



A generic probability based model to derive regional patterns of crops in time and space

Martin Wattenbach (1), Stefan Luedtke (1), Richard Redweik (1), Marcel van Oijen (2), Juraj Balkovic (3), and Gert Jan Reinds (4)

(1) Helmholtz Center Potsdam GFZ - German Research Centre for Geosciences, Hydrology, Potsdam, Germany (martin.wattenbach@gfz-potsdam.de), (2) Centre for Ecology & Hydrology, Bush Estate, Penicuik, EH26 0QB, U.K., (3) Ecosystems Services and Management Program (ESM) International Institute for Applied Systems Analysis (IIASA) Schlossplatz 1 A-2361 Laxenburg, Austria, (4) Alterra Wageningen UR, Netherlands

Croplands are not only the key to human food supply, they also change the biophysical and biogeochemical properties of the land surface leading to changes in the water cycle, energy partitioning, they influence soil erosion and substantially contribute to the amount of greenhouse gases entering the atmosphere. The effects of croplands on the environment depend on the type of crop and the associated management which both are related to the site conditions, economic boundary settings as well as preferences of individual farmers.

The method described here is designed to predict the most probable crop to appear at a given location and time. The method uses statistical crop area information on NUTS2 level from EUROSTAT and the Common Agricultural Policy Regionalized Impact Model (CAPRI) as observation. These crops are then spatially disaggregated to the 1 x 1 km grid scale within the region, using the assumption that the probability of a crop appearing at a given location and a given year depends on a) the suitability of the land for the cultivation of the crop derived from the MARS Crop Yield Forecast System (MCYFS) and b) expert knowledge of agricultural practices. The latter includes knowledge concerning the feasibility of one crop following another (e.g. a late-maturing crop might leave too little time for the establishment of a winter cereal crop) and the need to combat weed infestations or crop diseases. The model is implemented in R and PostGIS. The quality of the generated crop sequences per grid cell is evaluated on the basis of the given statistics reported by the joint EU/CAPRI database. The assessment is given on NUTS2 level using per cent bias as a measure with a threshold of 15% as minimum quality.

The results clearly indicates that crops with a large relative share within the administrative unit are not as error prone as crops that allocate only minor parts of the unit. However, still roughly 40% show an absolute per cent bias above the 15% threshold. This highlights the discrepancy between the best practice given the soil properties within an administrative unit and the effectively cultivated crops.