SOCIETY FOR VETERINARY EPIDEMIOLOGY
AND PREVENTIVE MEDICINE
http://www.svepm.org.uk

SVEPM PROPOSAL FORM FOR ORGANIZING A PRE-CONFERENCE WORKSHOP

Please complete the expandable table below and return by email by August 31st 2019 to the SVEPM Honorary Secretary, Philip Robinson at secretary@svepm.org.uk.

Title of the Workshop	Microbiome data analysis for veterinary epidemiologists
Workshop facilitators Please provide name, affiliation and email address Underline the name of the contact person One facilitator will receive free registration to the SVEPM annual meeting	Annelies (J.G.) Kers, Veterinary medicine, Department of Farm Animal Health, Utrecht, the Netherlands and Laboratory of Microbiology, Wageningen University & Research, Wageningen, the Netherlands: j.g.kers@uu.nl Egil A. J. Fischer Veterinary medicine, Department of Farm Animal Health, Utrecht, the Netherlands: E.A.J.Fischer@uu.nl
Learning objectives and expected outcomes	In veterinary epidemiology an increased number of researchers try to associate health with the microbiome of these animals and the environment. Rapid developments in sequencing technologies have led to decreasing costs per sample and a surge in available microbiome data and their meta-data. The analysis and interpretation of those datasets brings several challenges, such as increased resolution and the need to test multivariate factors to analyse the association of microbiome community composition and environmental covariates with health and other outcomes. The objective of this masterclass is to introduce microbiome data analysis, the interpretation, and limitations, in combination with a hands-on tutorial. The expected outcomes are to create awareness on how to perform microbiome research, increase the reproducibility in veterinary microbiome research, and to provide an overview of the different statistical tool to analysis 16S ribosomal RNA gene amplicon sequenced data. This workshop is based on the Masterclass "*Analysis and interpretation of microbiome and metagenomics data*" at Utrecht University held in March 2019. For this workshop, we will focus on the methodological subjects that are part of microbiome research.
Content and structure	Introduction to the microbiome data analysis - The definitions of the microbiome - The 16S rRNA gene amplicon sequencing workflow - Microbiota data analysis: comparing ecosystems 1. Alpha and beta diversity

Committee: K.M. McIntyre (President); M. Brennan (Senior Vice-President); G. van Schaik (Junior Vice-President); P. Robinson (Honorary Secretary); D. Brodbelt (Honorary Treasurer); L. Boden; F. Dórea; T. Vergne; L.P.Carmo; D. Barrett (co-opted)

1

	2. Visualization
	3. Ordination
	- Hands-on tutorial in R
Materials provided by the facilitators	We will provide a lecture to introduce veterinary epidemiologists into microbiome data analysis. The hands-on tutorial will introduce people to the basics of microbial community analysis. All materials will be provided on-line.
Maximum number of participants	30
Assumed knowledge of participants	Basic use of R
Required meeting room set-up and equipment, including number of power points (for laptops)	Screen to present PowerPoint presentation. Power sockets for 30 laptops