

1. [A review of approaches for evapotranspiration partitioning](#)

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วารสาร: Agricultural and Forest Meteorology, Volume 184, 15 January 2014, Pages 56–70

Abstract: Partitioning of evapotranspiration (ET) into evaporation from the soil (E) and transpiration through the stomata of plants (T) is challenging but important in order to assess biomass production and the allocation of increasingly scarce water resources. Generally, T is the desired component with the water being used to enhance plant productivity; whereas, E is considered a source of water loss or inefficiency. The magnitude of E is expected to be quite significant in sparsely vegetated systems, particularly in dry areas or in very wet systems such as surface irrigated crops and wetlands. In these cases, ET partitioning is fundamental to accurately monitor system hydrology and to improve water management practices. This paper aims to evaluate and summarize available methods currently used to separately determine E and T components. We presuppose that, to test the accuracy of ET partitioning methods (measurements and/or modeling), all three components, i.e., E , T and ET , must be estimated independently, but recognize that sometimes one of the components is taken as the residual of the other two. Models that were validated against measurements for their ability to partition between E and T are briefly discussed. To compare approaches, 52 ET partitioning studies were considered regarding estimates of the relative amount of E and for success of agreement in closing the $ET = E + T$ equation. The E/ET ratio was found to exceed 30% in 32 of the studies, which confirms the hypothesis that E often constitutes a large fraction of ET and deserves independent consideration. Only 20 studies estimated E and T as well as ET , and had varied results. A number of studies succeeded to estimate $E + T$ to within 10% of measured ET . Future challenges include development of models simulating the components of ET separately and advancement of methods for continuous measurement of E , T and/or the ratio between the two.

2. [Photographic measurement of leaf angles in field crops](#)

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วารสาร: Agricultural and Forest Meteorology, Volume 184, 15 January 2014, Pages 137–146

Abstract: Leaf angle distribution (LAD) is one of the most important parameters used to describe the structure of horizontally homogeneous vegetation canopies such as field crops. LAD affects how incident photosynthetically active radiation is distributed on plant leaves, thus directly affecting plant productivity. Knowledge of LAD is also required for retrieval of other important biophysical variables from measurements of canopy radiation transmittance or spectral reflectance. Unfortunately, its determination is laborious and measured data is rarely available. In this study, we applied a recently developed method for determination of the inclination angles using leveled digital photography to the leaves of six cool-temperate crops: faba bean, narrow-leafed lupin, turnip rape, wheat, barley, and oat. The method, previously applied only to small and flat leaves of broadleaved trees and bushes, was extended to be applicable to the narrow and curved leaves of cereals. A reasonable match

was found between the leaf angles determined by photographic measurements and the mean leaf tilt angles (MTA) measured using a LAI-2000 plant canopy analyzer for five out of the six species ($R^2 = 0.92$). The error caused by assuming a spherical LAD, when calculating LAI from canopy transmittance measurements, varied between 0 and 1.5 LAI units, depending on species. Finally, we analyzed the correlation between photographically determined species-specific LADs and airborne imaging spectroscopy data acquired for the same species in a similar growth stage. The highest correlation between spectral reflectance factor and leaf mean tilt angle was found at a wavelength of 748 nm ($R = 0.80$). The high correlation between MTA and this red edge waveband can be useful for MTA determination from imaging spectroscopy.

[3. Simulation of stand transpiration based on a xylem water flow model for individual trees](#)

ผู้แต่ง: Rainer Hentschel, Sebastian Bittner, Michael Janott, Christian Biernath, Jutta Holst, Juan Pedro Ferrio, Arthur Gessler, Eckart Priesack

วารสาร: Agricultural and Forest Meteorology, Volumes 182–183, 15 December 2013, Pages 31–42

Abstract: Quantifying the water exchange between a forest stand and the atmosphere is of major interest for the prediction of future growth conditions and the planning of silvicultural treatments. In the present study, we address (i) the uncertainties of sap flow estimations at the tree level and (ii) the performance of the simulation of stand transpiration. Terrestrial laser scan images (*TLS*) of a mature beech stand (*Fagus sylvatica* L.) in Southwestern Germany serve as input data for a representation of the aboveground tree architecture of the study stand. In the single-tree xylem water flow model (*XWF*) used here, 98 beech trees are represented by 3D graphs of connected cylinders with explicit orientation and size. Beech-specific hydraulic parameters and physical properties of individual trees determine the physiological response of the tree model to environmental conditions.

The *XWF* simulations are performed without further calibration to sap flow measurements. The simulations reliably match up with sap flow estimates derived from sap flow density measurements. The density measurements strongly depend on individual sapwood area estimates and the characterization of radial sap flow density gradients with xylem depth. Although the observed pure beech stand is even-aged, we observe a high variability in sap flow rates among the individual trees. Simulations of the individual sap flow rates show a corresponding variability due to the distribution of the crown projection area in the canopy and the different proportions of sapwood area.

Stand transpiration is obtained by taking the sum of 98 single-tree simulations and the corresponding sap flow estimations, which are then compared with the stand-level root water uptake model (*RWU* model) simulation. Using the *RWU* model results in a 35% higher simulation of seasonal stand transpiration relative to the *XWF* model. These findings demonstrate the importance of individual tree dimensions and stand heterogeneity assessments in estimating stand water use. As a consequence of species-specific model parameterization and precise *TLS*-based stand characterization, the *XWF* model is applicable to various sites and tree species and is a promising tool for predicting the possible water supply limitations of pure and mixed forest stands.

[4. Selecting traits that explain species–environment relationships: a generalized linear mixed model approach](#)

ผู้แต่ง: Jamil, T., Ozinga, W. A., Kleyer, M., ter Braak, C. J.F.

วารสาร: Journal of Vegetation Science, *Volume 24, Issue 6*, pages 988–1000, November 2013

Abstract:

Question

Quantification of the effect of species traits on the assembly of communities is challenging from a statistical point of view. A key question is how species occurrence and abundance can be explained by the trait values of the species and the environmental values at the sites.

Methods

Using a sites × species abundance table, a site × environment data table and a species × trait data table, we address the above question using a novel generalized linear mixed model (GLMM) approach. The GLMM overcomes problems of pseudo-replication and heteroscedastic variance by including sites and species as random factors. The method is equally applicable to presence–absence data as to count and multinomial data. We present a tiered forward selection approach for obtaining a parsimonious model and compare the results with alternative methods (the fourth corner method and RLQ ordination).

Results

We illustrate the approach on a presence–absence version on two data sets. In the Dune Meadow data, species presence is parsimoniously explained by moisture and manure on the meadows in combination with seed mass and specific leaf area (SLA). In the Grazed Grassland data, species presence is parsimoniously explained by the grazing intensity and soil phosphorus in combination with the C:N ratio and flowering mode.

Conclusions

Our GLMM approach can be used to identify which species traits and environmental variables best explain the species distribution, and which traits are significantly correlated with environmental variables. We argue that the method is better suited for providing an interpretable and predictive model than the fourth corner method and RLQ.

[5. Correlations between genetic and species diversity: effects of resource quantity and heterogeneity](#)

ผู้แต่ง: Avolio, M. L., Smith, M. D.

วารสาร: Journal of Vegetation Science, *Volume 24, Issue 6*, pages 1185–1194, November 2013

Abstract:

Questions

It is hypothesized that species and genetic diversity are correlated because niche differentiation among species and genotypes is either affected by the same processes (positive) or each level restricts the amount of diversity in the other (negative). Although many studies have observed both positive and negative relationships, others have found no correlation between the two diversity measures. Are measures of species (richness, diversity and evenness) and genetic diversity correlated, and how does resource (soil moisture, light, nitrogen and phosphorus) quantities and heterogeneity affect both levels of diversity?

Location

Intact tallgrass prairie at Konza Prairie Biological Station, northeast Kansas, US.

Methods

We investigate the correlation between plant species and genetic diversity in a long-term precipitation manipulation experiment – the Rainfall Manipulation Plots (RaMPs) – located in intact tallgrass prairie as well as adjacent non-manipulated prairie. The RaMPs experiment has been imposing ambient and more variable precipitation regimes (a 50% increase in timing between rainfall events without changing total rainfall amount) during the growing season since 1998, resulting in reduced mean soil moisture and increased soil moisture variability. Thus, the RaMPs and non-manipulated prairie plots capture a range of soil moisture amounts and variability. Genetic diversity (measured as genotype richness and genomic dissimilarity among individuals) was quantified for the dominant grass species, *Andropogon gerardii*, which has large impacts on plant community structure and ecosystem function.

Results

We found species and genetic diversity were not significantly correlated. Genotypic richness was negatively related to soil moisture variability, but measures of species diversity were not. In the non-manipulated plots only, we found generally negative relationships between resource quantity (light and nitrogen) and community diversity, and positive relationships between resource heterogeneity (CV of light) and community diversity.

Conclusions

Our results suggest that a lack of a positive or negative relationship between species and genetic diversity could be due to these two levels of diversity responding differently to the identity, quantity and heterogeneity of resources.

6. [Coupling ordination techniques and GAM to spatially predict vegetation assemblages along a climatic gradient in an ENSO-affected region of extremely high climate variability](#)

ผู้แต่ง: Muenchow, J., Feilhauer, H., Bräuning, A., Rodríguez, E. F., Bayer, F., Rodríguez, R. A., von Wehrden, H.

วารสาร: Journal of Vegetation Science, Volume 24, Issue 6, pages 1154–1166, November 2013

Abstract:

Questions

El Niño Southern Oscillation (ENSO) is a strong driver of climatic and ecosystem variability in coastal NW Peru. La Niña amplifies the already dry local conditions, and led to depleted ecosystems in 2011. However, the 2012 La Niña event triggered rainfall far above the average. (1) Did plant species diversity, primary productivity and vegetation assemblages change along a climatic gradient between two climatologically different La Niña years; (2) Is there a difference in explanatory power of environmental predictors between the 2 yr; and (iii) is it possible to predict the observed vegetation patterns spatially?

Location

Transect along a climatic gradient in the Sechura Desert of Piura, NW Peru (corresponds to the terrestrial part of the El Niño region 1 + 2) – a region of extremely high climatic variability.

Methods

We visited 50 30 m × 30 m randomly sampled plots in 2011 and 2012. A Procrustes analysis of two non-metric multidimensional scaling (NMDS) ordinations provided information on the temporal change of species assemblages. Variation partitioning revealed the differences in explanatory power of the predictors. We employed a generalized additive model (GAM) to fit the scores of the first ordination axis with a floristic gradient map as a result.

Results

Generally, higher rainfall resulted in a positive feedback when considering biodiversity, productivity and vegetation assemblages. The floristic gradient map resulting from the GAM displayed the spatial distribution of the three main assemblages along the climatic gradient. Edaphic variables added no independent portion to the explanation of the vegetation assemblages, but explained in conjunction with topography and NDVI a considerable amount of the variance.

Conclusions

Strong Atlantic easterly winds crossing the Andes can boost plant growth even during a La Niña situation. This underscores the need for a deeper understanding of ENSO-related climate variability of ENSO. Combining vegetation maps with accurate predictions of such climatic anomalies would aid the effective execution of conservation and recovery strategies. Additionally, coupling an unconstrained ordination with a GAM appears to be a promising tool for vegetation mapping, especially in the presence of a non-linear gradient.

7. [Effects of organic and inorganic fertilizers on greenhouse gas \(GHG\) emissions in tropical forestry](#)

ผู้แต่ง: Danilo Ignacio de Urzedo, Mariana Pires Franco, Leonardo Machado Pitombo, Janaina Braga do Carmo

วารสาร: Forest Ecology and Management, Volume 310, 15 December 2013, Pages 37–44

Abstract: The production of organic wastes tends to increase in a manner that is proportional to human population growth. Currently, applying these wastes to soils is being considered as an alternative solution for the over production of organic waste. However, the levels of greenhouse gas (GHG) emissions from organic waste applications in tropical forestry are unknown. The aim of the present study was to quantify soil carbon dioxide (CO₂), nitrous oxide (N₂O) and methane (CH₄) emissions from a reforestation project, where trees (*Calophyllum brasiliense*) were fertilized with different mineral and organic waste materials. A randomized trial was established to measure soil GHG emissions from plots fertilized with sewage sludge compost (SSC), sewage sludge (SS), mineral fertilizer (Min Fert) and a control (C). *C. brasiliense* seedling spaced in 3 m × 2 m intervals were place into a planting hole which had fertilizer incorporated for seedling establishment. Soil GHG were measured using the static chamber method, placing chambers on the surface of the soil and taking measurements over time, during 172 days in a dry season. Organic wastes (SS and SSC treatments) had significantly higher soil CO₂ fluxes than mineral fertilizer and control plots, with soil CO₂ fluxes of 6.35 ± 1.17 and 9.33 ± 0.96 g C m⁻² day⁻¹, respectively. The application of organic wastes promoted a drastic increase in soil N₂O emissions treated with SSC (141.19 mg ± 21 N m⁻² day⁻¹, $p < 0.01$), which had a higher emission factor (2.11%). Average soil CH₄ flux on collection days was -0.1 ± 0.2 mg C m⁻² day⁻¹, although cumulative soil CH₄ emissions over the 5 months study period was positive for the SS treatment, demonstrating the potential emission of

GHG from this treatment. Apparently, the variation in fluxes between treatments with organic residues was influenced by differences in the physical and chemical compositions of the wastes and the amounts of labile carbon added.

8. [A 100-year conservation experiment: Impacts on forest carbon stocks and fluxes](#)

ผู้แต่ง: Tara Sharma, Werner A. Kurz, Graham Stinson, Marlow G. Pellatt, Qinglin Li

วารสาร: Forest Ecology and Management, Volume 310, 15 December 2013, Pages 242–255

Abstract: Forest conservation is an important climate change mitigation strategy. National parks in Canada's Rocky and Purcell Mountains offer a rare opportunity to evaluate the impacts of a century of conservation on forest carbon (C) stocks and fluxes. We studied forest ecosystem C dynamics of three national parks in the Rocky and Purcell Mountains of British Columbia – Yoho, Kootenay, and Glacier National Parks – over the period 1970–2008 using the CBM-CFS3 inventory-based forest C budget model. We hypothesized that parks and protected areas would contain higher forest C density and have lower CO₂ uptake rates compared to their surrounding reference areas because of the exclusion of timber harvesting and resulting predominance of older, slower growing forest stands. Results for Glacier National Park relative to its reference area were consistent with our hypothesis. Forests in Kootenay National Park were substantially younger than those in its reference area despite the exclusion of harvesting because natural disturbances affected large areas within the park over the past century. Site productivity in Kootenay National Park was also generally higher in the park than in its reference area. Consequently, Kootenay National Park had both higher C density and higher CO₂ uptake than its reference area. Yoho National Park forests were similar in age to reference area forests and more productive, and therefore had both higher C stocks and greater CO₂ uptake. C density was higher in all 3 parks compared to their surrounding areas, and parks with younger forests than reference areas had higher CO₂ uptake. The results of this study indicate that forest conservation in protected areas such as national parks can preserve existing C stocks where natural disturbances are rare. Where natural disturbances are an important part of the forest ecology, conservation may or may not contribute to climate change mitigation because of the risk of C loss in the event of wildfire or insect-caused tree mortality. Anticipated increases in natural disturbance resulting from global warming may further reduce the climate change mitigation potential of forest conservation in disturbance-prone ecosystems. We show that managing for the ecological integrity of landscapes can also have carbon mitigation co-benefits.

9. [High genetic diversity of in situ and ex situ populations of Madagascar coffee species: further implications for the management of coffee genetic resources](#)

ผู้แต่ง: Domohina N. Andrianasolo, Aaron P. Davis, Norosoa J. Razafinarivo, Serge Hamon, Jean-Jacques Rakotomalala, Sylvie-Annabel Sabatier, Perla Hamon

วารสาร: Tree Genetics & Genomes, October 2013, Volume 9, Issue 5, pp 1295-1312

Abstract: The genetic diversity of endemic Madagascan *Coffea* species has not received any considerable attention, despite the high extinction threat facing most of the species on the island. In order to address this shortfall, we assessed and compared the genetic diversity and allelic richness of ex situ and in situ populations for four selected species, and 18 ex situ

populations maintained at the Kianjavato Coffee Research Station. We also investigated the possibility of in situ and ex situ hybridization events for Madagascan coffee, both within and between species. For these purposes, we used 18 nuclear microsatellite markers, on a total of 37 *Coffea* populations (4 in situ and 33 ex situ) representing a total of 398 genotypes (96 in situ and 302 ex situ) for 23 species. Our study showed (1) strong differentiation between Madagascan *Coffea* species; (2) good differentiation between all the populations studied, including those from the same locality (even when the area of the locality was restricted); (3) good evidence for both in situ and ex situ hybridization, although in situ hybridization appeared to be limited; (4) much higher genetic diversity within in situ collections compared to ex situ collections; and (5) that, despite limitations, the Kianjavato Coffee Research Station collection is an extremely valuable resource of Madagascan coffee germplasm. Recommendations for in situ and ex situ germplasm conservation are discussed.

10. [The effects of artificial selection on sugar metabolism and transporter genes in grape](#)

ผู้แต่ง: Haiping Xin, Jisen Zhang, Wei Zhu, Nian Wang, Peige Fang, Yuepeng Han, Ray Ming, Shaohua Li

วารสาร: Tree Genetics & Genomes, October 2013, Volume 9, Issue 5, pp 1343-1349

Abstract: Sugar content is a key feature of grape quality. The sugar content of grapes has been significantly improved after nearly a thousand years of artificial selection. However, the mechanism underlying the changes in the grape sugar content during the process of artificial selection remains largely unknown although several genes involved in sugar metabolism and transportation in grape have been identified. In this study, the genomes of 13 wild *Vitis* species and 14 cultivated *Vitis vinifera* accessions were resequenced to 2–5 X depth using the Illumina Hiseq2000 platform. Genetic variation of 138 genes involved in sugar biosynthesis and transport was investigated, and 7,690 and 12,717 single nucleotide polymorphisms/insertions and deletions (SNPs/InDel) were identified within the cultivated *V. vinifera* and wild *Vitis* species, respectively. The percentages of SNPs/InDels were 0.93 and 1.54 % in cultivated and wild species, respectively, and the wild *Vitis* species had 1.65-fold more SNPs/InDels than the cultivated *V. vinifera*. Moreover, the distribution of SNPs/InDels in gene regions was also investigated. Eight genes (HT4, PPFTK4, PPFTK6, PMT3, SPS1, HT8, HT15, SUSy1) showed low level of allelic diversity in cultivated species, suggesting they might have undergone purifying selection during the domestication process of grapes. Our genome DNA resequencing data provided a valuable resource for analyzing the effects of artificial selection on trait-related pathways in grape. The result that eight genes showed lower level of DNA variation in cultivated species than in wild species will be very helpful in understanding sugar accumulation in grapes.