by ecological selection). We concluded that, within the context of our simplified model conditions, a host-symbiont system with mixed-mode transmission is evolutionarily stable unconditionally only if the host can maximize the Malthusian parameters of the infected and non-infected lineages using the same strategy. Finally, we performed a game-theoretical analysis of our selection situation and compared two stability definitions.

Transformer-based log anomaly detection with cross-dataset generalization

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A novel method with a strong generalization ability for detecting anomalies in log data is presented, which enables the detection of anomalies even in log types that were not seen during training. To achieve this, a transformer-based encoder is trained in a self-supervised manner on a large volume of multiple log data sets simultaneously.

Using the representation generated by the encoder as a fundamental model, the detector part of the method is trained in a supervised manner on one or more data sets, where training with more data sets leads to better results. Furthermore, when trained with multiple data sets, the method can also generalize to a log data set that was not included in the training. The study employs two encoder models which differ in the tokenization of digits. Together, these models can achieve results that are at least as good as, or better than, those of the state-of-the-art solutions on the most important log data benchmarks. Our results are supported by numerous measurements, for which we make the codes available.

Global dynamics of a within-host model for Usutu virus

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We propose a within-host mathematical model for the dynamics of Usutu virus infection, incorporating Crowley–Martin functional response. The basic reproduction number $\mathfrak{R}_0$ is found by applying the next-generation matrix approach. Depending on this threshold, parameter, global asymptotic stability of one of the two possible equilibria is also established via constructing appropriate Lyapunov functions and using LaSalle's invariance principle. We present numerical simulations to illustrate the results and a sensitivity analysis of $\mathfrak{R}_0$

was also completed. Finally, we fit the model to actual data on Usutu virus titers. Our study provides new insights into the dynamics of Usutu virus infection.

Microsecond scale 3D real time motion correction for in-vivo brain imaging

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In-vivo imaging of the central nervous system is inherently hampered by the motion of behaving animals, particularly when using voltage sensitive dyes where the signal is acquired from small regions of interest to get maximal temporal resolution. Here we present an FPGA-based acousto-optical scanning solution for 3D online motion correction for signal extraction with a high temporal resolution of 100 kHz within a volume of $900 \times 900 \times 400$ um up to 0-100 Hz of motion with a residual motion under 1 um at a sufficient signal-to-noise ratio. The timescale of the intervention loop is shorter than 500 μs. The correction can be applied on somatic and dendritic measurements, including volumetric imaging. The mathematical algorithm had to be optimized for the very low amount of memory in the FPGA.

The closed-loop online motion compensation has been validated with recordings in the cortex of awake mice, via 3kHz voltage imaging of Parvalbumin neurons using the Jedi2P sensor, and acquisition of 4D datasets (3 space + time) in collaboration with the *German Center for Neurodegenerative Diseases*. The project has won a Hungarian Innovation Award in March 2024.