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ABSTRACTS

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Multimetric assessment of spatial interpolation methods for soil mapping

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The aim of this study was to identify the most effective spatial interpolation techniques for mapping soil variables. The analysis was based on soil data from the European LUCAS database, provided by the European Soil Data Centre (ESDAC). The dataset included two sampling campaigns (2015 and 2018), with samples collected predominantly from the same locations, ensuring spatial consistency and enabling reliable temporal comparisons.

The objective of the study was to overcome the limitations associated with evaluating interpolation accuracy using a single metric. Instead, a broad set of indicators was applied, including classical error measures (RMSE, MAPE), quantile-based indices, and inequality and asymmetry metrics. This approach enabled a comprehensive assessment of interpolation methods, highlighting their strengths and weaknesses, which is crucial for environmental mapping and monitoring soil changes over time.

Both probabilistic methods (e.g., kriging variants) and deterministic techniques (nearest neighbor, natural neighbor, triangulation with linear interpolation, modified Shepard's method, inverse distance weighting, and radial basis functions) were employed. Their performance was further evaluated using multivariate analysis tools such as principal component analysis and cluster analysis. The results indicate that the choice of interpolation method should be tailored to the specific soil parameter and temporal context, requiring a complex and multifaceted evaluation of interpolation quality.

Keywords: spatial interpolation accuracy, multimeric evaluation, multivariate analysis, soil property mapping, environmental monitoring

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Changes in C and N concentration in wood dry mass during decomposition

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Dead wood constitutes a substantial proportion of forest biomass and is considered a significant carbon reservoir that varies over time and space. The decomposition process is one of the factors determining its size. Unlike carbon, the concentration of nitrogen in woody plant tissues is very low. However, the availability of nitrogen affects the rate at which carbon is released. This study is the first to describe the variability in the physical (density) and chemical (carbon and nitrogen concentration) characteristics of dead wood from selected European tree species on a continental scale, depending on the degree of decomposition, the position of the dead wood, the fertility of the habitat, and the moisture conditions.

We used the generalized least squares (GLS) method to analyze carbon concentration in dead wood, correcting for a lack of homogeneity of variance, which increased significantly with wood decomposition and could not be eliminated by data transformation. Changes in relative wood density, nitrogen concentration, and the C:N ratio (log N and log C:N) during decomposition were examined using mixed-effects linear models. To avoid the negative impact of strong collinearity of predictors on the model, the maximum correlation coefficient between the included explanatory variables was set to $|r| > 0.7$.

The carbon concentration in dry mass was less than 50% (except for highly decomposed coniferous wood), a value commonly used to model the carbon budget of ecosystems. This suggests a possible significant overestimation of the amount of carbon bound in dead wood tissues. Differences between coniferous and deciduous wood increase as decomposition advances. Using values specific to species groups (coniferous or deciduous) and decomposition classes can significantly improve the accuracy of carbon pool and flow estimations. The high variability in C and N content within these groups, but not at the level of individual species, suggests that, whenever high accuracy is required, the optimal solution is to use species-specific values. At the species level, values obtained in other parts of the geographical range can be used. When modeling carbon cycling in forest ecosystems, especially after large-scale disturbances, it is important to consider the dynamics of dead tree falls.

Keywords: dead wood, carbon concentration, decomposition

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Random forest models in detection of crop damage in rapeseed using RGB imagery acquired using UAV

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The objective of the study was to assess the accuracy of classifying crop damage caused by wild boar using Random Forest models based on data collected from UAVs. The re-search focused on rapeseed crops at full maturity, just prior to harvest. The study was conducted in 2021 in central-western Poland on a rapeseed field shortly before harvest. The study demonstrated that UAVs with RGB sensors can effectively assess crop damage before rapeseed harvest. Combining RGB imagery with a digital surface model (DSM) and topographic position index (TPI) improved classification accuracy to 95%. The F1-score was 0.97 for undamaged and 0.70 for damaged areas. TPI was the most influential variable, highlighting the importance of DSM-derived data alongside RGB images in late growth stage.

Keywords: random forest, drones, rapeseed, crop damage

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Industrial hemp solid hydro-distillation residue − properties and diversity

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The paper presents the profile of solid residue from the industrial hemp hydro-distillation. No comprehensive data exist on the chemical composition of solid residues produced during hydro-distillation. To address this gap, residues from seven hemp cultivars were analyzed for moisture (87.27 %), volatile matter (64.83 % dry mass (d.m.)), fixed carbon (14.02 % d.m.), ash (21.15 % d.m.), higher heating value (15.92 MJ kg^{-1} d.m.), lower heating value (12.48 MJ kg^{-1}), carbon (36.99 % d.m.), hydrogen (4.05 % d.m.), sulfur (0.126 % d.m.), nitrogen (3.17 % d.m.), chlorine (0.126 % d.m.), cellulose (18.88 % d.m.), hemicellulose (19.11 % d.m.), lignin (7.96 % d.m.), and extractives (54.05 % d.m.). To better capture the diversity among cultivars, a cluster analysis was performed using the chemical and energetic traits. The generated dendrograms revealed distinct cultivar groupings, highlighting Finola as a clearly separated cluster due to its unique elemental composition and structural fractions. This approach not only allowed the identification of cultivars with similar quality potential but also distinguished genotypes with specific properties, which is highly relevant for biomass valorization and targeted applications. These findings contribute new knowledge relevant to biomass valorization and circular economy practices involving industrial hemp.

Keywords: Cannabis sativa, industrial hemp, hydro-distillation, distillation residue

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Agronomic practices to maximize seed and straw yield of monoecious hemp cultivar ‘Henola’

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Hemp (*Cannabis sativa L.*) is a valuable resource used as a source of biomass, utilized for textile purposes, the production of environmentally friendly polymeric materials, modern composites, and paper. Moreover, hemp can be used for biofuel production. The main goal of this study was to establish the optimal agronomic practices – sowing date, row spacing, and mineral fertilization – to maximize straw and seed yield of the monoecious hemp cultivar ‘Henola’ under temperate climate conditions. Field experiments were conducted over three growing seasons using a randomized block design, testing five fertilization treatments, three sowing dates, and three row spacings. Statistical analysis revealed that high nitrogen doses (PK + 120 N) significantly increased both straw and seed yields. The optimal sowing period was from late April to early May. Narrower row spacings (0.2 m and 0.35 m) favored higher seed yields, while row spacing had no significant effect on straw biomass.

Keywords: Cannabis sativa L., fertilization, row spacing, sowing date, biomass, agronomy

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Vitiligo is associated with an increased risk of cardiovascular diseases: a large-scale, propensity-matched, US-based retrospective study

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The paper presents the link between vitiligo and the risk of cardiovascular diseases development (CVDs). Utilizing a retrospective analysis of de-identified electronic health records from the US Collaborative Network (USCN) via the TriNetX platform, the study established two cohorts of 96,581 individuals each: a vitiligo patient group and a propensity-score-matched control group. The research analyzed the risk of 94 different CVD diagnoses over a 15-year period following the initial diagnosis. The findings showed a higher risk of developing CVD in the vitiligo group. Specifically, 54 of the 94 diagnoses displayed a statistically significant increased risk. Notably, diagnoses such as cerebral infarction (HR 1.21), venous thromboembolism (HR 1.27), and a composite endpoint of Major Adverse Cardiovascular Events (MACE) (HR 1.28) all showed a significantly increased risk in vitiligo patients. The results suggest that patients with vitiligo have an increased risk of developing cardiovascular diseases compared to healthy individuals. This implies that vitiligo may require more precise monitoring and systemic treatment, given its potential association with serious cardiovascular comorbidities.

Keywords: vitiligo, cardiovascular disease, heart failure, heart disease, MACE, TriNetX

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Application of XLSTAT by Lumivero in multivariate analyses for environmental sciences

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XLSTAT by Lumivero (https://www.xlstat.com) is a user-friendly statistical package that integrates more than 300 advanced analytical tools directly into Microsoft Excel, offering an accessible environment for scientists working with complex datasets. Its intuitive menus and wide range of multivariate techniques, including PCA, PLS regression, discriminant analysis, and clustering, make it especially suitable for interdisciplinary research teams, particularly in environmental sciences. The software allows direct use of raw spreadsheets, speeding up data handling and enabling clear visualization of results, which is crucial for both exploratory analyses and predictive modelling as well as interpretation of the results. By reducing the need for extensive programming skills, XLSTAT accelerates data exploration and interpretation, allowing researchers to focus on ecological meaning rather than coding.

Key advantages of XLSTAT include its user-friendly interface, reliable computation, and effective visualization options that enhance communication of findings across disciplines. While handling of very large datasets may be limited compared with dedicated statistical platforms such as R or Python, XLSTAT provides a practical balance between ease of use and analytical depth. Overall, it serves as a robust and supportive tool, strengthening scientific insight and evidence-based environmental management.

Keywords: XLSTAT, statistical package, multivariate techniques

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Multivariate analysis using PCA and clustering methods in the study of heterogeneous regional data

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The aim of the study was to apply advanced multivariate methods to assess regional diversity in highly correlated data. The analysis was conducted on the example of data concerning pro-environmental activities in agriculture, using a set of financial, structural, and ecological variables. The data were standardized and then subjected to principal component analysis (PCA), which reduced the dimensionality from over a dozen variables to three main components explaining 85.6% of the variance. Interpretation of PC1 revealed a structural–investment dimension, PC2 - an ecological one, and PC3 - a financial–administrative dimension. The next stage involved hierarchical cluster analysis using squared Euclidean distance and Ward's method, which enabled the classification of voivodeships into groups with similar profiles. The results confirmed a high consistency between the PCA space and the partition obtained in the cluster analysis. The presented approach demonstrates the usefulness of integrating PCA and taxonomic methods in exploring heterogeneous data and applying them in economic–environmental research.

Keywords: PCA, cluster analysis, dimensionality reduction, heterogeneous regional data

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How water stress affects the growth, development, and gene expression of Yellow Mealworm

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Water is essential for life, and its deficiency affects organisms, including insects. In insects, water deficiency slows growth and development and reduces immunity. In the case of mealworm farming, a controlled reduction of the applied water rate can bring economic benefits by reducing the costs associated with maintaining the farm. The study aimed to assess the effect of different water rates on the development and survival of mealworm larvae (*Tenebrio molitor* L.) while searching for genes whose expression may indicate disruptions in development caused by water deficiency. The experiment was conducted using three rates of water: full water requirement (H_2O-100), half of the water requirement (H_2O-50), and no additional water source (H_2O-0). Growth dynamics, survival, total biomass, and changes in the expression of genes associated with stress response were measured. The results indicate that insects given a full water rate (H_2O-100) achieved the highest final individual weight and total insect biomass, confirming water's key role in providing optimal development conditions. The H_2O-50 group did not differ significantly from H_2O-100 in terms of growth and productivity, suggesting the ability of larvae to adapt to moderate water restriction. On the other hand, no water addition significantly reduced the growth rate, final larval weight, and total biomass, activating defence mechanisms at the molecular level. Gene expression analysis showed that genes responsible for the expression of HSP70 and Coleoptericin B were most active in insects from H_2O-0 group, which emphasises their role in the response to water stress. These results have practical implications for sustainable insect farming and may contribute to optimising insect mass rearing reducing water footprint and production costs.

Keywords: Tenebrio molitor, water stress, gene expression, insect farming, larvae development

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AI methods for medical and environmental data analysis

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This paper is a review of selected applications of artificial intelligence (AI) models in medical research, including the use of deep neural networks to identify retinal diseases (Jeyasri & Karthiyayini, 2025) and breast cancer (McKinney et al., 2020), as well as a system for histopathological analysis for cancer diagnosis developed by PathAI (Diao et al., 2021). Artificial intelligence models are also widely used in environmental research. The paper presents the application of AI to model air quality and forecast PM_{10}, NO_x, and O_3 concentrations in Stockholm (Zhang et al., 2024), to analyze satellite images for monitoring forest cover (Siddha, 2024), and to assess water quality (Bai et al., 2025).

Keywords: artificial intelligence, medical research, environmental monitoring

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Selected methods for assessing alder pollen concentration

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Here, we study the problems connected with determinig regions within Poland that exhibit comparable characteristics with respect to the investigated variable, namely the atmospheric concentration of alder pollen.

To achieve this, functional data analysis techniques were employed to identify spatial units with analogous levels of the observed phenomenon. The empirical results were processed using advanced statistical approaches, which facilitated the detection of intricate relationships and the aggregation of objects sharing similar variability profiles.

The outcomes of the analyses enabled the identification and demarcation of areas characterized by homogeneous levels of pollen concentration. Moreover, the applied statistical procedures proved effective in capturing spatial distribution patterns, thereby allowing for the recognition of regions with uniform aeroallergen characteristics.

Keywords: functional data, pollen concentration

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Optimal grouping for Weibull models: Improved parameter estimation for the compressive strength of fertilizer granules

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This study evaluates how data grouping influences parameter estimation for the Weibull distribution in analyses of fertilizer-granule compressive strength. We propose an MLE framework for interval-grouped data with optimally selected bins (D-optimality; maximization of the Fisher information determinant) and derive correct closed-form expressions for the Fisher information matrix in the grouped-data setting. The method is tested on real data for three fertilizers (Salmag, Superphosphate, Polifoska 8), comparing optimal bins against commonly used equal-width bins. As performance measures we use asymptotic relative efficiency (ARE) and the χ^2 goodness-of-fit test. Results indicate that optimal grouping consistently increases estimation precision (ARE closer to 1) and often improves fit (higher χ^2 p-values) relative to equal-width grouping.

Keywords: Weibull distribution, grouped data, D-optimality, MLE, χ^2 test, asymptotic relative efficiency

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Comparing machine learning methods in detecting Fahr's disease

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The paper presents research results on comparing different machine learning methods, including neural networks, for the detection of Fahr's disease. Fahr's disease is a rare neurodegenerative disorder characterized by calcifications in the basal ganglia, thalamus, and other brain structures, and requires accurate diagnosis. Diagnosis is primarily based on the analysis of computed tomography (CT) images. For this study, a unique dataset of brain CT scans with confirmed diagnoses was created, along with a dataset of healthy brain images for training and testing. Several methods, including ResNet and EfficientNet, were evaluated. Most approaches achieved high performance across multiple metrics. The findings demonstrate the potential of machine learning for supporting diagnosis of Fahr's disease and highlight directions for further research. Specific examples, method effectiveness, and detailed results will be presented during the talk.

Keywords: machine learning, CNN, Fahr's disease, CT

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Prediction of calving time based on sensor measurements of behavior in cattle

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Although the expected calving date is known, it remains imprecise due to individual physical and hormonal changes affecting cows' behavior. Proper management during calving is crucial for the health of cows and calves. This study aimed to predict calving time based on behavioral symptoms in two breeds: 38 Polish Holstein-Friesian and 14 Brown Swiss cows from a single farm. Using CowManager sensors, 24-hour behavior of dairy cows was monitored, with data from 3D accelerometers classified into specific activities (feeding, rumination, resting, low/high activity). As the study was conducted on a single farm, the generalizability of the results to other herd management systems or environmental conditions may be limited. A preliminary graphical analysis identified changes in behavior in the last hours before calving. Statistical analysis included bootstrap method, logistic regression and analysis of change points in the time series (separately for each cow and trait, for moving averages covering six hours). One-day periods were taken for the analysis, starting from 168 hours before calving. The daily period was shifted by one hour until six hours before calving. The applied methodology has shown satisfactory effectiveness (recall of 81.03% for PHF cows). Differences in pre-calving behavior between breeds were observed.

Keywords: bootstrap method, Brown Swiss, Holstein-Fresian, sensor

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Statistical and bioinformatics methods for whole genome sequencing analysis of rare genetic disorders

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Whole genome sequencing (WGS) has emerged as a powerful tool for identifying genetic variants underlying rare diseases and developmental disorders, enabling comprehensive analysis of genomic variation at unprecedented resolution. This study proposes a comprehensive statistical and bioinformatics methodology for the analysis of complex genetic conditions, as evidenced by an investigation of XX male syndrome in a Maine Coon cat. We performed WGS analysis on four samples: the affected individual, both parents, and an additional control sample. The presentation will provide a comprehensive overview of bioinformatics methodologies, encompassing the instruments and criteria employed for quality assessment, variant calling algorithms, and filtration strategies. The validation of suspected pathogenic variants was conducted using Sanger sequencing in a cohort representing diverse genetic backgrounds. This approach was employed to ascertain population frequencies and evaluate pathogenicity. The findings contribute to our understanding of sex determination disorders and establish a reproducible workflow for genetic investigation of rare developmental conditions.

Keywords: whole genome sequencing, bioinformatics pipeline, statistical analysis, variant discovery

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Phenolic acid content in fly agaric fruit bodies (*Amanita muscaria)* depending on the type of habitat and the end of harvest

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The research included the analysis of fly agaric (*Amanita muscaria*) fruiting bodies from two types of stands: an 88-year-old *Pinus sylvestris* with a group of 10-year-old understory trees of *P. sylvestris* and *Picea abies*, growing on podzolic soils, and from a mixed stand of *P. sylvestris* (11-year-old) and *Betula pendula* (12-year-old) growing on rusty soil (a type of podzolic soil) with an understory of *Prunus padus* and *Robinia pseudoacacia* and with single mature specimens of *P. sylvestris*, *P. nigra*, *B. pendula* and Quercus robur in August and September 2022 and 2023. The collected fruiting bodies were frozen and freeze-dried (at -53°C, at 0.025 mBar). After drying, the ground fruiting bodies were extracted. Phenolic acids were analyzed using ultra-performance gas chromatography (UPLC) with a DAD detector.

The study aimed to assess the influence of the habitat, year and date of harvest on the level of phenolic acids in fly agaric fruit bodies. Before performing statistical analysis, it was verified whether the data were normally distributed and whether the data variances were homogeneous. Due to the failure to meet these conditions for the considered data, the nonparametric equivalent of two-way analysis of variance - the Scheirer-Ray-Hare test, was used.

The relationship between samples and variables was presented using a heatmap. They show the content of phenolic acids in individual samples in relation to the habitat, year and date of collection. Dendrograms were generated using hierarchical cluster analysis. These allowed for the assessment of similarity between samples in terms of their chemical profiles.

Based on the analyses performed, it can be concluded that the content of individual phenolic acids depends on a number of environmental factors. Fruiting bodies from coniferous forests differ in composition from those from deciduous forests.

Keywords: fly agaric fruit bodies, phenolic acids, nonparametric statistical methods

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Distribution of energy required to crush mineral fertilizer granules

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The use of modern fertilizers allows for increased food production capacity and reduced environmental impact. Granulated fertilizers undergo comprehensive quality control, and one of the criteria for their evaluation is a compression strength test, which determines their suitability for handling (transport, storage) and application.

Compression tests were carried out on selected compound fertilizers to compute the energy required to crush the granules. The consistency of empirical distributions with selected theoretical distributions was checked, and the distributions that best describe the energy distribution were identified.

Keywords: mineral fertilizers, crushing energy

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Exploring image representations for airborne pollen recognition

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In pollen monitoring, pollen grains are typically identified and counted manually under a microscope which is a tedious and time-consuming task. To automate this process, we investigate the use of deep learning-based object detectors for recognizing and counting pollen grains in microscopic images.

This study focuses on the impact of different color representations on detection performance. We evaluated five color spaces: RGB, AvgRGB, STRESS, CMYK, and Magenta. Two image sets were used: one captured with an Olympus DP23 microscope and the other with an HDCE-x5 micro camera, covering three pollen taxa. For object detection, we employed the YOLO architecture (v12s), which has shown strong performance in related tasks.

To assess detection precision across varying imaging conditions, we used a nonparametric statistical approach based on relative treatment effects (RTE) within the F1.LD.F2 design. An ANOVA-type statistic was applied to test differences in precision distributions.

Our results show that average precision exceeds 98% when both training and test images are from the same camera. However, precision decreases when the test images are captured using a different device. Notably, only the Magenta color representation maintains high detection precision in cross-device scenarios, indicating its robustness and suitability for broader use in automated pollen monitoring.

Keywords: image processing, image recognition, pollen monitoring

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The application of multivariate analysis in studies of the variability of cereal breeding materials

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The results of long-term studies on the variability of phenotypic traits of grains of various cereal species conducted at the Department of Genetics, Plant Breeding, and Bioresource Engineering are presented. The research material consisted of hybrids of common wheat and spelt, accessions of Polish wheat, cultivars of durum wheat, and Tritordeum breeding lines. In our investigations, we used the principal component analysis (PCA), the hierarchical analysis, and the k-means method. The foregoing methods enabled the discrimination of the examined materials in terms of grain morphometric characteristics (wheat and spelt hybrids), phenolic acid and flavonoid content in grain (Polish wheat and durum wheat), mycotoxin content in the grain (Polish wheat), and the traits determining the technological quality of the grain and flour (wheat and spelt hybrids and Tritordeum).

Keywords: cereals, grain, multivariate analysis

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Spatio-temporal patterns of methane emissions from 2019 onwards: A satellite-based comparison of high- and low-emission regions

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Methane is a potent greenhouse gas with a significant impact on short- and medium-term climate forcing, and its atmospheric concentration has been increasing rapidly in recent decades. This study aims to analyze spatio-temporal patterns of atmospheric methane concentrations between 2019 and 2025, focusing on comparisons between regions characterized by high and low emission intensities. Level-3 XCH_4 data from the TROPOspheric Monitoring Instrument onboard the Sentinel-5 Precursor satellite were used, which were aggregated into seasonal and annual composites. High-emission regions, such as the Mekong Delta, Nile Delta, Eastern Uttar Pradesh and Bihar, Central Thailand, Lake Victoria Basin, and Eastern Arkansas, were contrasted with low-emission areas including Patagonia, the Mongolian Steppe, Northern Scandinavia, the Australian Outback, the Sahara Desert, and the Canadian Shield. The results show that high-emission regions exhibit substantially higher seasonal amplitude in XCH4 concentrations, with an average seasonal variation of approximately 30.00 ppb, compared to 17.39 ppb in low-emission regions. Methane concentrations generally peaked at the end of the year and reached their lowest levels during the first half of the year, particularly in agriculturally dominated regions. Principal component and cluster analyses further confirmed a strong spatial differentiation between high- and low-emission regions based on both temporal trends and seasonal behavior. These findings demonstrate the potential of satellite remote sensing to monitor regional methane dynamics and highlight the need for targeted mitigation strategies in major agricultural and wetland zones.

Keywords: methane emissions, satellite remote sensing, TROPOMI, Sentinel-5P, seasonal variability, atmospheric methane trends

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