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Mapping a spatial and temporal phenoregions: a case study for the contiguous US at a 1 km spatial resolution

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Phenology is the science that studies the timings of recurrent biological events, as well as their causes, interrelations, and variations in space and time. Because these timings are driven by environmental conditions (notably by temperature in temperate regions), phenological information is regularly used to study climate change. In this context, several studies have investigated approaches to extract and analyse regions with similar plant phenology (i.e. phenoregions). Phenoregions can be used to study the impact of climate change on vegetated canopies, build (forest) monitoring and warning systems, create new land cover maps. Phenoregions are often found by means of unsupervised classification methods such as k-means clustering. However, these approaches only analyse phenological data across one dimension: either spatial or temporal. Recent studies have presented novel clustering approaches that permit analysing the data across the spatial and temporal dimensions.

A well-tested co-clustering algorithm is the Bregman block average co-clustering (BBAC), which has been used to extract coarse spatial resolution phenoregions over European continent. However, new phenological products at high spatial resolution (1km) are nowadays available. Here, we analyse the Extended Spring Indices, which are available over the contiguous United States from 1980 to 2017, to map regions and years with similar first leaf and first bloom phenology. These two phenological indices are extracted using daily minimum and maximum temperature data extracted from Daymet. To realize our co-clustering analysis, we integrated the BBAC algorithm into a cloud-based computational platform that permits storing, analysing, and visualizing big geodata. This work contributes to a better understanding of the inter-annual variations in spring plant phenology, and reveals the impact of global warming at continental scales.