* 6.5 (2013), 1080–1088.

[77] Massimo M. Santoro. "Zebrafish as a model to explore cell metabolism". *Trends in Endocrinology and Metabolism* 25.10 (2014), 546–554.

[78] Kerstin Howe et al. "The zebrafish reference genome sequence and its relationship to the human genome". *Nature* 496.7446 (2013), 498–503.

[79] Nannan Chang et al. "Genome editing with RNA-guided Cas9 nuclease in Zebrafish embryos". *Cell Research* 23.4 (2013), 465–472.

[80] Rob C. van Wijk et al. "Systems pharmacology of hepatic metabolism in zebrafish larvae". *Drug Discovery Today: Disease Models* 22 (2016), 27–34.

[81] Jeremy S Edwards and Bernhard O Palsson. "Systems properties of the Haemophilus influenzae Rd metabolic genotype." *The Journal of biological chemistry* 274.25 (1999), 17410–6.

[82] Daniel Segrè, Dennis Vitkup, and George M Church. "Analysis of optimality in natural and perturbed metabolic networks." *Proceedings of the National Academy of Sciences of the United States of America* 99.23 (2002), 15112–7.

[83] Caroline Colijn et al. "Interpreting Expression Data with Metabolic Flux Models: Predicting Mycobacterium tuberculosis Mycolic Acid Production". *PLoS Computational Biology* 5.8 (2009), e1000489.

[84] Mats Åkesson, Jochen Förster, and Jens Nielsen. "Integration of gene expression data into genome-scale metabolic models". *Metabolic Engineering* 6.4 (2004), 285–293.

[85] Jochen Förster et al. "Genome-scale reconstruction of the Saccharomyces cerevisiae metabolic network." *Genome research* 13.2 (2003), 244–53.

[86] Markus J Herrgård et al. "A consensus yeast metabolic network reconstruction obtained from a community approach to systems biology". *Nature Biotechnology* 26.10 (2008), 1155–1160.

[87] Ines Thiele et al. “A community effort towards a knowledge-base and mathematical model of the human pathogen Salmonella Typhimurium LT2”. *BMC Systems Biology* 5.1 (2011), 8.

[88] Neema Jamshidi and Bernhard Ø Palsson. “Investigating the metabolic capabilities of Mycobacterium tuberculosis H37Rv using the in silico strain iNJ661 and proposing alternative drug targets”. *BMC Systems Biology* 1.1 (2007), 26.

[89] Shuzhao Li et al. “Constructing a fish metabolic network model”. *Genome Biology* 11.11 (2010), R115.

[90] Aarash Bordbar, Neema Jamshidi, and Bernhard O Palsson. “iAB-RBC-283: A proteomically derived knowledge-base of erythrocyte metabolism that can be used to simulate its physiological and patho-physiological states”. *BMC Systems Biology* 5.1 (2011), 110.

[91] Aarash Bordbar et al. “A multi-tissue type genome-scale metabolic network for analysis of whole-body systems physiology.” En. *BMC systems biology* 5.1 (2011), 180.

[92] Herman P Spaink, Hans J Jansen, and Ron P Dirks. “Advances in genomics of bony fish”. *Briefings in Functional Genomics* 13.2 (2014), 144–156.

[93] Yen-Chia Chang et al. “Taurine homeostasis requires de novo synthesis via cysteine sulfinic acid decarboxylase during zebrafish early embryogenesis”. *Amino acids* 44.2 (2013), 615–629.

[94] Zachary A. King et al. “BiGG Models: A platform for integrating, standardizing and sharing genome-scale models”. *Nucleic Acids Research* 44.D1 (2016), D515–D522.

[95] Nathan E. Lewis et al. “Omic data from evolved E. coli are consistent with computed optimal growth from genome-scale models”. *Molecular Systems Biology* 6 (2010), 390.

[96] Ali Ebrahim et al. “COBRApy: COnstraints-Based Reconstruction and Analysis for Python”. *BMC Systems Biology* 7.1 (2013), 74.

[97] Daniel Machado and Markus Herrgård. “Systematic Evaluation of Methods for Integration of Transcriptomic Data into Constraint-Based Models of Metabolism”. *PLoS Computational Biology* 10.4 (2014), e1003580.

[98] Rajib Saha, Anupam Chowdhury, and Costas D Maranas. “Recent advances in the reconstruction of metabolic models and integration of omics data”. *Current Opinion in Biotechnology* 29 (2014), 39–45.

[99] Ehsan Motamedian et al. “TRFBA: an algorithm to integrate genome-scale metabolic and transcriptional regulatory networks with incorporation of expression data”. *Bioinformatics* 33.7 (2016), 1057–1063.

[100] Nick Fyson et al. “Gene-centric constraint of metabolic models”. *bioRxiv* (2017), 116558.

[101] Daniel Machado, Markus J. Herrgård, and Isabel Rocha. "Stoichiometric Representation of Gene–Protein–Reaction Associations Leverages Constraint-Based Analysis from Reaction to Gene-Level Phenotype Prediction". *PLoS Computational Biology* 12.10 (2016), 1–24.

[102] Young-Mo Kim et al. "Salmonella modulates metabolism during growth under conditions that induce expression of virulence genes". *Molecular BioSystems* 9.6 (2013), 1522.

[103] Michael Hucka et al. "The systems biology markup language (SBML): a medium for representation and exchange of biochemical network models." *Bioinformatics (Oxford, England)* 19.4 (2003), 524–31.

[104] Brett G. Olivier and Frank T. Bergmann. "The Systems Biology Markup Language (SBML) Level 3 Package: Flux Balance Constraints". *Journal of Integrative Bioinformatics* 12.2 (2017), 660–690.

[105] Eric W. Sayers et al. "Database resources of the National Center for Biotechnology Information". *Nucleic Acids Research* 47.D1 (2019), D23–D28.

[106] Hiroyuki Ogata et al. "KEGG: Kyoto encyclopedia of genes and genomes". *Nucleic Acids Research* 27.1 (1999), 29–34.

[107] Minoru Kanehisa et al. "KEGG as a reference resource for gene and protein annotation". *Nucleic Acids Research* 44.D1 (2016), D457–D462.

[108] Minoru Kanehisa et al. "KEGG: New perspectives on genomes, pathways, diseases and drugs". *Nucleic Acids Research* 45.D1 (2017), D353–D361.

[109] Elizabeth Brunk et al. "Recon3D enables a three-dimensional view of gene variation in human metabolism". *Nature Biotechnology* 36.3 (2018), 272–281.

[110] Stefanía Magnúsdóttir et al. "Generation of genome-scale metabolic reconstructions for 773 members of the human gut microbiota". *Nature Biotechnology* 35.1 (2016), 81–89.

[111] Scott A. Becker and Bernhard O. Palsson. "Context-specific metabolic networks are consistent with experiments". *PLoS Computational Biology* 4.5 (2008), e1000082.

[112] Ed Reznik, Pankaj Mehta, and Daniel Segrè. "Flux Imbalance Analysis and the Sensitivity of Cellular Growth to Changes in Metabolite Pools". *PLoS Computational Biology* 9.8 (2013), e1003195.

[113] Adam M. Feist and Bernhard O. Palsson. "The biomass objective function". *Current Opinion in Microbiology* 13.3 (2010), 344–349.

[114] Chih Hung Chou et al. "FMM: A web server for metabolic pathway reconstruction and comparative analysis". *Nucleic Acids Research* 37.SUPPL. 2 (2009), W129–W134.

[115] Wei-Dan Jiang et al. "Growth, digestive capacity and intestinal microflora of juvenile Jian carp (Cyprinus carpio var. Jian) fed graded levels of dietary inositol". *Aquaculture Research* 40.8 (2009), 955–962.

[116] Sanaz Khosravi et al. “Dietary myo-inositol requirement of parrot fish, Oplegnathus fasciatus”. *Aquaculture* 436 (2015), 1–7.

[117] Shi-Yen Shiau and Shu-Lin Su. “Juvenile tilapia (Oreochromis niloticus × Oreochromis aureus) requires dietary myo-inositol for maximal growth”. *Aquaculture* 243.1-4 (2005), 273–277.

[118] Yann Gibert, Sean L McGee, and Alister C Ward. “Metabolic profile analysis of zebrafish embryos.” *Journal of visualized experiments : JoVE* 14.71 (2013), e4300.

[119] Adam Amsterdam et al. “Identification of 315 genes essential for early zebrafish development.” *Proceedings of the National Academy of Sciences of the United States of America* 101.35 (2004), 12792–12797.

[120] Gregory Golling et al. “Insertional mutagenesis in zebrafish rapidly identifies genes essential for early vertebrate development”. *Nature Genetics* 31.2 (2002), 135–140.

[121] Adam Amsterdam et al. “A large-scale insertional mutagenesis screen in zebrafish”. *Genes and Development* 13.20 (1999), 2713–2724.

[122] W. Driever et al. “A genetic screen for mutations affecting embryogenesis in zebrafish”. *Development* 123.1 (1996), 37–46.

[123] Akira Muto et al. “Forward Genetic Analysis of Visual Behavior in Zebrafish”. *PLoS Genetics* 1.5 (2005), e66.

[124] Laurence D. Covassin et al. “A genetic screen for vascular mutants in zebrafish reveals dynamic roles for Vegf/Plcg1 signaling during artery development”. *Developmental Biology* 329.2 (2009), 212–226.

[125] Norimasa Iwanami et al. “Forward Genetic Screens in Zebrafish Identify Pre-mRNA-Processing Pathways Regulating Early T Cell Development”. *Cell Reports* 17.9 (2016), 2259–2270.

[126] Susan E Brockerhoff et al. “A behavioral screen for isolating zebrafish mutants with visual system defects”. *Proceedings of the National Academy of Sciences* 92.23 (1995), 10545–10549.

[127] Richard N Smith et al. “InterMine: a flexible data warehouse system for the integration and analysis of heterogeneous biological data”. *Bioinformatics* 28.23 (2012), 3163–3165.

[128] Wouter J Veneman et al. “Analysis of RNAseq datasets from a comparative infectious disease zebrafish model using GeneTiles bioinformatics”. *Immunogenetics* 67.3 (2014), 135–147.

[129] Vinay Satish Kumar and Costas D. Maranas. “GrowMatch: An Automated Method for Reconciling In Silico/In Vivo Growth Predictions”. *PLoS Computational Biology* 5.3 (2009), e1000308.

[130] Jennifer L. Reed et al. “Systems approach to refining genome annotation”. *Proceedings of the National Academy of Sciences of the United States of America* 103.46 (2006), 17480–17484.

[131] Markus J Herrgård, Stephen S Fong, and Bernhard Ø Palsson. "Identification of genome-scale metabolic network models using experimentally measured flux profiles". *PLoS computational biology* 2.7 (2006), e72.

[132] Sylvain Prigent et al. "Meneco, a Topology-Based Gap-Filling Tool Applicable to Degraded Genome-Wide Metabolic Networks". *PLoS Computational Biology* 13.1 (2017), e1005276.

[133] Alex Thomas et al. "Network reconstruction of platelet metabolism identifies metabolic signature for aspirin resistance". *Scientific Reports* 4.1 (2015), 3925.

[134] Daniel Fraher et al. "Zebrafish embryonic lipidomic analysis reveals that the yolk cell is metabolically active in processing lipid". *Cell Reports* 14.6 (2016), 1317–1329.

[135] Douglas R Tocher et al. "Nutritional regulation of hepatocyte fatty acid desaturation and polyunsaturated fatty acid composition in zebrafish (Danio rerio) and tilapia (Oreochromis niloticus)". *Fish Physiology and Biochemistry* 24.4 (2001), 309–320.

[136] Daniel A. Beard, Shou-dan Liang, and Hong Qian. "Energy balance for analysis of complex metabolic networks". *Biophysical Journal* 83.1 (2002), 79–86.

[137] Giorgio Volpe and Giovanni Volpe. "The topography of the environment alters the optimal search strategy for active particles". *Proceedings of the National Academy of Sciences of the United States of America* 114.43 (2017), 11350–11355.

[138] Vincent Tejedor, Raphael Voituriez, and Olivier Bénichou. "Optimizing persistent random searches". *Physical Review Letters* 108.8 (2012), 088103.

[139] G. M. Viswanathan et al. "Optimizing the success of random searches". *Nature* 401.6756 (1999), 911–914.

[140] F. Bartumeus et al. "Optimizing the Encounter Rate in Biological Interactions: Lévy versus Brownian Strategies". *Physical Review Letters* 88.9 (2002), 097901.

[141] Paulus Mrass et al. "Cell-autonomous and environmental contributions to the interstitial migration of T cells". *Seminars in Immunopathology* 32.3 (2010), 257–274.

[142] Matthew F. Krummel, Frederic Bartumeus, and Audrey Gérard. "T cell migration, search strategies and mechanisms". *Nature Reviews Immunology* 16.3 (2016), 193–201.

[143] Javier Rey-Barroso et al. "Switching between individual and collective motility in B lymphocytes is controlled by cell-matrix adhesion and intercellular interactions". *Scientific Reports* 8.1 (2018), 5800.

[144] Jordan Jacobelli et al. "Myosin-IIA and ICAM-1 regulate the interchange between two distinct modes of T cell migration." *Journal of immunology (Baltimore, Md. : 1950)* 182.4 (2009), 2041–50.

[145] Calina A. Copos et al. “Mechanosensitive Adhesion Explains Stepping Motility in Amoeboid Cells”. *Biophysical Journal* 112.12 (2017), 2672–2682.

[146] Guangyuan Yu et al. “Phenomenological modeling of durotaxis”. *Physical Review E* 96.1 (2017), 010402.

[147] Inge M. N. Wortel et al. “Actin-inspired feedback couples speed and persistence in a Cellular Potts Model of cell migration”. *bioRxiv* (2020).

[148] James A. Glazier and François Graner. “Simulation of the differential adhesion driven rearrangement of biological cells”. *Physical Review E* 47.3 (1993), 2128–2154.

[149] Mark S. Alber et al. “On Cellular Automaton Approaches to Modeling Biological Cells”. In: *Mathematical systems theory in biology, communications, computation, and finance*. 2003, 1–39.

[150] Raïssa Houmadi et al. “The Wiskott-Aldrich Syndrome Protein Contributes to the Assembly of the LFA-1 Nanocluster Belt at the Lytic Synapse”. *Cell Reports* 22.4 (2018), 979–991.

[151] Kris A DeMali, Christy A Barlow, and Keith Burridge. “Recruitment of the Arp2/3 complex to vinculin: coupling membrane protrusion to matrix adhesion.” *The Journal of cell biology* 159.5 (2002), 881–91.

[152] Grégory Giannone et al. “Lamellipodial Actin Mechanically Links Myosin Activity with Adhesion-Site Formation”. *Cell* 128.3 (2007), 561–575.

[153] Paula Stanley et al. “Intermediate-affinity LFA-1 binds α-actinin-1 to control migration at the leading edge of the T cell”. *EMBO Journal* 27.1 (2008), 62–75.

[154] Ana-Sunčana Smith and Udo Seifert. “Effective adhesion strength of specifically bound vesicles”. *Physical Review E* 71.6 (2005), 061902.

[155] R Bruinsma, M Goulian, and P Pincus. “Self-assembly of membrane junctions.” *Biophysical Journal* 67.2 (1994), 746.

[156] Erich Sackmann and Robijn F. Bruinsma. “Cell Adhesion as Wetting Transition?” *ChemPhysChem* 3.3 (2002), 262.

[157] Murray Eden. “A two-dimensional growth process”. *Dynamics of fractal surfaces* 4 (1961), 223–239.

[158] David Selmeczi et al. “Cell motility as persistent random motion: Theories from experiments”. *Biophysical Journal* 89.2 (2005), 912–931.

[159] Maria Zeitz, Katrin Wolff, and Holger Stark. “Active Brownian particles moving in a random Lorentz gas”. *The European Physical Journal E* 40.2 (2017), 23.

[160] Peter Dieterich et al. “Anomalous dynamics of cell migration.” *Proceedings of the National Academy of Sciences of the United States of America* 105.2 (2008), 459–63.

[161] Clarence E. Chan and David J. Odde. “Traction dynamics of filopodia on compliant substrates”. *Science* 322.5908 (2008), 1687–1691.

[162] Ke Hu et al. “Differential transmission of actin motion within focal adhesions”. *Science* 315.5808 (2007), 111–115.

[163] Carlos Jurado, John R. Haserick, and Juliet Lee. “Slipping or Gripping? Fluorescent Speckle Microscopy in Fish Keratocytes Reveals Two Different Mechanisms for Generating a Retrograde Flow of Actin”. *Molecular Biology of the Cell* 16.2 (2005), 507–518.

[164] Azadeh Samadani, Jerome Mettetal, and Alexander Van Oudenaarden. “Cellular asymmetry and individuality in directional sensing”. *Proceedings of the National Academy of Sciences of the United States of America* 103.31 (2006), 11549–11554.

[165] Edward J. Banigan et al. “Heterogeneous CD8+ T Cell Migration in the Lymph Node in the Absence of Inflammation Revealed by Quantitative Migration Analysis”. *PLoS Computational Biology* 11.2 (2015), e1004058.

[166] K. Scott Weber, Mark J. Miller, and Paul M. Allen. “Th17 Cells Exhibit a Distinct Calcium Profile from Th1 and Th2 Cells and Have Th1-Like Motility and NF-AT Nuclear Localization”. *The Journal of Immunology* 180.3 (2008), 1442–1450.

[167] Alison Gaylo-Moynihan et al. “Programming of Distinct Chemokine-Dependent and -Independent Search Strategies for Th1 and Th2 Cells Optimizes Function at Inflamed Sites”. *Immunity* 51.2 (2019), 298–309.e6.

[168] Paolo Maiuri et al. “Actin flows mediate a universal coupling between cell speed and cell persistence”. *Cell* 161.2 (2015), 374–386.

[169] Begoña Álvarez-González et al. “Three-dimensional balance of cortical tension and axial contractility enables fast amoeboid migration”. *Biophysical Journal* 108.4 (2015), 821–832.

[170] Herbert B. Schiller et al. “β 1 - And α v -class integrins cooperate to regulate myosin II during rigidity sensing of fibronectin-based microenvironments”. *Nature Cell Biology* 15.6 (2013), 625–636.

[171] René F.M. van Oers et al. “Mechanical Cell-Matrix Feedback Explains Pairwise and Collective Endothelial Cell Behavior In Vitro”. *PLoS Computational Biology* 10.8 (2014), e1003774.

[172] Elisabeth G. Rens and Roeland M.H. Merks. “Cell Contractility Facilitates Alignment of Cells and Tissues to Static Uniaxial Stretch”. *Biophysical Journal* 112.4 (2017), 755–766.

[173] Elisabeth G. Rens and Roeland M. H. Merks. “Cell Shape and Durotaxis Explained from Cell-Extracellular Matrix Forces and Focal Adhesion Dynamics”. *iScience* 23.9 (2020), 101488.

[174] Jordan Jacobelli et al. “Confinement-optimized three-dimensional T cell amoeboid motility is modulated via myosin IIA-regulated adhesions”. *Nature Immunology* 11.10 (2010), 953–961.

[175] Philip Vitorino et al. “MAP4K4 regulates integrin-FERM binding to control endothelial cell motility”. *Nature* 519.7544 (2015), 425–430.

[176] Jorn Starruß et al. “Morpheus: A user-friendly modeling environment for multiscale and multicellular systems biology”. *Bioinformatics* 30.9 (2014), 1331–1332.

[177] Pierre-François Lenne and Alice Nicolas. “Physics puzzles on membrane domains posed by cell biology”. *Soft Matter* 5.15 (2009), 2841.

[178] Rudolf Merkel et al. “Energy landscapes of receptor–ligand bonds explored with dynamic force spectroscopy”. *Nature* 397.6714 (1999), 50–53.

[179] Bryan T. Marshall et al. “Direct observation of catch bonds involving cell-adhesion molecules”. *Nature* 423.6936 (2003), 190–193.

[180] Amit Pathak and Sanjay Kumar. “Independent regulation of tumor cell migration by matrix stiffness and confinement”. *Proceedings of the National Academy of Sciences of the United States of America* 109.26 (2012), 10334–10339.

[181] Anthony Han et al. “Crowding tunes 3D collagen fibrils and reveals matrix regulation of cancer cell morphogenesis”. *bioRxiv* (2018).

[182] Matthew F Krummel, Rachel S Friedman, and Jordan Jacobelli. “Modes and mechanisms of T cell motility: roles for confinement and Myosin-IIA”. *Current Opinion in Cell Biology* 30 (2014), 9–16.

[183] Jennet Toyjanova et al. “Matrix confinement plays a pivotal role in regulating neutrophil-generated tractions, speed, and integrin utilization”. *Journal of Biological Chemistry* 290.6 (2015), 3752–3763.

[184] Janina K. Hellmann et al. “Environmental constraints guide migration of malaria parasites during transmission”. *PLoS Pathogens* 7.6 (2011), e1002080.

[185] Anna Battista, Friedrich Frischknecht, and Ulrich S. Schwarz. “Geometrical model for malaria parasite migration in structured environments”. *Physical Review E - Statistical, Nonlinear, and Soft Matter Physics* 90.4 (2014), 042720.

[186] Jin Seok Park et al. “Directed migration of cancer cells guided by the graded texture of the underlying matrix”. *Nature Materials* 15.7 (2016), 792–801.

[187] Chaejeong Heo et al. “Cellular behavior controlled by bio-inspired and geometry-tunable nanohairs”. *Nanoscale* 9.45 (2017), 17743–17751.

[188] Goher Mahmud et al. “Directing cell motions on micropatterned ratchets”. *Nature Physics* 5.8 (2009), 606–612.

[189] David Caballero et al. “Ratchetaxis: Long-Range Directed Cell Migration by Local Cues.” *Trends in cell biology* 25.12 (2015), 815–827.

[190] Delphine Arcizet et al. “Contact-controlled amoeboid motility induces dynamic cell trapping in 3D-microstructured surfaces”. *Soft Matter* 8.5 (2012), 1473.

[191] Mari Gorelashvili et al. “Amoeboid migration mode adaption in quasi-3D spatial density gradients of varying lattice geometry”. *New Journal of Physics* 16 (2014), 1–22.

[192] Liang Li, Edward C Cox, and Henrik Flyvbjerg. "'Dicty dynamics': Dictyostelium motility as persistent random motion." *Physical biology* 8.4 (2011), 046006.

[193] Elizaveta A. Novikova et al. "Persistence-Driven Durotaxis: Generic, Directed Motility in Rigidity Gradients". *Physical Review Letters* 118.7 (2017), 078103.

[194] Howard C. Berg and Douglas A. Brown. "Chemotaxis in Escherichia coli analysed by three-dimensional tracking". *Nature* 239.5374 (1972), 500–504.

[195] Ka Ming Pang, Eunkyung Lee, and David A. Knecht. "Use of a fusion protein between GFP and an actin-binding domain to visualize transient filamentous-actin structures". *Current Biology* 8.7 (1998), 405–408.

[196] Till Bretschneider et al. "Dynamic Actin Patterns and Arp2/3 Assembly at the Substrate-Attached Surface of Motile Cells". *Current Biology* 14.1 (2004), 1–10.

[197] Pascal Vallotton et al. "Tracking retrograde flow in keratocytes: News from the front". *Molecular Biology of the Cell* 16.3 (2005), 1223–1231.

[198] Shin I. Nishimura, Masahiro Ueda, and Masaki Sasai. "Non-Brownian dynamics and strategy of amoeboid cell locomotion". *Physical Review E - Statistical, Nonlinear, and Soft Matter Physics* 85.4 (2012), 041909.

[199] Eric J. Campbell and Prosenjit Bagchi. "A computational model of amoeboid cell motility in the presence of obstacles". *Soft Matter* 14.28 (2018), 5741–5763.

[200] Andrew D. Doyle et al. "One-dimensional topography underlies three-dimensional fibrillar cell migration". *The Journal of Cell Biology* 184.4 (2009), 481–490.

[201] Laurent Pieuchot et al. "Curvotaxis directs cell migration through cell-scale curvature landscapes". *Nature Communications* 9.1 (2018), 1–13.

[202] Kwang Hoon Song et al. "Sinusoidal wavy surfaces for curvature-guided migration of Tlymphocytes". *Biomaterials* 51 (2015), 151–160.

[203] Jennifer A. Mitchel and Diane Hoffman-Kim. "Cellular scale anisotropic topography guides Schwann cell motility". *PLoS ONE* 6.9 (2011), e24316.

[204] Noritaka Masaki et al. "Robustness of self-organizing chemoattractant field arising from precise pulse induction of its breakdown enzyme: A single-cell level analysis of pde expression in dictyostelium". *Biophysical Journal* 104.5 (2013), 1191–1202.

[205] Daniele Proverbio and Marco Maggiora. "Dynamical strategies for obstacle avoidance during Dictyostelium discoideum aggregation: A Multi-agent system model". *arXiv* (2019).

[206] Ramon Grima. "Directed cell migration in the presence of obstacles". *Theoretical Biology and Medical Modelling* 4.1 (2007), 1–12.

[207] Cally Scherber et al. "Epithelial cell guidance by self-generated EGF gradients". *Integrative Biology* 4.3 (2012), 259.

[208] Elliot J. Marsden et al. "Chemotactic clusters in confined run-and-tumble bacteria: a numerical investigation". *Soft Matter* 10.1 (2014), 157–165.

[209] Rachelle N. Palchesko et al. "Development of Polydimethylsiloxane Substrates with Tunable Elastic Modulus to Study Cell Mechanobiology in Muscle and Nerve". *PLoS ONE* 7.12 (2012), e51499.

[210] Simon Youssef, Sebastian Gude, and Joachim O. Rädler. "Automated tracking in live-cell time-lapse movies". *Integrative Biology* 3.11 (2011), 1095–1101.

[211] Wanbin Hu et al. "A novel function of TLR2 and MyD88 in the regulation of leukocyte cell migration behavior during wounding in zebrafish larvae". *Frontiers in Cell and Developmental Biology* 9 (2021), 210.

[212] Graham J. Lieschke et al. "Morphologic and functional characterization of granulocytes and macrophages in embryonic and adult zebrafish". *Blood* 98.10 (2001), 3087–3096.

[213] Oliver Soehnlein and Lennart Lindbom. "Phagocyte partnership during the onset and resolution of inflammation". *Nature Reviews Immunology* 10.6 (2010), 427–439.

[214] Charles N. Serhan et al. "Resolution of in flammation: state of the art, definitions and terms". *The FASEB Journal* 21.2 (2007), 325–332.

[215] Li Li et al. "Live imaging reveals differing roles of macrophages and neutrophils during zebrafish tail fin regeneration". *Journal of Biological Chemistry* 287.30 (2012), 25353–25360.

[216] Carl Nathan. "Neutrophils and immunity: Challenges and opportunities". *Nature Reviews Immunology* 6.3 (2006), 173–182.

[217] Franklin H. Epstein and Stephen J. Weiss. "Tissue Destruction by Neutrophils". *New England Journal of Medicine* 320.6 (1989), 365–376.

[218] Jennifer C. Brazil, Nancy A. Louis, and Charles A. Parkos. "The role of polymorphonuclear leukocyte trafficking in the perpetuation of inflammation during inflammatory bowel disease". *Inflammatory Bowel Diseases* 19.7 (2013), 1556–1565.

[219] Paul Martin and S. Joseph Leibovich. "Inflammatory cells during wound repair: The good, the bad and the ugly". *Trends in Cell Biology* 15.11 (2005), 599–607.

[220] Anthony L. Mescher. "Macrophages and fibroblasts during inflammation and tissue repair in models of organ regeneration". *Regeneration* 4.2 (2017), 39–53.

[221] Sophie J. Hopkin et al. "Triggering the Resolution of Immune Mediated Inflammatory Diseases: Can Targeting Leukocyte Migration Be the Answer?" *Frontiers in Pharmacology* 10 (2019), 184.

[222] Takashi Hato and Pierre C. Dagher. “How the innate immune system senses trouble and causes trouble”. *Clinical Journal of the American Society of Nephrology* 10.8 (2015), 1459–1469.

[223] Charles A. Janeway and Ruslan Medzhitov. “Innate immune recognition”. *Annual Review of Immunology* 20 (2002), 197–216.

[224] Philipp Niethammer. “The early wound signals”. *Current Opinion in Genetics and Development* 40 (2016), 17–22.

[225] Li Yu, Liantang Wang, and Shangwu Chen. “Endogenous toll-like receptor ligands and their biological significance”. *Journal of Cellular and Molecular Medicine* 14.11 (2010), 2592–2603.

[226] Kumar Vijay. “Toll-like receptors in immunity and inflammatory diseases: Past, present, and future”. *International Immunopharmacology* 59 (2018), 391–412.

[227] Valerie J. Quesniaux et al. “Toll-Like Receptor 2 (TLR2)-Dependent-Positive and TLR2-Independent-Negative Regulation of Proinflammatory Cytokines by Mycobacterial Lipomannans”. *The Journal of Immunology* 172.7 (2004), 4425–4434.

[228] Alexander Poltorak et al. “Defective LPS signaling in C3H/HeJ and C57BL/10ScCr mice: Mutations in Tlr4 gene”. *Science* 282.5396 (1998), 2085–2088.

[229] Marco E. Bianchi. “HMGB1 loves company”. *Journal of Leukocyte Biology* 86.3 (2009), 573–576.

[230] Hideyuki Yanai et al. “HMGB proteins function as universal sentinels for nucleic-acid-mediated innate immune responses”. *Nature* 462.7269 (2009), 99–103.

[231] Hellen S. Teixeira et al. “TLR3-Dependent Activation of TLR2 Endogenous Ligands via the MyD88 Signaling Pathway Augments the Innate Immune Response”. *Cells* 9.8 (2020).

[232] Laura Oliveira-Nascimento, Paola Massari, and Lee M. Wetzler. “The role of TLR2 ininfection and immunity”. *Frontiers in Immunology* 3.APR (2012), 79.

[233] Jürgen Schauber et al. “Injury enhances TLR2 function and antimicrobial peptide expression through a vitamin D-dependent mechanism”. *Journal of Clinical Investigation* 117.3 (2007), 803–811.

[234] Angela Castoldi et al. “TLR2, TLR4 and the Myd88 signaling pathway are crucial for neutrophil migration in acute kidney injury induced by sepsis”. *PLoS ONE* 7.5 (2012), e37584.

[235] Yifei Xu et al. “Toll-like receptor 2 in promoting angiogenesis after acute ischemic injury”. *International Journal of Molecular Medicine* 31.3 (2013), 555–560.

[236] Anna Moles et al. “A TLR2/S100A9/CXCL-2 signaling network is necessary for neutrophil recruitment in acute and chronic liver injury in the mouse”. *Journal of Hepatology* 60.4 (2014), 782–791.

[237] Kamalika Mojumdar et al. "Divergent impact of Toll-like receptor 2 deficiency on repair mechanisms in healthy muscle versus Duchenne muscular dystrophy". *Journal of Pathology* 239.1 (2016), 10–22.

[238] Donghoon Kim et al. "Toll-like receptor 2 contributes to chemokine gene expression and macrophage infiltration in the dorsal root ganglia after peripheral nerve injury". *Molecular Pain* 7 (2011), 74.

[239] Ekihiro Seki, Eekjoong Park, and Jiro Fujimoto. "Toll-like receptor signaling in liver regeneration, fibrosis and carcinogenesis". *Hepatology Research* 41.7 (2011), 597–610.

[240] Kouichi Miura et al. "Toll-like receptor 2 and palmitic acid cooperatively contribute to the development of nonalcoholic steatohepatitis through inflammasome activation in mice". *Hepatology* 57.2 (2013), 577–589.

[241] Lingling Ji et al. "Toll like receptor 2 knock-out attenuates carbon tetrachloride (CCl 4)-induced liver fibrosis by downregulating MAPK and NF-κB signaling pathways". *FEBS Letters* 588.12 (2014), 2095–2100.

[242] Qing Deng, Elizabeth A. Harvie, and Anna Huttenlocher. "Distinct signalling mechanisms mediate neutrophil attraction to bacterial infection and tissue injury". *Cellular Microbiology* 14.4 (2012), 517–528.

[243] Kiyoshi Takeda and Shizuo Akira. "Microbial recognition by Toll-like receptors". *Journal of Dermatological Science* 34.2 (2004), 73–82.

[244] Lingfeng Chen et al. "Myeloid Differentiation Primary Response Protein 88 (MyD88): The Central Hub of TLR/IL-1R Signaling". *Journal of Medicinal Chemistry* 63.22 (2020), 13316–13329.

[245] Natalie Wagner et al. "Microglia Activation in Retinal Ischemia Triggers Cytokine and Toll-Like Receptor Response". *Journal of Molecular Neuroscience* (2020).

[246] Mohan R. Dasu et al. "TLR2 expression and signaling-dependent inflammation impair wound healing in diabetic mice". *Laboratory Investigation* 90.11 (2010), 1628–1636.

[247] Lisa Macedo et al. "Wound healing is impaired in MyD88-deficient mice: A role for MyD88 in the regulation of wound healing by adenosine A2A receptors". *American Journal of Pathology* 171.6 (2007), 1774–1788.

[248] Ruth A. Houseright et al. "Cell type specific gene expression profiling reveals a role for complement component C3 in neutrophil responses to tissue damage". *Scientific Reports* 10.1 (2020), 15716.

[249] Annemarie H. Meijer and Herman P. Spaink. "Host-Pathogen Interactions Made Transparent with the Zebrafish Model". *Current Drug Targets* 12.7 (2011), 1000–1017.

[250] Stephen A. Renshaw et al. "Atransgenic zebrafish model of neutrophilic inflammation". *Blood* 108.13 (2006), 3976–3978.

[251] Philipp Niethammer et al. “A tissue-scale gradient of hydrogen peroxide mediates rapid wound detection in zebrafish”. *Nature* 459.7249 (2009), 996–999.

[252] Yufei Xie et al. “Glucocorticoids inhibit macrophage differentiation towards a pro-inflammatory phenotype upon wounding without affecting their migration”. *DMM Disease Models and Mechanisms* 12.5 (2019).

[253] Audrey Bernut et al. “Deletion of cftr Leads to an Excessive Neutrophilic Response and Defective Tissue Repair in a Zebrafish Model of Sterile Inflammation”. *Frontiers in Immunology* 11 (2020), 1733.

[254] Anushka Katikaneni et al. “Lipid peroxidation regulates long-range wound detection through 5-lipoxygenase in zebrafish”. *Nature Cell Biology* 22.9 (2020), 1049–1055.

[255] Frida Sommer et al. “Frontline Science: Antagonism between regular and atypical Cxcr3 receptors regulates macrophage migration during infection and injury in zebrafish”. *Journal of Leukocyte Biology* 107.2 (2020), 185–203.

[256] Katherine M. Henry et al. “Zebrafish as a model for the study of neutrophil biology”. *Journal of Leukocyte Biology* 94.4 (2013), 633–642.

[257] Michiel van der Vaart et al. “Functional analysis of a zebrafish myd88 mutant identifies key transcriptional components of the innate immune system”. *DMM Disease Models and Mechanisms* 6.3 (2013), 841–854.

[258] Wanbin Hu et al. “Infection and RNA-seq analysis of a zebrafish tlr2 mutant shows a broad function of this toll-like receptor in transcriptional and metabolic control and defense to Mycobacterium marinum infection”. *BMC Genomics* 20.1 (2019), 878.

[259] Annemarie H. Meijer et al. “Expression analysis of the Toll-like receptor and TIR domain adaptor families of zebrafish”. *Molecular Immunology* 40.11 (2004), 773–783.

[260] Shuxin Yang et al. “Common and specific downstream signaling targets controlled by Tlr2 and Tlr5 innate immune signaling in zebrafish”. *BMC Genomics* 16.1 (2015), 547.

[261] Audrey Bernut et al. “Mycobacterium abscessus cording prevents phagocytosis and promotes abscess formation”. *Proceedings of the National Academy of Sciences of the United States of America* 111.10 (2014), 943–52.

[262] Antonia Chatzopoulou et al. “Glucocorticoid-induced attenuation of the inflammatory response in zebrafish”. *Endocrinology* 157.7 (2016), 2772–2784.

[263] Erik Meijering, Oleh Dzyubachyk, and Ihor Smal. “Methods for cell and particle tracking”. *Methods in Enzymology* 504 (2012), 183–200.

[264] Vincenzo Torraca et al. “The CXCR3-CXCL11 signaling axis mediates macrophage recruitment and dissemination of mycobacterial infection.” *Disease models & mechanisms* 8.3 (2015), 253–69.

[265] Cynthia L. Stokes, Douglas A. Lauffenburger, and Stuart K. Williams. "Migration of individual microvessel endothelial cells: Stochastic model and parameter measurement". *Journal of Cell Science* 99.2 (1991), 419–430.

[266] Harriet B. Taylor et al. "P38 and JNK have opposing effects on persistence of in vivo leukocyte migration in zebrafish". *Immunology and Cell Biology* 91.1 (2013), 60–69.

[267] Caroline Gray et al. "Simultaneous intravital imaging of macrophage and neutrophil behaviour during inflammation using a novel transgenic zebrafish". *Thrombosis and Haemostasis* 105.5 (2011), 811–819.

[268] Dianhua Jiang et al. "Regulation of lung injury and repair by Toll-like receptors and hyaluronan". *Nature Medicine* 11.11 (2005), 1173–1179.

[269] Kyoko Komai et al. "Role of scavenger receptors as damage-associated molecular pattern receptors in Toll-like receptor activation". *International Immunology* 29.2 (2017), 59–70.

[270] Shinichiro Yamamoto et al. "TRPM2-mediated Ca2+ influx induces chemokine production in monocytes that aggravates inflammatory neutrophil infiltration". *Nature Medicine* 14.7 (2008), 738–747.

[271] Manish Mittal et al. "Reactive oxygen species in inflammation and tissue injury". *Antioxidants and Redox Signaling* 20.7 (2014), 1126–1167.

[272] Tetsuro Shishido et al. "Central role of endogenous Toll-like receptor-2 activation in regulating inflammation, reactive oxygen species production, and subsequent neointimal formation after vascular injury". *Biochemical and Biophysical Research Communications* 345.4 (2006), 1446–1453.

[273] Erika Donà et al. "Directional tissue migration through a self-generated chemokine gradient". *Nature* 503.7475 (2013), 285–289.

[274] Luke Tweedy et al. "Self-Generated Chemoattractant Gradients: Attractant Depletion Extends the Range and Robustness of Chemotaxis". *PLOS Biology* 14.3 (2016), e1002404.

[275] Ioanna Manolopoulou et al. "Bayesian spatio-dynamic modeling in cell motility studies: Learning nonlinear taxic fields guiding the immune response". *Journal of the American Statistical Association* 107.499 (2012), 855–865.

[276] Jean Yves Tinevez et al. "TrackMate: An open and extensible platform for single-particle tracking". *Methods* 115 (2017), 80–90.

[277] Vladimír Ulman et al. "An objective comparison of cell-tracking algorithms". *Nature Methods* 14.12 (2017), 1141–1152.

[278] Klas E.G. Magnusson et al. "Global linking of cell tracks using the viterbi algorithm". *IEEE Transactions on Medical Imaging* 34.4 (2015), 911–929.

[279] Bjørn E.V. Koch et al. "Correction to: Intestinal microbiome adjusts the innate immune setpoint during colonization through negative regulation of MyD88 (Nature Communications, (2018), 9, 1, (4099), 10.1038/s41467-018-06658-4)". *Nature Communications* 10.1 (2019), 526.

[280] January Weiner et al. “Biomarkers of inflammation, immunosuppression and stress with active disease are revealed by metabolomic profiling of tuberculosis patients”. *PLoS ONE* 7.7 (2012), e40221.

[281] Yi Ding et al. “Tuberculosis causes highly conserved metabolic changes in human patients, mycobacteria-infected mice and zebrafish larvae”. *Scientific Reports* 10.1 (2020), 11635.

[282] Thomas Pfau et al. “IDARE2—Simultaneous Visualisation of Multiomics Data in Cytoscape”. *Metabolites* 11.5 (2021).

[283] Ang Li et al. “Are the Effects of Independent Biophysical Factors Linearly Additive? A 3D Tumor Migration Model”. *Biophysical Journal* 117.9 (2019), 1702–1713.

[284] Inbal Hecht et al. “"Self-Assisted" Amoeboid Navigation in Complex Environments”. *PLoS ONE* 6.8 (2011), e21955.

[285] Luke Tweedy et al. “Seeing around corners: Cells solve mazes and respond at a distance using attractant breakdown”. *Science* 369.6507 (2020).

[286] Harshana Rajakaruna et al. “Environment-imposed constraints make Brownian walkers efficient searchers”. *bioRxiv* (2020).

[287] Ben Lambert et al. “Bayesian inference of agent-based models: a tool for studying kidney branching morphogenesis”. *Journal of Mathematical Biology* 76.7 (2018), 1673–1697.

[288] Jochen Kursawe, Ruth E. Baker, and Alexander G. Fletcher. “Approximate Bayesian computation reveals the importance of repeated measurements for parameterising cell-based models of growing tissues”. *Journal of Theoretical Biology* 443 (2018), 66–81.

[289] Alex Graudenzi, Davide Maspero, and Chiara Damiani. “Modeling Spatio-Temporal Dynamics of Metabolic Networks with Cellular Automata and Constraint-Based Methods”. In: *Lecture Notes in Computer Science (including subseries Lecture Notes in Artificial Intelligence and Lecture Notes in Bioinformatics)*. Vol. 11115 LNCS. 2018, 16–29.