11th Workshop Dynamical Systems Applied to Biology and Natural Sciences DSABNS 2020 Trento, Italy, February 4-7, 2020

TIME SCALE SEPARATION: COMPARISON OF SINGULAR PERTURBATION AND CENTER MANIFOLD ANALYSIS UNDER SCALING

Nico Stollenwerk

Centro de Matemática, Aplicações Fundamentais e Investigação Operacional (CMAF-CIO), Faculdade de Ciências, Universidade de Lisboa, Portugal

nico@ptmat.fc.ul.pt

To analayse time scale separation for model reduction to lower dimensional effective models we compare singular perturbation and center manifold analysis, giving special attention to the scaling of small parameters appearing in the dynamic equations.

Examples shown are models for vector borne diseases, SISUV and SIRUV models, as examples of low dimensional analytically treatable models. The first, the SISUV model, is naturally a singular perturbation problem, not the other one, the SIRUV model, which initially appears in the form of a regular perturbation problem, but leading to singular behaviour due to the non-linearity of the dynamics, making it an initially harder problem than models with naturally appearing classical singular perturbation form.

The main result is that in lowest order in the naturally small parameters, the SIRUV model gives in lowest order a $V(S, I) = \frac{\vartheta}{\nu} \cdot \frac{M}{N} \cdot I$ as required for effective SIR models for human disease dynamics only, whereas the SISUV model gives in lowest order a Holling type II functional form $V(S, I) = \frac{\frac{\vartheta}{\nu}I}{N + \frac{\vartheta}{\nu}I} \cdot M$ where the saturation still matters due to eventually large numbers of infected *I* because of the long recovery period in the SISUV model (as opposed to the SIRUV model). In this respect the SISUV model is a sketching model for e.g. malaria with long re-appearing disease, wheras the SIRUV model with its short recovery time is a sketching model for e.g. dengue fever and other fast recovering vector-borne diseases.

The scaling analysis of the spectral gap of eigenvalues around the endemic fixed point, as required in center manifold analysis, can be extended to numerical analysis of spectral gaps also in Lyapunov spectra as signs of time scale separation and possible model reduction, applied to multi-strain epidemiological models as examples of not only higher dimensional models but also with complex dynamical behaviour, i.e. bifurcations into chaos with positive Lyapunov exponents.

References

[1] Rocha, F., Aguiar, M., Souza, M., & Stollenwerk, N. (2013) Time-scale separation and center manifold analysis describing vector-borne disease dynamics, *Int. Journal. Computer Math.* **90**, 2105–2125.

©DSABNS

11th Workshop Dynamical Systems Applied to Biology and Natural Sciences DSABNS 2020 Trento, Italy, February 4-7, 2020

- [2] Rocha, F., Mateus, L., Skwara, U., Aguiar, M., & Stollenwerk, N. (2016) Understanding dengue fever dynamics: a study of seasonality in vector borne disease models, *International Journal of Computer Mathematics*, 93, 1405–1422.
- [3] Rashkov, P., Venturino, E., Aguiar, M., Stollenwerk, N., & Kooi, B. (2019) On the role of vector modelling in a minimalistic epidemiological model, *Mathematical Biosciences and Engineering* **16**, 4314–4338.
- [4] Aguiar, M., Kooi, B., Pugliese, A., Sensi, M., & Stollenwerk, N. (2020) Time scale separation in the vector borne disease model SIRUV via center manifold analysis, *in preparation*.