Geoderma 329 (2018) 27–42

Contents lists available at ScienceDirect

Geoderma

journal homepage: www.elsevier.com/locate/geoderma

Mapping the transition from pre-European settlement to contemporary soil conditions in the Lower Hunter Valley, Australia

Jingyi Huang*, Alex B. McBratney, Brendan P. Malone, Damien J. Field

Sydney Institute of Agriculture & School of Life and Environmental Sciences, The University of Sydney, Eveleigh, NSW 2015, Australia

ARTICLE INFO

Handling Editor: M. Vepraskas

Keywords:
Soil security
Soil genesis
Digital soil mapping
Human activities
Soil monitoring

ABSTRACT

The concept of soil security has been proposed with the dimensions of capability, condition, capital, connectivity, and codification of soil. However, it remains a challenge to accurately and efficiently assess the soil's capability and condition as a function of soil change. The idea of genoform and phenoform was proposed 20 years ago and recently revitalized. Herein, we were inspired by these concepts to develop a general approach and concepts of genosoils and phenosoils for distinguishing the soil changes within soil mapping units as affected by human activities. Across a 220 km^2 district with a diversity in landforms, parent materials, and land use types, we generated maps of Pre-European (soil classes that existed prior to agricultural development) soil classes using a digital soil mapping approach. Based on the land use change, Pre-European genosoils and present genosoils and phenosoils were identified and mapped within each of the Pre-European soil classes. The measured topsoil (0–10 cm) and subsoil (40–50 cm) properties have shown differences between the present genosoils and phenosoils. By objectively calculating the distances between the present genosoils and phenosoils in a principal component space using a recently published comprehensive soil classification system, several present phenosoils displayed significant differences among several soil properties (distance > 8% of overall distance) and were redefined as new genosoils. The approach has successfully mapped genosoils and phenosoils within Pre-European soil classes at the district scale and identified shifts between present genosoils and phenosoils. It showed potential in detecting areas of soil changes due to human activities. Future work is required to separate seasonal fluctuations from long-term variations in NDVI and improve land use classification using remote sensing data. The method developed here can be applied in areas without remnant vegetation to separate the soil condition from capability by gauging phenosoils against genosoils.

1. Introduction

Soil serves as the intersection of the lithosphere, hydrosphere, atmosphere and biosphere as a global resource to produce food, fibre, and fresh water, contribute to energy and climate sustainability, and to maintain the biodiversity and the overall protection of the ecosystem (De Groot et al., 2002; Lavelle and Spain, 2001). To secure the soil resource, it is necessary to monitor the spatial variations and temporal changes of soil properties (Arrouays et al., 2012; Jandl et al., 2014; Chauveau et al., 2014).

To frame this, the concept of soil security has been proposed with the dimensions of capability, condition, capital, connectivity, and codification of soil which encompass the social, economic and biophysical sciences and recognize policy and legal frameworks (McBratney et al., 2014; Kidd et al., 2018). However, it remains a challenge to accurately and efficiently assess the soil's capability and condition as a function of soil change. This is because soils are formed as a result of climate, organisms, relief, parent material, and humans and are susceptible to natural but more importantly anthropogenic disturbance over time (Amundson and Jenny, 1991; Pulleman et al., 2000).

The idea of genoform and phenoform was proposed 20 years ago (Droogers and Bouma, 1997) and recently revitalized by Rossiter and Bouma (2018). Genoforms are defined as soil classes as identified by the soil classification system used as the basis for detailed soil mapping in a given area while soil phenoforms are defined as persistent variants of a genoform with sufficient physical or chemical differences to substantially affect soil functions. These concepts are potentially useful in identifying the soil spatial variations and monitoring the soil changes through time (Rossiter and Bouma, 2018). However, Rossiter and Bouma (2018) only focused on the current soil survey map (i.e. soil series) to identify the genoforms and phenoforms at one stage. As the soil may change with time, the soil phenoform identified in the past can become a new genoform at the present time. More specifically, depending on the extent of change, people may wish to distinguish

* Corresponding author.
E-mail address: jingyi.huang@sydney.edu.au (J. Huang).

https://doi.org/10.1016/j.geoderma.2018.05.016
Received 28 December 2017; Received in revised form 2 May 2018; Accepted 13 May 2018
0016-7061/ © 2018 Published by Elsevier B.V.

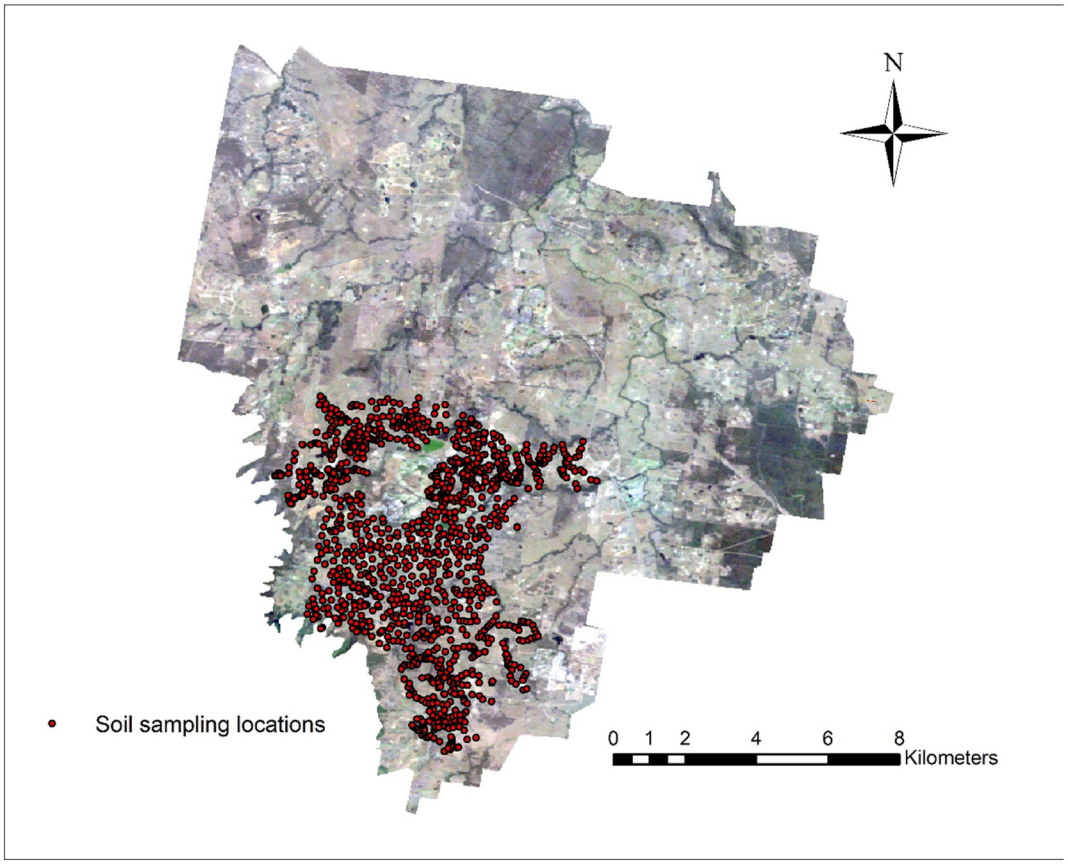

Fig. 1. Landsat 5 Image of the Hunter Wine Country Private Irrigation District (HWCPID), NSW, Australia. Note: the red dots indicated the locations of the soil samples collected during 2001 and 2011. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

differences among phenoforms. In addition, there is a need to apply these concepts to soil mapping units across large areas, particularly when maps of soil series are not available. Based on the concepts of genoforms and phenoforms, we proposed genosoils and phenosoils to monitor soil changes within different soil mapping units as affected by human activities. The aims of this study were to 1) develop a method to identify genosoils using a digital soil mapping approach, 2) using remote sensing data to delineate phenosoils and monitor human-induced soil changes from an initial genosoil to different phenosoils and from a previous genosoil to a new genosoil, 3) propose a quantitative method to define the various genosoils and phenosoils based on soil properties, and 4) ultimately provide guidance for soil monitoring and land conservation for soil security.

2. Materials and methods

2.1. Study area

The study area is located in the Hunter Wine Country Private Irrigation District (HWCPID), NSW, Australia (32.83°S, 151.35°E). It covers an area of approximately 220 km^2 (Fig. 1). The climate of the HWCPID is temperate, with warm humid summers, and relatively cool and humid winters. The average annual rainfall is ~750 mm and is mostly uniformly distributed throughout the year (Bureau of Meteorology, 2017). Topographically, this area consists mostly of undulating hills that ascend to low mountains to the south-west. The underlying geology of the HWCPID includes predominantly Early Permian siltstones, marl, and some minor sandstone (Hawley et al., 1995). Other extensive parent material includes Late Permian siltstones, and Middle Permian conglomerates, sandstones, and siltstones. The soils are variable and predominantly weathered kaolinitic–smectitic, ranging from light to medium texture grade. In terms of land use, an expansive viticultural industry is situated in the area and is possibly the most widespread in rural industries, followed by dryland agricultural grazing systems and forest. It is this diversity in landforms, parent material, and land use that make this a suitable area to address the research aims.

2.2. Soil data

Soil data used in this study are based on a collection of 1354 soil profiles that have been collected and described in the years including and between 2001 and 2011 (Fig. 1). Primarily located in the southern area of the HWCPID, each soil profile was described to the sub-order level of the Australian Soil Classification (ASC) (Isbell, 2002). Unlike the USDA Soil Taxonomy (Smith and Ahmad, 1986), the ASC does not rely extensively on quantitative diagnostic characteristics and horizons to classify the soils. Instead, the ASC system uses a key to allocate a soil profile to a certain order in turn. By evaluating the criteria of different orders sequentially, a soil profile will be classified into a soil order. In addition, ASC also uses soil colors (e.g. Red, Brown, Yellow, Grey, Black) to differentiate the suborders of certain soil orders (e.g. Kurosols, Sodosols, Chromosols, Ferrosols, Dermosols, Kandosols).

A number of soil properties were recorded for each soil profile horizon including soil texture, color and pH and electrical conductivity (1:5 soil: water) for the 0–10 cm and 40–50 cm depth intervals. Soil organic carbon concentration was also estimated for these depth intervals using an a priori calibrated vis-NIR soil spectral model developed from soil spectra of the data set described in Geeves et al. (1995). In general, the description of data used in the study has been given previously in Malone et al. (2014) and Odgers et al. (2011). The use of these data in this study was for the dual purpose of first mapping soil types (soil class data) and for verification of genosoils and phenosoils

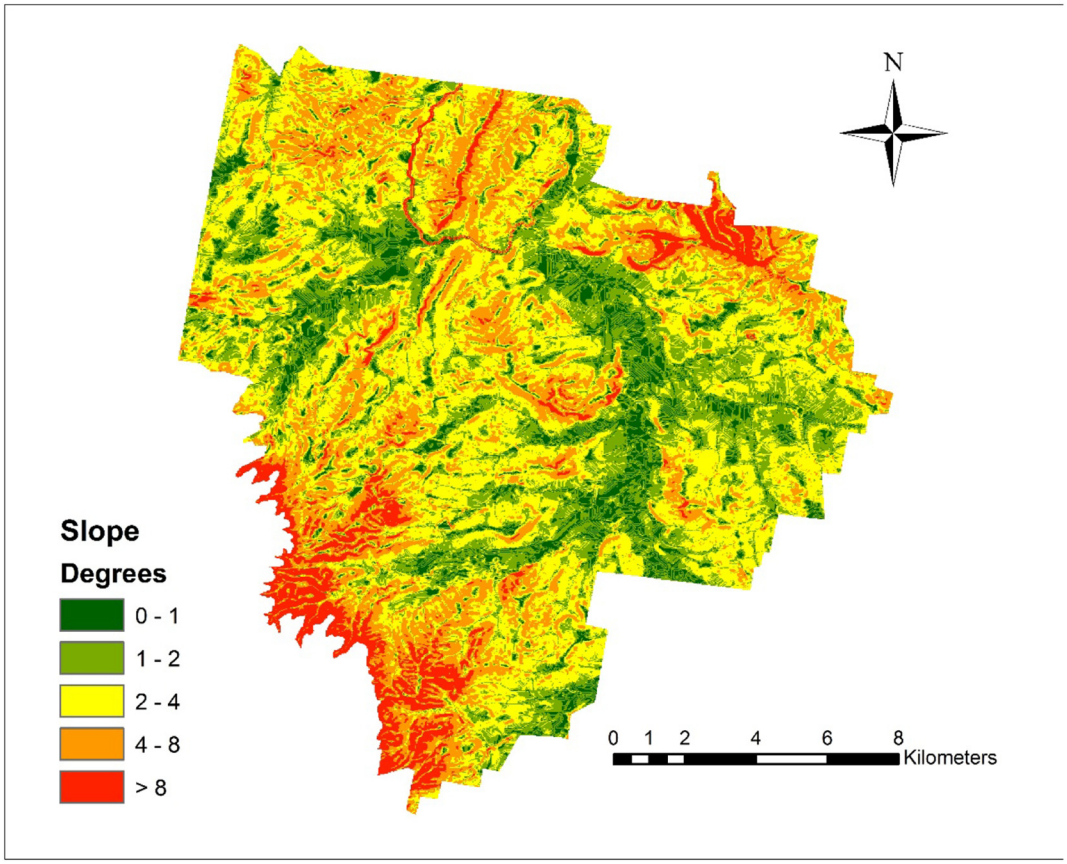

Fig. 2. Spatial distribution of slope values (degrees) across the study area.

using soil profile data, specifically the 0–10 cm and 40–50 cm information.

2.3. Ancillary data

2.3.1. Digital elevation model (DEM) and its derivatives

In terms of the terrain parameters, a 25-m resolution DEM was used. From the DEM the following 6 variables were extracted:

1) Slope: measured in degrees, the first derivative of elevation in the direction of greatest slope (shown in Fig. 2).
2) Topographic wetness index (TWI): a secondary landform parameter which estimates for each pixel, its tendency to accumulate water (Quinn et al., 1995).
3) Multi-resolution valley bottom flatness index (MRVBF): derived using slope and elevation to classify valley bottoms as flat, low areas (Gallant and Dowling, 2003). MRVBF has been used extensively for the delineation and grading of valley floor units corresponding to areas of alluvial and colluvial deposits.
4) Diffuse incoming solar radiation (ISR): Measure of potential incoming solar radiation, and used as a parameter for evaluating the positional aspect effect. This parameter was evaluated over the duration of a single calendar year with a 5-day time step.
5) Mid-slope position (MSP): A relative slope position parameter which gives a classification of the slope position in both valley and crest positions.
6) Terrain Ruggedness Index (TRI): an index to quantify topographic heterogeneity.

Algorithms for deriving these variables were implemented using the SAGA GIS software (http://www.saga-gis.org/en/index.html).

2.3.2. Gamma-ray spectrometry data

Natural radioactive emissions of gamma-ray (γ-ray) from the decay of potassium (K – %), uranium (U – ppm), thorium (Th – ppm) and across the whole spectrum (total counts [TC] – cps) have been widely used in soil and regolith mapping. In this study, both airborne and ground γ-ray spectrometry data were used.

Airborne γ-ray spectrometry data were obtained from the Geoscience Australia Data Delivery System. In the Hunter Valley area, the airborne collected data consisted of flight lines with a spacing of about 1500 m and height of 200 m with measurements every 60 m. Compared to other parts of Australia, this data collection density is relatively poor, where flight lines can have a spacing of 250 m and height of 60 m. The reason for the relatively coarser data collection strategy is due to the topographic heterogeneity of the region. For the airborne survey, the γ-ray detector consisted of sodium iodide (NaI) treated with thallium (4 L). Three detector packages were used; each contained four crystal detectors, giving a total volume of 48 L. An Ashtech XII GPS Receiver was used for geo-referencing the γ-ray data.

Because of the poor resolution of the airborne γ-ray spectrometry data, a collection of a few farm-scale ground-based γ-ray surveys were used within an extrapolation model to improve the overall information content across the Hunter Valley. The farm-scale surveys have previously contributed to other soil research studies in the Hunter Valley and are described in Stockmann et al. (2015, 2017) and Malone et al. (2018). To extrapolate the ground-based γ-ray spectrometry data across the whole study area, the Random Forest (Liaw and Wiener, 2002) machine learning algorithm was used. In brief, DEM data (i.e. elevation) and its derivatives as shown in Section 2.3.1 were used in combination with the air-borne γ-ray data (i.e. K, U, Th, TC) to predict random forest models of ground-based γ-ray data (i.e. K, Th, TC) onto the same 25-m grid. γ-ray U data was not predicted and used in the following analysis because its spatial distribution pattern was essential

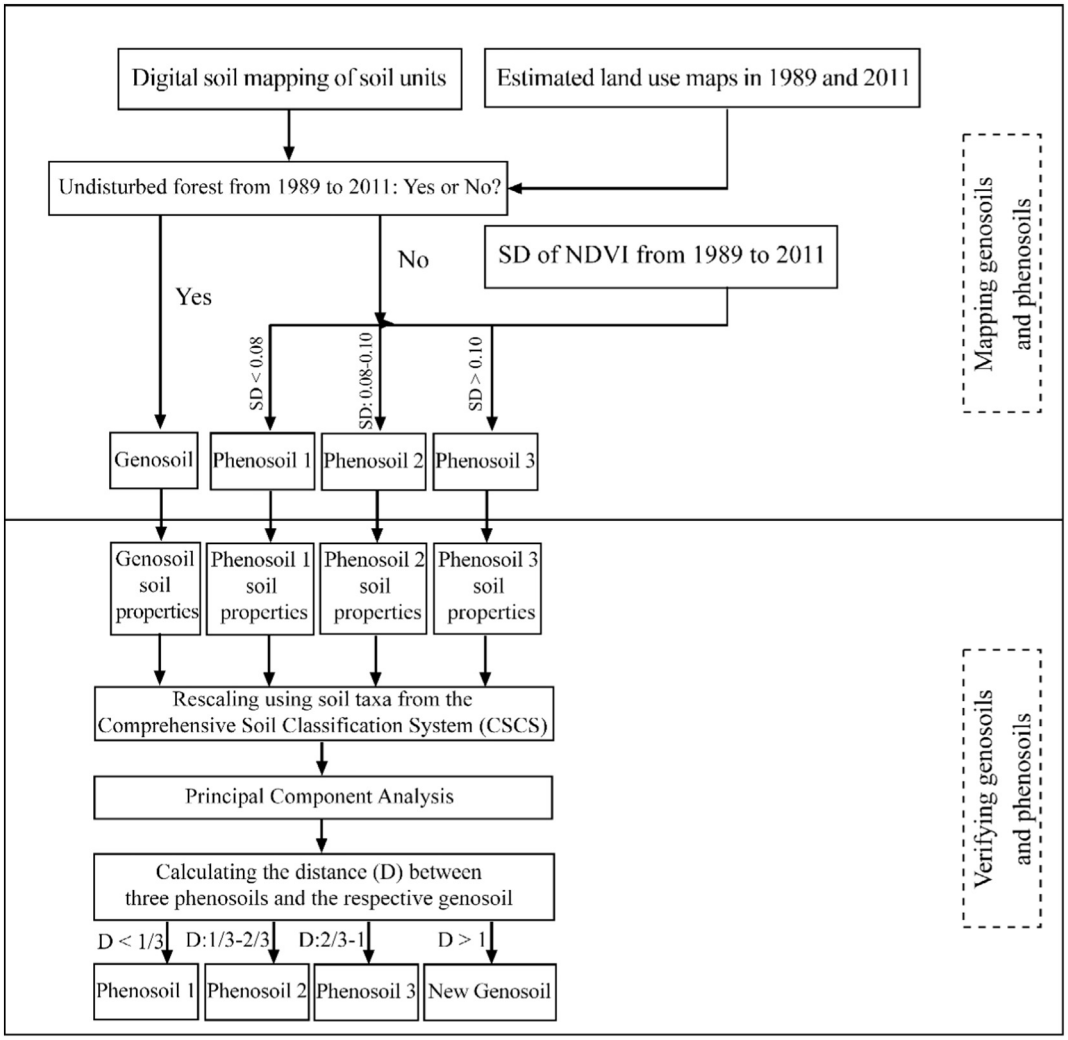

Fig. 3. Flowchart of the method to map and verify genosoils and phenosoils. Note: CSCS refers to the Comprehensive Soil Classification System (after Hughes et al., 2017).

Table 1
Summary of pre-European soil classes and present soil classes according to Australian Soil Classification across the study area.

No. of observed soil profiles	Present soil classes	Equivalent present day World Reference Base for Soil Resources Soil Groups	Pre-European soil classes
36	Calcarosols	Calcisols	Calcarosols
122	Red Chromosols	Luvisols	Red Chromosols
190	Brown Chromosols	Luvisols	Brown Chromosols
45	Other Chromosols	Luvisols	Other Chromosols
368	Red Dermosols	Luvisols/Acrisols	Red Kurosols/Red Chromosols
427	Brown Dermosols	Luvisols/Acrisols	Brown Kurosols/Brown Chromosols
122	Other Dermosols	Luvisols/Acrisols	Other Kurosols/Other Chromosols
45	Hydrosols	Fluvisols	Hydrosols
51	Red Kurosols	Acrisols	Red Kurosols
58	Brown Kurosols	Acrisols	Brown Kurosols
13	Other Kurosols	Acrisols	Other Kurosols
50	Rudosols	Regosols	Rudosols/Tenosols

random noise in the study area.

2.3.3. Landsat 5 datasets

USGS Landsat 5 data were obtained using the Google Earth Engine platform (Gorelick et al., 2017). The Landsat scenes with the highest available data quality (Tier 1) were used, which consists of Level-1 Precision Terrain (L1TP) processed data that have well-characterized radiometry and are inter-calibrated across the different Landsat sensors. All the preprocessed Tier 1 Landsat data on the Google Earth Engine platform can be considered consistent and inter-calibrated (regardless of the sensor) across the full collection.

For creating simple cloud-free Landsat composites, the "ee.Algorithms.Landsat.simpleComposite" function available in the Google Earth Engine was used. Herein, a subset of scenes at each location over every 3 consecutive months (i.e. January 1 – March 31; April 1 to June 30; July 1 to September 30; October 1 to December 31) was selected, converted from raw digital numbers to the top of atmosphere reflectance. The simple cloud score (https://developers.google.

Table 2
Mean values of various soil properties of different Pre-European soil classes measured at topsoil (0–10 cm) and subsoil (40–50 cm).

Pre-European soil class	No. Samples	Soil Organic Carbon (Topsoil, %)	Soil Organic Carbon (Subsoil, %)	Clay Content (Topsoil, %)	Clay Content (Subsoil, %)	Silt Content (Topsoil, %)	Silt Content (Subsoil, %)	Sand Content (Topsoil, %)	Sand Content (Subsoil, %)	pH (Topsoil)	pH (Subsoil)
Red Chromosols	242	3.4	1.1	27.2	42.9	28.2	23.7	44.6	33.4	6.2	6.3
Brown Chromosols	642	3.1	0.9	24.1	40.4	29.3	22.9	46.6	36.7	6.1	6.1
Other Chromosols	3	3.1	2.4	31.3	34.8	7.4	14.3	61.3	50.9	6.6	7.5
Hydrosols	7	3.6	1.3	25.5	29.9	34.3	23.3	40.2	46.8	6.4	7.0
Red Kurosols	246	3.2	0.7	23.7	50.0	35.2	24.0	41.1	26.1	6.1	5.5
Brown Kurosols	76	2.9	0.7	29.7	54.8	35.0	22.9	35.3	22.3	6.3	5.2
Other Kurosols	9	1.8	0.5	27.0	66.3	41.4	18.0	31.6	15.7	6.0	5.1
Rudosols	8	3.2	1.3	28.2	39.7	18.9	15.6	52.9	44.7	6.3	6.8
Tenosols	9	2.1	1.3	17.5	20.0	25.1	22.4	57.4	57.7	6.3	6.8
Calcarosols	112	4.3	2.0	29.9	47.4	23.7	21.9	46.4	30.7	6.8	7.5

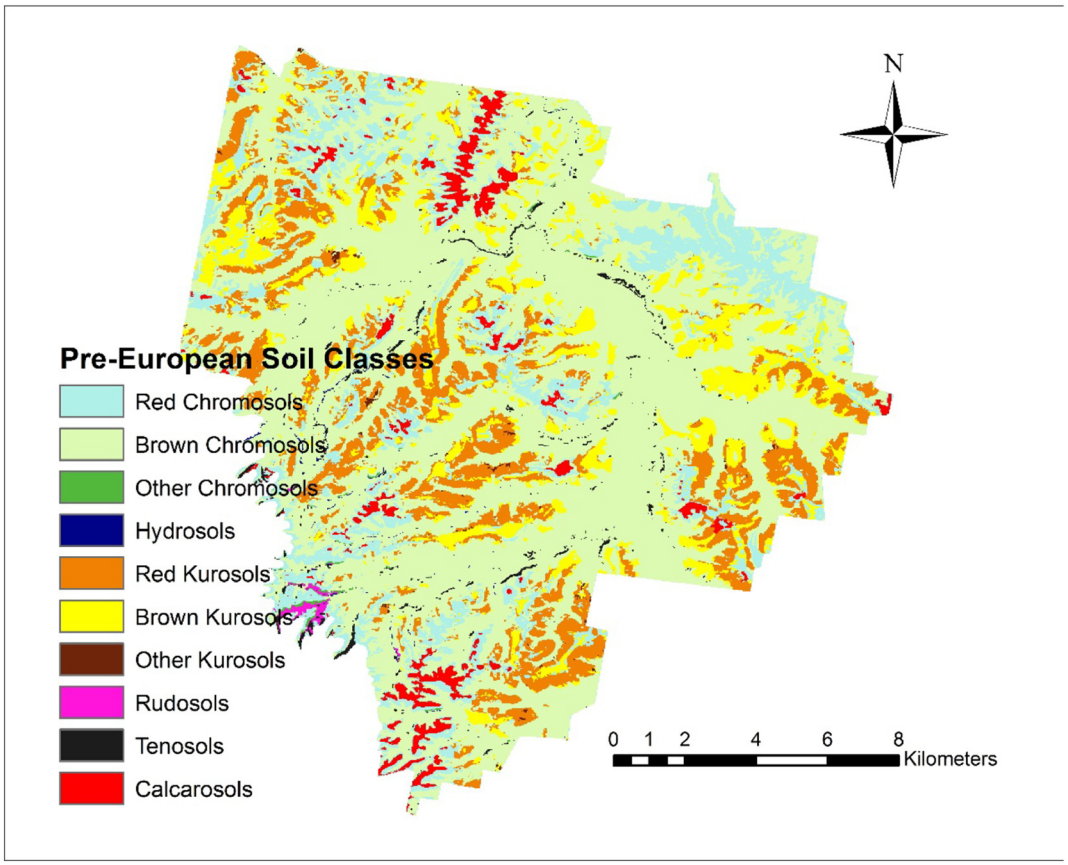

Fig. 4. Spatial distribution of the back-predicted Pre-European soil classes (initial genoforms) across the study area.

com/earth-engine/landsat#simple-cloud-score) was then calculated and the median of the least cloudy pixels was retained in the composites.

The Normalized Difference Vegetation Index (NDVI) was computed for each of the composites from 1989 to 2011. The standard deviation of the NDVI among all the composites was calculated on a pixel basis and used for detecting soil disturbance due to human activities (e.g. seasonal cultivation and grazing or long-term land use changes) in the following analysis.

2.4. Mapping pre-European soil classes and genosoils

Rossiter and Bouma (2018) defined the genoforms and phenoforms at the detailed mapping scale (i.e. soil series of the ST system). Given that soil series maps are not always available, we proposed the concept of genosoil based on the soil mapping units that were least disturbed by human activities. Given the spatial extent of the study area (220 km^2) and the resolution of the ancillary data (25 m), we attempted to create genosoils within the identified soil classes at the order/suborder levels of the Australian Soil Classification (ASC) (Isbell, 2002). The flowchart of the method to map genosoils and phenosoils is shown in Fig. 3.

In this study, we assumed that several soil classes existed prior to agricultural development and considered them as Pre-European settlement soil classes. European settlement of the Hunter Valley began in the 1820s (Hoyle et al., 2008). There are still tracts of land which have native vegetation and which have not been cultivated. The spatial distribution of Pre-European soil classes was back-predicted across the study area. This relied largely on a significant understanding of soils in the study area with soil profile data acquired from 2001 to the present time. Based on these soil profile data, more than half of the soils are

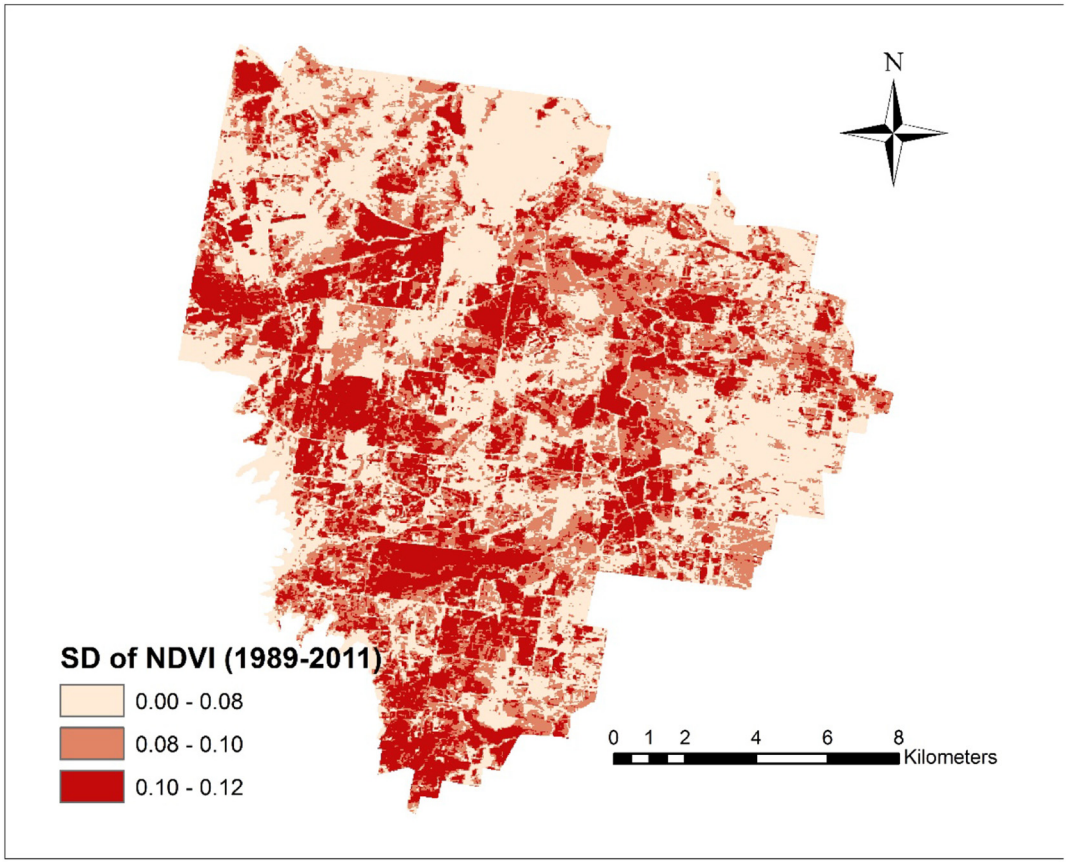

Fig. 5. Spatial distribution of the standard deviation (SD) of the Normalized difference vegetation index (NDVI) calculated using Landsat 5 imagery collected during 1989–2011 across the study area.

classified as Dermosols using the ASC system (Odgers et al., 2011). The remaining are the unchanged soils including Kurosols, Chromosols, and other soil orders.

According to the ASC, Dermosols are soils that lack a clear or abrupt textural B horizon and are moderate to strong structure throughout (Isbell, 2002). In Australia, the most common occurrences are of igneous and metamorphic materials and are most widespread in the high rainfall coastal locations of eastern Australia (Isbell, 2002). Dermosols may also occur unintendedly when soils are mixed due to agriculture which has not been taken into account in the ASC.

While the climate of the HWCPID may not preclude the development of Dermosols here, we know that mechanical disturbance has created these soils insomuch that in undisturbed areas texture contrast soils dominate (light textured topsoil of varying thickness over clay dominated subsoil). This is likely due to the parent materials which are predominantly sedimentary. In these undisturbed areas the soils would normally either classify out to some sub-order of Kurosols or Chromosols depending on whether the soil was acidic (subsoil pH < 5.5) or not. In other undisturbed locations soils other than Chromosols and Kurosols also exist. For example, in areas where marl is highly concentrated, Calcarosols exist, and soils near waterways are generally Hydrosols, and some Rudosols and Tenosols are often found either in steep-sloped areas or on ridge tops.

With this acquired field knowledge, we reinterpreted the currently observed soil classes from our available dataset into the Pre-European soil classes. In brief, we used all the soil forming factors except human activities and hold them constant. Focusing primarily on the observed Dermosol soils, and the associated soil information at these sites such as the measured soil pH, we allocated these soils to either Chromosols or Kurosols. Allocating to the sub-order level was trivial because this was based on the dominant subsoil color. Therefore, using the example of an acidic Red Dermosol, our Pre-European allocation method would classify this soil out to be a Red Kurosol. To ensure stable modelling in the next step requiring digital soil mapping, some soil sub-order classes required aggregation with others. For example, red and brown soils (or Dermosol, Chromosols, and Kurosols) are much more dominant than their yellow, grey and black counterparts. Being familiar with the hydrological regime of soils in the study area, the aggregation of these lesser observed soil classes is a pragmatic step because soils that are yellow, grey or black tend to be those that don't drain so well or are periodically wet soils due to the low lying position in the landscape.

Table 1 shows the present soil classes and the back-predicted Pre-European soil classes. The equivalent Soil Groups of the World Reference Base for Soil Resources are also presented for reference. Note that the aggregated soil classes were defined as other types of the soil order than those already explicit defined to the sub-order level. Note also that all Hydrosols were aggregated into a single grouping, and similarly for Calcarosols. Rudosols and Tenosols were also grouped together as they have the minimal pedological organisation and composed largely of coarse grain materials. They are also found in similar landscape positions. Their aggregation was necessary due to their low prevalence throughout the study area.

With the newly allocated soil classes, we mapped their distribution across the study area using a multinomial logistic regression model. Environmental covariates used in the model included those previously described in Section 2.3 except for Landsat 5 datasets. Landsat 5 datasets were excluded because they were correlated with human activities and should be considered as constant over time to predict the Pre-European soil classes. From an independent validation (assuming the marginal distributions of the validation data is the same to the calibration data), using a withheld data set (30% of the full available data set) our model had an overall accuracy of 38% with Kappa coefficient of

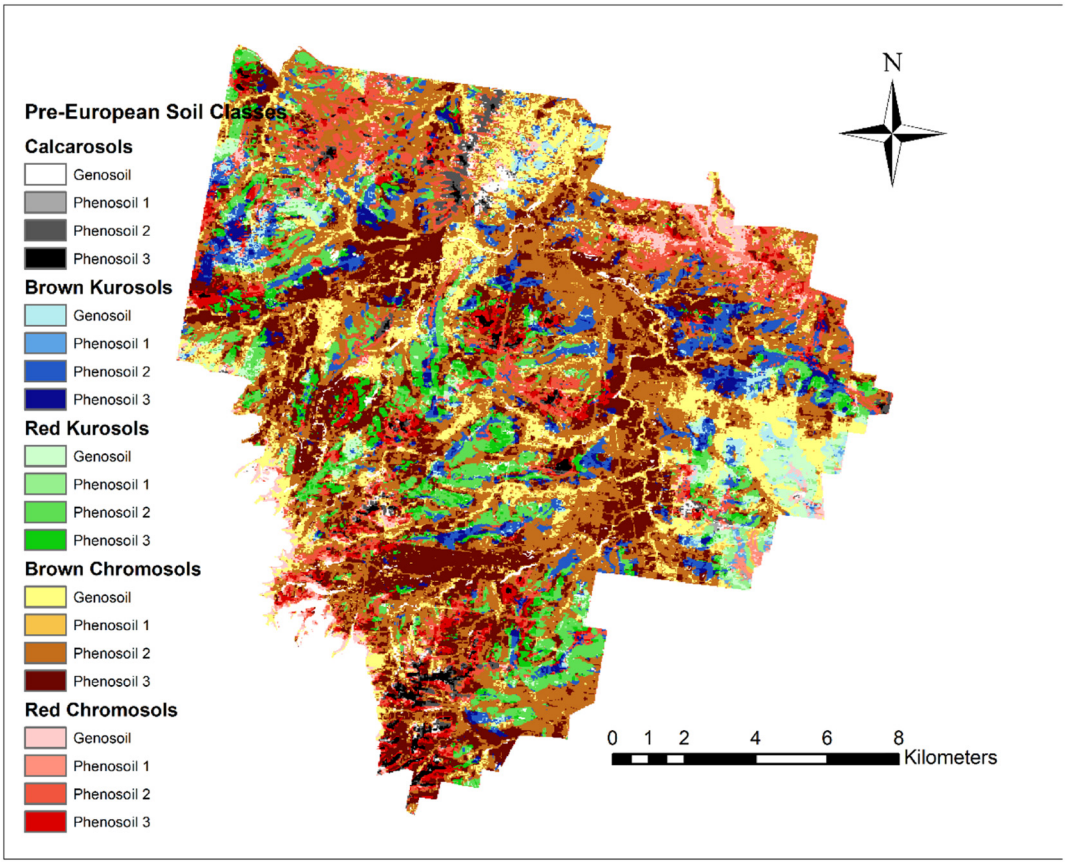

Fig. 6. Spatial distribution of the genosoils and phenosoils of several major Pre-European soil classes across the study area.

0.17. Assuming minimal agricultural activities occurred at the Pre-European time, the mapped different Pre-European soil classes were considered as different genosoils.

2.5. Mapping present genosoils and phenosoils

Rossiter and Bouma's (2018) soil phenoforms are persistent variants of a genoform with sufficient physical or chemical differences to substantially affect soil functions. In this study, we proposed phenosoils as the significant changes of soil physical and chemical properties within the soil mapping units. To delineate genosoils within each Pre-European soil class at the present time and the associated phenosoils, the spatial distribution of soil disturbance is required. It was assumed that human activities (e.g. seasonal cultivation and grazing and long-term land use changes) will change certain soil properties (to be presented in Table 2).

A georeferenced land use map generated in 2000 (the only map available during 1989–2011) across the study area was obtained from the NSW government (http://data.environment.nsw.gov.au/dataset/nsw-landuseac11c). A Random Forest model (Liaw and Wiener, 2002) was established to classify the land use types across the study area using the 7 bands and NDVI of Landsat 5 composite collected over the first three months of 2000 in Section 2.3.3. The performance of the model was acceptable given that the overall accuracy of 65% and the Kappa coefficient of 0.56 from an independent validation using a withheld data set (25% of the full available data set). The model was used to predict the land use types in 1989 and 2011.

It was reasonable to argue that the soils may experience different levels of disturbance, due to anthropogenic activities. Given that there was remnant vegetation distributed across the study area, for each Pre-European soil class, if the soil within it was predicted to be forest soil in both 1989 and 2011, it remained as the same genosoil at the present time. This was because the soil in these areas is most likely to be least disturbed with negligible differences in physical (e.g. clay content) or chemical (pH) properties.

Otherwise, the soil was assigned to different phenosoils depending how big the changes of soils properties were. In this study, the standard deviation (SD) of the NDVI calculated in Section 2.3.3 was used an indication of land use change. We did not separate the seasonal variations in NDVI across the agricultural land (due to the growing cycles of the crops and pastures) from the long-term variations in NDVI across the study area (due to the land use change between forest and agricultural land). This was because we hypothesised that the change of NDVI indicated soil disturbance and led to change of soil physical and chemical properties in the long term.

Therefore, various phenosoils were defined based on SD values of the NDVI, including phenosoil 1 (SD: < 0.08), phenosoil 2 (SD: 0.08–0.10), and phenosoil 3 (SD: > 0.10) (Fig. 3). Note that these threshold SD values were empirically determined and 0.08 and 0.10 were the median and 75% quantile of the SD values from 1989 to 2011 and across the study area. Based on the extent of soil change, phenosoils 1, 2, and 3 would approximately represent the sparse forest, pasture, and vineyard, respectively.

2.6. Assessing present genosoils and phenosoils using topsoil and subsoil properties

The identified genosoils and phenosoils were assessed using soil profile data described previously. Four soil properties measured at two depth intervals (topsoil: 0–10 cm; subsoil: 40–50 cm) were used in this study and include 1) pH, 2) clay percentage, 3) soil organic carbon and 4) exchangeable cations (Bishop et al., 1999; Malone et al., 2014). These soil variables were selected for two main reasons: 1) to achieve a reasonable cross-section of attributes describing the physical, chemical

Table 3
Mean values of various soil properties of different soil genosoils and phenosoils measured at topsoil (0–10 cm) and subsoil (40–50 cm). Note: – indicates number of samples is < 4; soil organic carbon, SOC.

Pre-European soil class/ genosoils	Present genosoils and phenosoils	Land use	No. Samples	SOC (Topsoil, %)	SOC (Subsoil, %)	Clay (Topsoil, %)	Clay (Subsoil, %)	Silt (Topsoil, %)	Silt (Subsoil, %)	Sand (Topsoil, %)	Sand (Subsoil, %)	pH (Topsoil)	pH (Subsoil)
Red Chromosols	Genosoil 1	Dense forest	22	3.5	0.9	24.0	40.4	23.8	23.0	52.2	36.7	6.0	5.6
Red Chromosols	Phenosoil 1	Sparse forest	–	–	–	–	–	–	–	–	–	–	–
Red Chromosols	Phenosoil 2	Pasture	112	3.3	1.1	27.1	39.8	27.8	23.6	45.0	36.6	6.1	6.2
Red Chromosols	Phenosoil 3	Vineyard	104	3.4	1.1	28.2	47.7	30.1	24.4	41.7	27.9	6.4	6.6
Brown Chromosols	Genosoil 1	Dense forest	68	3.3	0.9	18.4	32.9	30.4	25.6	51.3	41.5	5.8	5.9
Brown Chromosols	Phenosoil 1	Sparse forest	23	2.8	1.1	26.7	47.4	25.2	17.8	48.1	34.8	6.5	6.2
Brown Chromosols	Phenosoil 2	Pasture	294	3.0	0.8	25.8	41.4	29.3	23.9	44.9	34.8	6.1	6.0
Brown Chromosols	Phenosoil 3	Vineyard	257	3.1	0.9	23.3	40.5	29.3	21.8	47.4	37.7	6.1	6.3
Red Kurosols	Genosoil 1	Dense forest	28	4.1	0.2	14.9	38.6	25.0	26.6	60.1	34.8	5.5	5.2
Red Kurosols	Phenosoil 1	Sparse forest	–	–	–	–	–	–	–	–	–	–	–
Red Kurosols	Phenosoil 2	Pasture	148	3.4	0.7	24.9	52.6	37.8	23.0	37.3	24.4	6.1	5.4
Red Kurosols	Phenosoil 3	Vineyard	67	2.4	0.7	23.8	50.0	31.7	24.9	44.5	25.1	6.3	5.8
Brown Kurosols	Genosoil 1	Dense forest	4	3.3	0.7	24.6	28.4	48.5	37.8	26.9	33.8	6.1	5.9
Brown Kurosols	Phenosoil 1	Sparse forest	–	–	–	–	–	–	–	–	–	–	–
Brown Kurosols	Phenosoil 2	Pasture	44	3.2	0.8	27.6	58.6	34.4	21.4	38.0	20.0	6.2	5.1
Brown Kurosols	Phenosoil 3	Vineyard	28	2.4	0.5	32.8	55.9	34.1	21.1	33.1	23.1	6.5	5.3
Calcarosols	Genosoil 1	Dense forest	3	5.4	0.7	23.1	36.5	21.2	18.7	55.7	44.7	6.0	5.8
Calcarosols	Phenosoil 1	Sparse forest	7	5.4	2.5	27.7	38.0	37.7	31.2	34.6	30.9	6.3	7.0
Calcarosols	Phenosoil 2	Pasture	37	4.9	2.0	25.2	46.3	24.0	25.9	50.8	27.8	6.8	7.5
Calcarosols	Phenosoil 3	Vineyard	65	3.9	2.1	33.5	50.7	22.0	19.1	44.5	30.2	6.9	7.7

and mineralogical properties of the soil, and 2) to exploit whatever reliable data was stored within the available soil information database. Each of the soil profiles was assigned with a present genosoil or phenosoil and the mean values of the soil properties within each category were calculated and compared.

2.7. Verifying the present genosoils and phenosoils

The mapped genosoils and phenosoils should be verified using the soil properties. To propose a universal method that can be applied in different regions of the world and accounts for the inherent variations between the soils in different countries, we used a comprehensive soil classification system (CSCS) established by Hughes et al. (2017) as a reference to harmonise the soil properties and calculate the distances. In brief, the CSCS was established by sequentially adding soil taxa from existing global (i.e. US Soil Taxonomy and World Reference Base for Soil Resources) and regional (i.e. Australian Soil Classification and New Zealand Soil Classification) soil classification systems. To determine which soil taxa should be added to the CSCS, the distances between the soil taxa from different classification systems were calculated using a harmonised dataset of 23 soil properties measured at 18 depths from the soil surface to 1.5 m. The resultant CSCS currently has 493 soil taxa.

The flowchart of the method to verify genosoils and phenosoils is also shown in Fig. 3. Because the soil samples identified within the genosoils and phenosoils were collected at two depth intervals (i.e. 0–10 cm and 40–50 cm), we selected several soil properties (i.e. clay, silt, sand, SOC and pH) of the 493 soil taxa measured at the same soil depth intervals (a 493 × 10 matrix). The mean values of the soil properties were then scaled using the following formula:

$$\mathbf{A}_{i,j} = \frac{\mathbf{A}_{i,j} - \mathrm{mean}(\mathbf{A}_{i,j})}{\mathrm{SD}(\mathbf{A}_{i,j})} \quad (1)$$

where $\mathbf{A}_{i,\,j}$ was the jth soil property for the ith taxon, mean($\mathbf{A}_{i,\,j}$) and SD ($\mathbf{A}_{i,\,j}$) were the average and standard deviation of the jth soil property for all the 493 taxa, respectively, and $\mathbf{A}_{i,\,j}$ was the rescaled jth soil property for the ith taxon. Note that whenever additional soil properties and additional depths become available, they should be included for the analysis to better discriminate the differences between genosoils and phenosoils.

Principal component analysis (PCA) was then applied to the scaled soil database (the 493 × 10 matrix) to calculate a principal component space. Afterward, the centroids (mean values) of the genosoils and phenosoils 1–3 of several Pre-European classes (e.g. Red Chromosols, Brown Chromosols, Red Kurosols, Brown Kurosols, Calcarosols) were scaled using Eq. 1 and projected onto the predefined principal component space. The remaining Pre-European classes were not used in this analysis because the soil profile data collected within these classes were not sufficient. The Euclidean distances between the genosoils and the respective phenosoils of each Pre-European class were then calculated using all the principal components. PCA was used to avoid the collinearity between different soil variables and between same soil variables at different depths. All the calculations were conducted in R Software (R Core Team, 2017). The “prcomp” function of the “stats” Package was used to calculate the principal component space of the initial soil database and the “predict” function was used to project the different phenosoils of the various Pre-European classes onto the principal component space.

In biology, the 3% difference between the 16S rRNA genes has been used extensively to identify the operational taxonomic units of biological species (Schloss and Handelsman, 2005). If two species have differences in the 16S rRNA genes larger than 3% of the maximum distance of all the species, these two species are considered as different species. In this study, we proposed that if the difference between a soil phenosoil and its initial status (i.e. the respective genosoil) was larger than 8% of the maximum distance between the 493 soil taxa within the

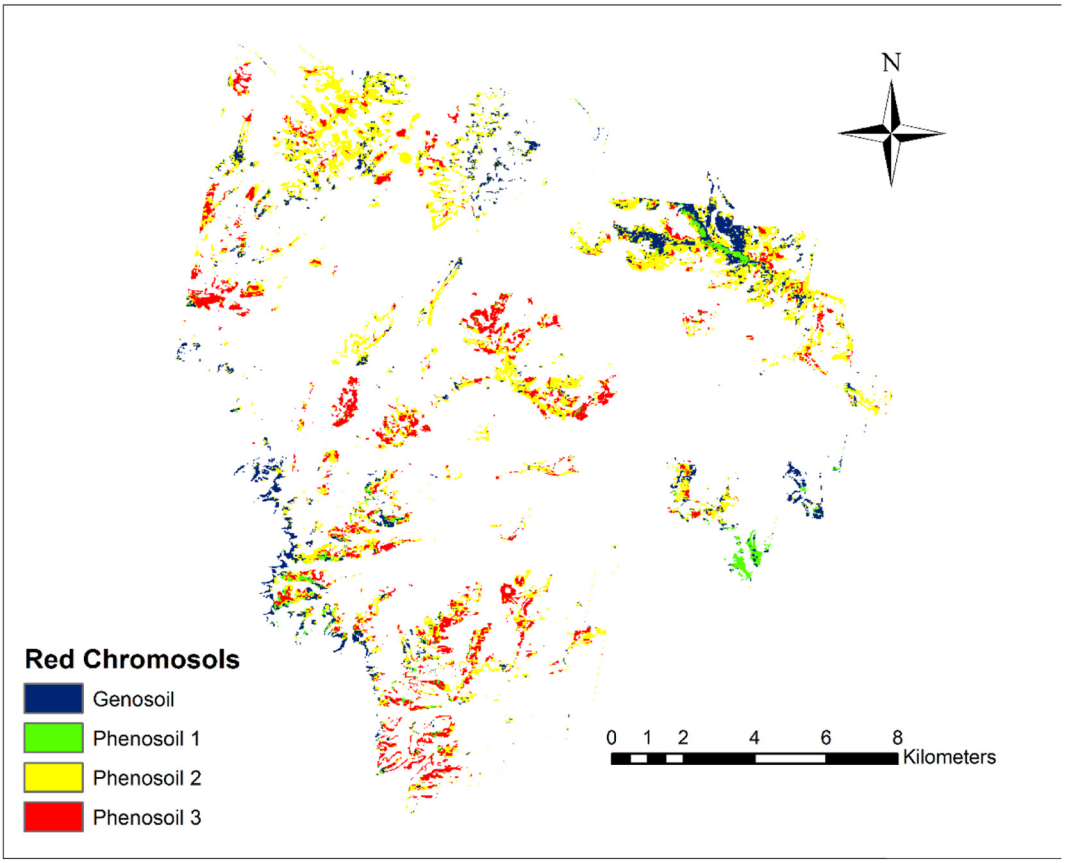

Fig. 7. Spatial distribution of the genosoil and phenosoils of Red Chromosols across the study area.

CSCS (i.e. ~1.0), we considered that the soil properties of the phenosoil changed significantly and should be redefined as a new genosoil. Similarly, the identified phenosoils should be verified and redefined using the distance to the corresponding genosoil and as follows: < 1/3, phenosoil 1; between 1/3 and 2/3, phenosoil 2; between 2/3 and 1.0, phenosoil 3. In this study, a larger distance threshold of 8% was used because we only used a selected set of soil properties (i.e. clay, silt, sand, SOC, and pH) at two depths, which were not sufficient to account for all variation between the genosoils and phenosoils. It should be noted that this threshold distance was empirically selected and needs to be adjusted when more soil variables become available. It should also be noted that different phenosoils were empirically classified using this threshold value so that the evolution process from one genosoil to other phenosoils can be delineated. To quantify the changes between the genosoils and phenosoils, one should still use the measured soil properties.

It should be also noted that Rossiter and Bouma (2018) argued that phenoforms are persistent, non-cyclical variants of a soil genoform with sufficient physical or chemical differences to substantially affect soil functions. By comparison, our concept of phenosoil is entirely based on the differences between soil properties. This is because soil properties are more basic and fundamental and different soil properties need to be measured to evaluate different soil functions (Lal, 2010).

3. Results and discussion

3.1. Spatial distribution of pre-European soil classes and genosoils

Fig. 4 shows the spatial distribution of 10 Pre-European soil classes representing 10 Pre-European genosoils across the study area. The mean values of topsoil and subsoil properties were presented in Table 2. Note that all the soil classes except other Chromosols and Calcarosols had a relatively low soil organic carbon (SOC) content in the topsoil (< 3.5%) and subsoil (< 1.5%) and were slightly acidic (pH: 5.5–6.5). By comparison, Calcarosols had a slightly larger SOC content in both topsoil (4.3%) and subsoil (2%) and was close to neutral in the topsoil (pH = 6.8) and slightly alkaline in the subsoil (7.5).

3.2. Spatial distribution of SD of the NDVI

Fig. 5 shows the SD of the NDVI from 1989 to 2011 across the study area. Compared with the distribution of the Pre-European soil classes (Fig. 4), Kurosols and Calcarosols were under significant disturbance (SD > 0.10) while the other soils were less disturbed (SD < 0.10). From the perspective of soil change, significant soil disturbance was attributed to the conversion of native forest to urban lands and vineyards (Fig. 1). By comparison, less disturbed soils were associated with remnant forests (Fig. 1), where soil conditions were relatively constant. The intermediate SD values (0.08–0.10) were mainly covered by agricultural lands (e.g. pasture) associated with intermediate soil changes whereby seasonal fluctuations of NDVI occurred due to the growth cycles of the crops and pasture.

3.3. Spatial distribution of present genosoils and phenosoils

The spatial distribution of present genosoil and other phenosoils (1–3) of some major Pre-European soil classes are presented in Fig. 6. The mean values of topsoil and subsoil properties for each present genosoils and phenosoils are shown in Table 3. We discuss the major soil classes below.

3.3.1. Red Chromosols and Brown Chromosols

Red Chromosols were divided into one genosoil and three phenosoils at the present time (refer to Fig. 7). As shown in Table 3, SOC

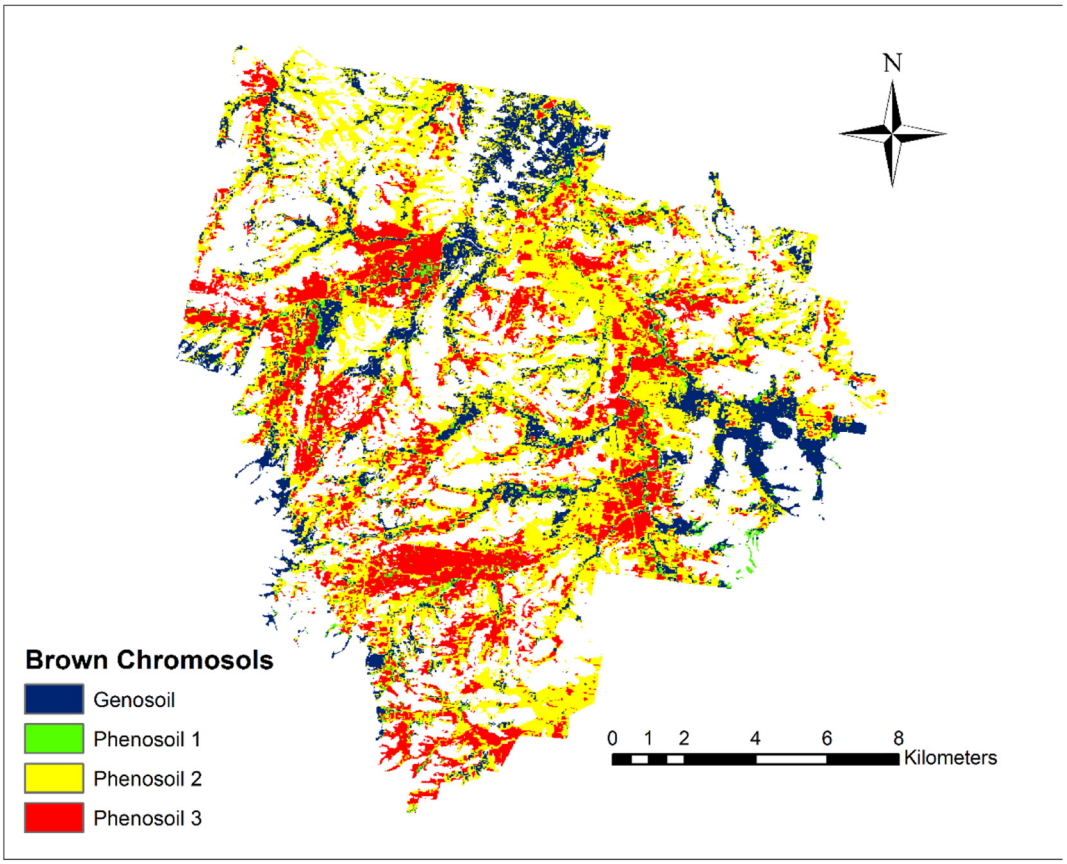

Fig. 8. Spatial distribution of the genosoil and phenosoils of Brown Chromosols across the study area.

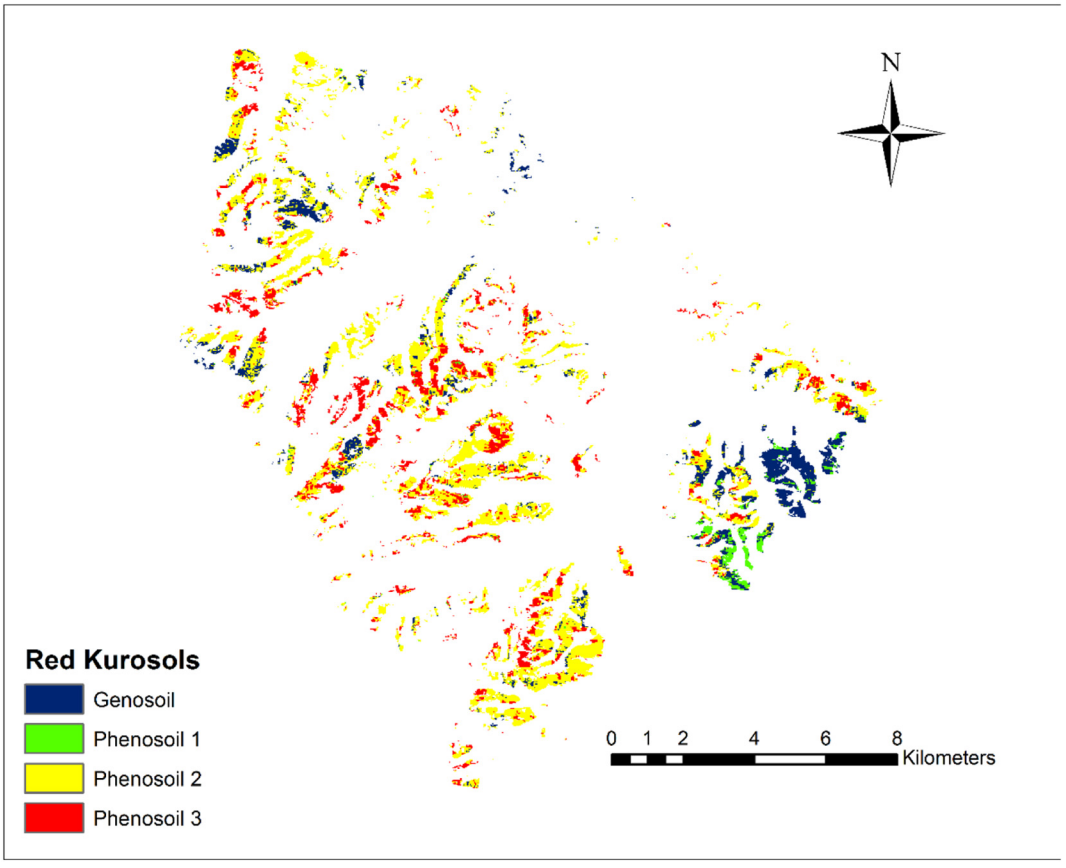

Fig. 9. Spatial distribution of the genosoil and phenosoils of Red Kurosols across the study area.

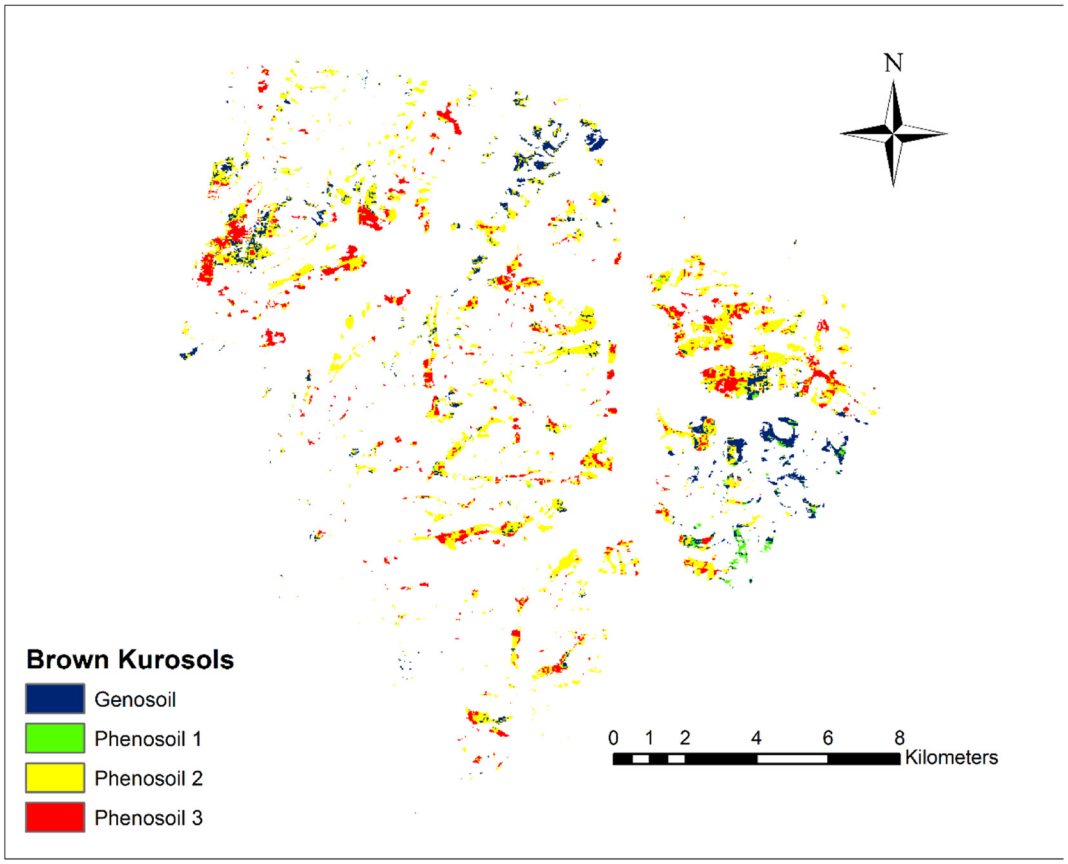

Fig. 10. Spatial distribution of the genosoil and phenosoils of Brown Kurosols across the study area.

content was very similar between the present genosoil and phenosoils (3–4%). This was also the case for clay content and the difference of clay content between topsoil and subsoil (i.e. texture contrast).

However, this was not the case for soil pH. If we exclude phenosoil 1 (due to insufficient soil samples), it can be found that pH values of Red Chromosols have increased from the genosoil to phenosoils 2 and 3 in both topsoil and subsoil. This suggested that these Red Chromosols have evolved from the initial status (i.e. genosoil 1) to the disturbed status (i.e. phenosoils 2 and 3). The practice of liming is common in the study area and this may have contributed to this. In this case, the disturbance can be viewed as persistent variants of a genosoil with sufficient chemical differences (change of pH: 0.4 and 1.0 in topsoil and subsoil, respectively) to substantially affect soil functions (Rossiter and Bouma, 2018), which are not only related to biomass production but also the store of archeological information, biodiversity and ecosystem services (McBratney et al., 2014). In addition, it is envisaged that soil pH may decrease and change back to the original status in the long term (< 5.5) if the liming practices have stopped. This also justifies why the soils have been considered as a phenosoil instead of genosoil.

Fig. 8 shows the distribution of the present genosoil and phenosoils for Brown Chromosols. Brown Chromosols have been classified into one genosoil (genosoil 1) and three phenosoils at the present time. As shown in Table 3, SOC contents and texture contrast were similar between the genosoils and phenosoils but pH values have varied slightly. Therefore, it can be argued that some Brown Chromosols have gradually changed from genosoil 1 to phenosoils 2 and 3. In this case, however, the disturbance was smaller as compared to the Red Chromosols (change of pH: 0.7 and 0.4 in topsoil and subsoil, respectively).

3.3.2. Red Kurosols and Brown Kurosols

Figs. 9 and 10 show the distributions of various present genosoils and phenosoils of Red Kurosols and Brown Kurosols. The spatial patterns were similar. Interestingly, a significant decrease of SOC was evident between genosoil 1 and phenosoils 2–3. This indicated that the soil has changed with time as a result of the agricultural activities. Similarly, pH values increased slightly when Kurosols shifted from genosoil 1 to phenosoils 2–3. This may be attributed to the application of lime associated with agricultural activities (e.g. pasture or vineyard). It was also noted that the difference of clay content between topsoil and subsoil (i.e. texture contrast) was much larger in phenosoils 2–3 compared with genosoil 1. This suggests that the topsoil within the phenosoils 2–3 may have eroded due to land use changes and particularly in areas where the slope is high (refer to Fig. 2).

3.3.3. Calcarosols

Fig. 11 shows the distributions of genosoil 1 and various phenosoils of Calcarosols. Most of the Calcarosols were disturbed and classified as phenosoils 2 and 3. As shown in Table 3, SOC content has decreased over time indicating Calcarosols has evolved from genosoil 1 to phenosoils 2 and 3. In addition, soil pH was found to increase from 6.0 to 6.9 in the topsoil and from 5.8 to 7.7 in the subsoil.

3.4. Potential shifts between genosoils

According to Rossiter and Bouma (2018), genosoils can be identified according to the soil classification system. Therefore, once the change of a soil is across a taxon boundary, then the soil will have shifted from one genosoil to another. Similarly, as shown in Table 3, the present genosoil 1 of Red Kurosols have pH values of 5.5 and 5.2 in the topsoil and subsoil. By comparison, phenosoil 3 of Red Kurosols have pH values of 6.3 and 5.8 in the topsoil and subsoil, respectively. According to the Australian Soil Classification (Isbell, 2002), if a texture contrast soil (i.e. duplex soil) is not strongly acidic (pH < 5.5), then it should be classified as Sodosol (exchangeable sodium percentage > 6%) or

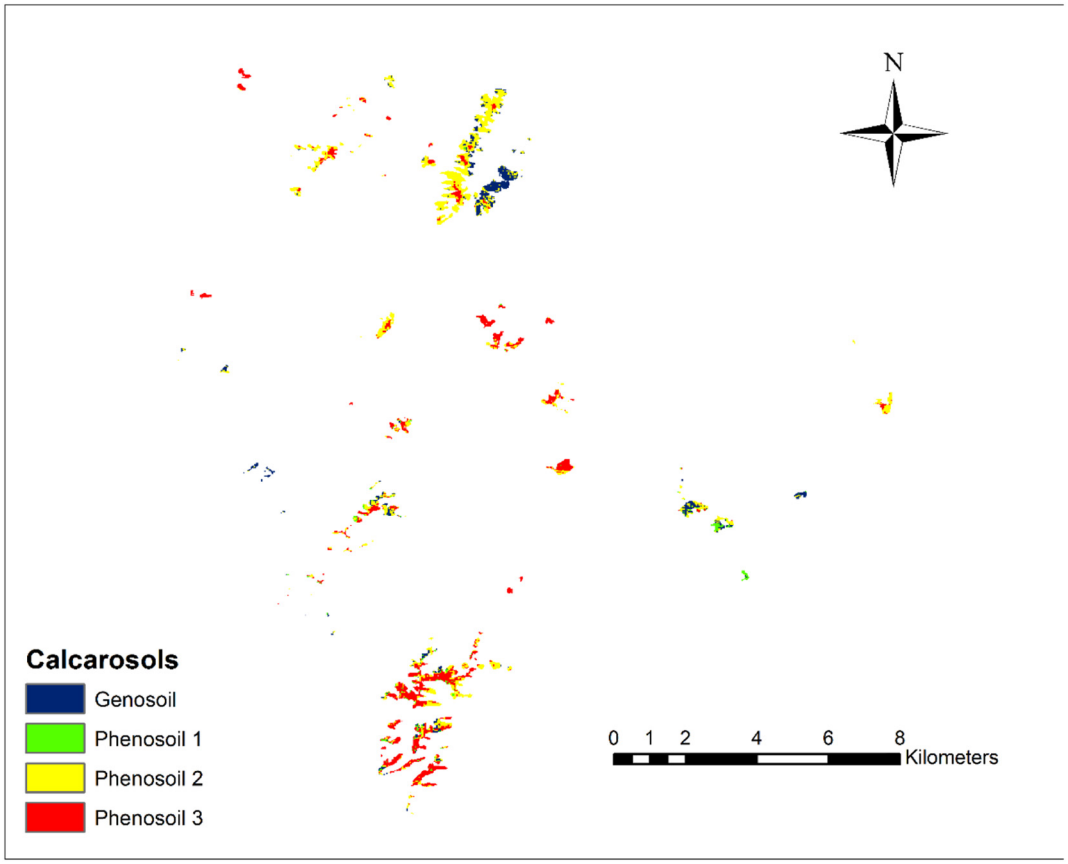

Fig. 11. Spatial distribution of the genosoil and phenosoils of Calcarosols across the study area.

Chromosol (exchangeable sodium percentage < 6%). Therefore, phenosoils 2 and 3 of Red Kurosols can be potentially defined as different genosoils, which can either be classified into one of the existing genosoils (e.g. Red Chromosols) or become a new genosoil (e.g. Red Dermosols). Fig. 12 shows the spatial distribution of present soil classes across the study area. Note that most of the phenosoils 2 and 3 of Red Chromosols are now classified as Red Dermosols. This issue will be further explored in the following section.

This suggests that if the intensive human activities (e.g. liming) occur, a soil phenosoil can have significant changes of soil properties and eventually shift towards to a new soil genosoil. This idea has also been discussed by Rossiter and Bouma (2018), who pointed out that intensive (e.g., deep ripping, additions of technogenic or transported materials) or long-term (e.g., additions of plaggen) management interventions, soil morphology and properties can have sufficient changes to be recognized in soil classification systems as separate soil types. Some examples of these intensive or long-term anthropogenic activities include Technosols (Rossiter, 2007) and Anthrosols reference groups of the World Reference Base for Soil Resources (Hern'andez and Galbraith, 1997), the Anthroposols of the Australian Soil Classification (Isbell, 2002) and paddy rice soils of Chinese Soil Taxonomy (Gong et al., 2001).

3.5. Verifying and redefining genosoils and phenosoils

Table 4 shows the distances calculated between the genosoils and various phenosoils within each Pre-European soil class using the comprehensive soil classification system (Hughes et al., 2017). In this study, such a potentially universal soil classification system was used as a reference to scale the soil variables so that the methodology can be applied elsewhere in the world and the changes between the genosoils and phenosoils can be compared consistently. Given that we did not have enough soil samples within phenosoil 1, we excluded it from the discussion. Based on the distances, several genosoils and phenosoils may be redefined objectively.

In terms of Red Chromosols, phenosoils 2 and 3 had distances of 0.6 and 1.2 from the genosoil, respectively (refer to Table 4). This suggested that phenosoil 2 (distance to genosoil 1: 1/3–2/3) should be considered as the same genosoil (phenosoil 1 of genosoil 1 of Red Chromosols, abbreviated as RCg1p1) while phenosoil 3 (distance to genosoil 1: > 1.0) can become a new genosoil (genosoil 2 of Red Chromosols, abbreviated as RCg2). When plotted in the principal component space (Fig. 13), the Red Chromosols have evolved from one genosoil (RCg1) to various phenosoils (i.e. RCg1p1 and RCg2) as indicated by different extents of soil change.

As for Brown Chromosols, phenosoil 1 and phenosoil 2 had distances larger than 2/3 but smaller than 1.0 from the genosoil. Therefore, both would be reconsidered as phenosoil 3 of Brown Chromosols (abbreviated as BCg1p3a and BCg1p3b). Similarly, this genosoil has evolved with time as a function of soil disturbance due to human activities (Fig. 13).

With regard to Red Kurosols, phenosoil 2 should be reconsidered as a new genosoil, RKg2 (distance to RKg1 > 1.0) (Table 4) while Phenosoil 3 should become the phenosoil 2 of this newly defined genosoil, namely, RKg2p2 (distance to RKg1 > 1.0; distance to RKg2: 1/3–2/3). This was the similar case of Brown Kurosols and Calcarosols (refer to Tables 4 and 5).

Fig. 13 also shows that different genosoils were generally clustered together. This suggested that the present map of genosoils was relatively accurate and able to pick up the differences in soil properties. However, a number of genosoils were found more close to each other than to the corresponding phenosoils. For example, RKg1 (genosoil 1 of Red Kurosols) was more close to BCg1 (genosoil 1 of Brown Chromosols) than to other Red Kurosols (e.g. RKg2 and RKg2p2) (refer to

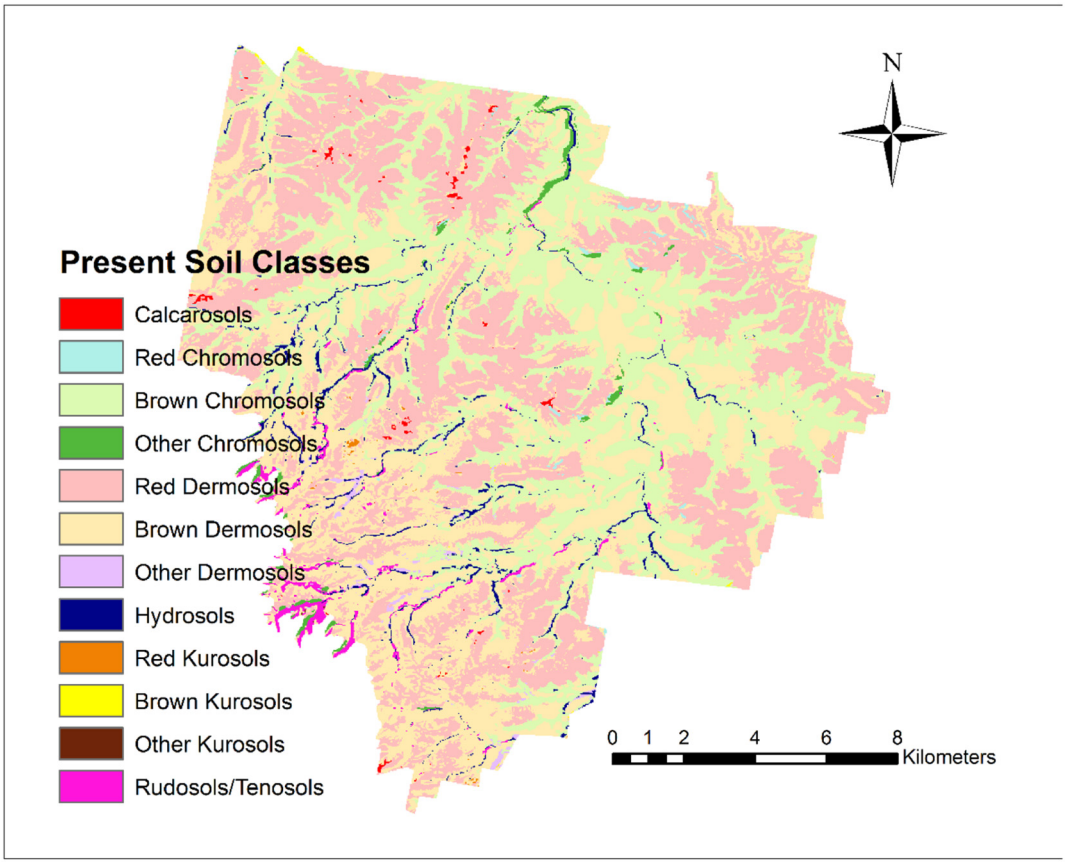

Fig. 12. Spatial distribution of the present soil classes across the study area.

Table 4
Distances between soil genosoil and phenosoils 2–3. Notes: Red Chromosols (RC), Brown Chromosols (BC), Red Kurosols (RK), Brown Kurosols (BK), and Calcarosols (CA) as well as genosoil 1 (g1), phenosoils 2 (p2) and 3 (p3) were abbreviated; e.g. RCg1p2 represents the second phenosoil of the first genosoil Red Chromosols.

	RCg1	RCg1p2	RCg1p3	BCg1	BCg1p2	BCg1p3	RKg1	RKg1p2	RKg1p3	BKg1	BKg1p2	BKg1p3	CAg1	CAg1p2	CAg1p3
RCg1	0.0	0.6	1.2	0.8	0.6	0.7	1.0	1.4	1.0	2.3	1.7	1.8	0.6	1.6	2.0
RCg1p2	–	0.0	0.8	0.9	0.2	0.4	1.5	1.3	0.9	2.0	1.7	1.6	1.0	1.3	1.6
RCg1p3	–	–	0.0	1.6	0.7	0.9	2.0	1.1	0.7	2.1	1.4	1.2	1.6	1.0	1.2
BCg1	–	–	–	0.0	0.9	0.8	0.9	1.8	1.4	1.9	2.2	2.3	1.0	1.9	2.4
BCg1p2	–	–	–	–	0.0	0.4	1.4	1.1	0.8	1.9	1.5	1.5	1.0	1.4	1.7
BCg1p3	–	–	–	–	–	0.0	1.4	1.3	0.9	2.0	1.7	1.7	0.9	1.3	1.7
RKg1	–	–	–	–	–	–	0.0	1.9	1.6	2.5	2.2	2.4	1.2	2.3	2.8
RKg1p2	–	–	–	–	–	–	–	0.0	0.7	2.1	0.6	0.8	1.9	2.0	2.2
RKg1p3	–	–	–	–	–	–	–	–	0.0	2.1	0.9	1.1	1.6	1.5	1.8
BKg1	–	–	–	–	–	–	–	–	–	0.0	2.5	2.4	2.6	2.7	3.1
BKg1p2	–	–	–	–	–	–	–	–	–	–	0.0	0.6	2.2	2.2	2.3
BKg1p3	–	–	–	–	–	–	–	–	–	–	–	0.0	2.2	2.1	2.0
CAg1	–	–	–	–	–	–	–	–	–	–	–	–	0.0	1.8	2.1
CAg1p2	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0	0.9
CAg1p3	–	–	–	–	–	–	–	–	–	–	–	–	–	–	0.0

Table 4 for details). This suggested that RKg1 may be redefined as a phenosoil of Brown Chromosols (e.g. BCg1p3). This was not unexpected because RKg1 had a similar texture contrast (duplex) to BCg1 according to the ASC system (Isbell, 2002) and change of soil pH in RKg1 (refer to Tables 2 and 3) may lead to a shift and reclassification from Kurosols to Chromosols.

3.6. Guidelines and implications for soil conservation and land management

The concepts of genoforms and phenoforms proposed by Droogers and Bouma (1997) are important in assessing and monitoring the change of soil condition (Bonfante and Bouma, 2015). The key differences and relationship between the concepts of genoform-phenoform and genosoil-phenosoil are summarised in Table 6. When a detailed soil series map is available, the concept of genoform and phenoform suggested by Droogers and Bouma (1997) and Rossiter and Bouma (2018) can be applied to identify soil change. However, when a detailed soil series map is not available (e.g. in some of the developing countries), or the change of soil properties is so significant that the soil has shifted from one series to another due to human activities (e.g. cultivation), the concepts of genosoils and phenosoils can be used to characterise the soil change within various soil classes identified by using a digital soil mapping approach (McBratney et al., 2003) for soil condition monitoring.

Particularly, the concepts of genosoils and phenosoils can be applied elsewhere with least human disturbance such as Tibet plateau (Li et al.,

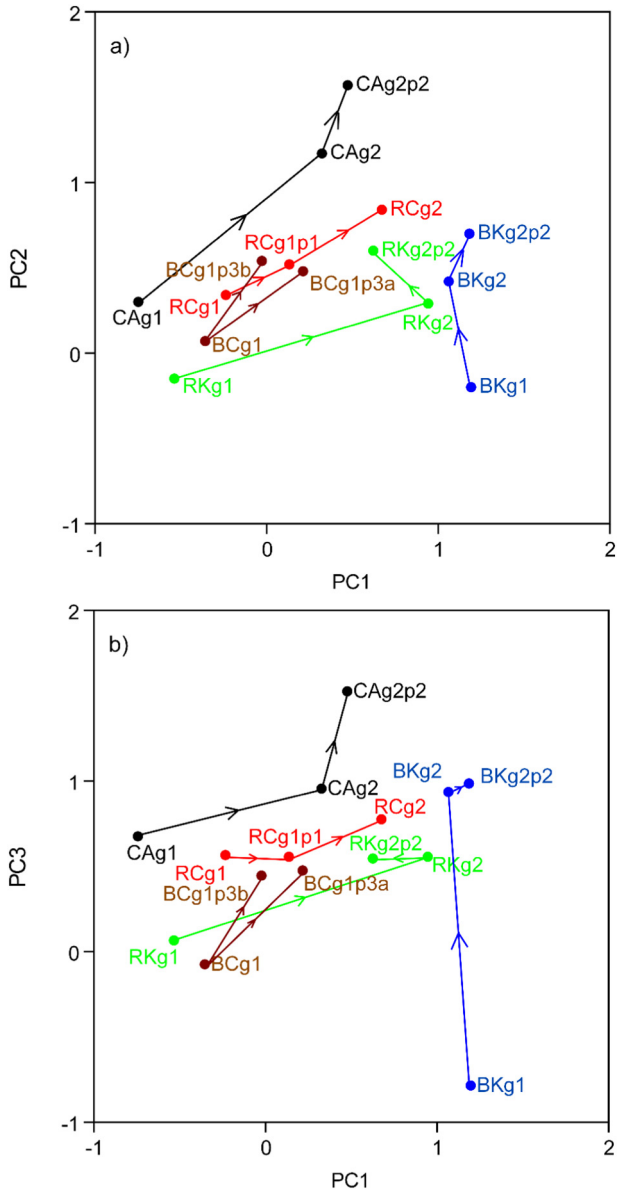

Fig. 13. Distribution of the centroids of redefined genosoils and phenosoils in the principal component (PC) spaces created using the comprehensive soil classification system (Hughes et al., 2017) and including a) PC1 versus PC2, b) PC1 versus PC3. The arrows of the solid lines indicated the direction of soil evolution as a function of human activities.

2015) or with extensive human disturbance such as land consolidation (Wang and Gong, 1998). In terms of the latter, whereby no remnant vegetation is present, some prior knowledge about the soil forming factors of the study area is required (Shi et al., 2004). As illustrated in Fig. 3, by using clustering all the soil forming factors except for human activities, we can generate different soil mapping units (not necessarily equivalent to soil series) and consider them as the reference states at the present time (McBratney et al., 2014; Kidd et al., 2018). Afterward, remote sensing datasets such as Landsat images can be used to delineate the extent of soil disturbance within these soil mapping units as a function of human activities and assign them different genosoils and phenosoils. Lastly, we can verify these genosoils and phenosoils by collecting soil samples within these genosoils and phenosoils and measuring the soil physical and chemical properties. To evaluate the changes of soil properties objectively, previously established comprehensive soil classification systems (Hughes et al., 2017) can be used as a reference to calculate the relative distance between the various genosoils and the respective phenosoils and determine whether new phenosoils and even genosoils should be created to indicate the soil change within and across soil mapping units.

Therefore, the concepts genosoils and phenosoils are important for soil and land conservation as it provides a feasible approach for rapid monitoring of soil change relative to the baseline conditions which is a quantification of soil capability (McBratney et al., 2014). The case study demonstrated here also shows the potential for monitoring and comparing the soil changes within and across different soil types, including monitoring soil changes 1) from an initial genosoil to different phenosoils, and 2) from a genosoil to a new genosoil. The shifts between genosoils and phenosoils could also be used to identify areas with soil change, which can be potentially employed by farmers, land managers, and government agencies to choose the soil sampling and surveying locations for improving the existing soil monitoring schemes (Tugel et al., 2005; Morvan et al., 2008).

3.7. Future work

A few issues need to be further explored in the future. First, it is worth developing a more robust pattern recognition algorithm to separate the seasonal fluctuations from long-term agricultural activities of multi-year NDVI data from remote sensing images and identify zones with different land management practices over time (Zhu and Woodcock, 2014; Homer et al., 2015).

Second, the creation of least disturbed (e.g. Pre-European) soil classes is relatively easy in this study because remnant vegetation exists. However, remnant vegetation is not a necessity to identify genosoils and phenosoils across a landscape. In regions with a long-term history of land reclamation (e.g. Africa, Europe and Asia), a current soil class map created using a digital soil mapping approach (McBratney et al., 2003) can be used to delineate genosoils and phenosoils. The soils

Table 5
A reinterpretation of Table 4 removing phenosoil 1 showing the sequence from the genosoil to phenosoils 2 and 3. Note: elements in bold represent new genosoils. Red Chromosols (RC), Brown Chromosols (BC), Red Kurosols (RK), Brown Kurosols (BK), and Calcarosols (CA) as well as genosoils 1 (g1) and 2 (g2), phenosoils 2 (p2) and 3 (p3) were abbreviated; e.g. RCg1p2 represents the second phenosoil of the first genosoil Red Chromosols. If two phenosoils were assigned to a same new phenosoil, they were labelled using 'a' and 'b'. The soil classes in the brackets under the present genosoil, phenosoils 2 and 3 are the present soil classes allocated using the soil sampling data.

Pre-European soil class/ genosoil	Present genosoil	Present phenosoil 2	Present phenosoil 3
RC	RCg1 (Red Dermosols, Brown Dermosols, Chromosols)	RCg1p1 (Red Dermosols and Brown Dermosols)	**RCg2** (Red Dermosols and Brown Dermosols)
BC	BCg1 (Brown Dermosols and Brown Chromosols)	BCg1p3a (Brown Dermosols and Brown Chromosols)	BCg1p3b (Brown Dermosols and Brown Chromosols)
RK	RKg1 (Red Kurosols)	**RKg2** (Red Dermosols and Brown Dermosols)	RKg2p2 (Red Dermosols and Brown Dermosols)
BK	BKg1 (Brown Kurosols)	**BKg2** (Brown Dermosols and Red Dermosols)	BKg2p2 (Brown Dermosols and Red Dermosols)
CA	CAg1 (Brown Dermosols)	**CAg2** (Brown Dermosols, Red Dermosols and Calcarosols)	CAg2p2 (Brown Dermosols, Red Dermosols and Calcarosols)

Table 6
Summary of key differences and relationship between the concepts of genoform-phenoform and genosoil-phenosoil.

Concept	Definition	Differentiation criteria	Application	Relationship
Genoform	Soil classes as identified by the soil classification system used as the basis for detailed soil mapping in a given area	Soil classes (e.g. soil series)	When detailed soil survey map (e.g. soil series map) is available and the users want to understand the changes in soil properties/functions relative to different soil classes.	When a soil series map is available, soil mapping units are used as a starting point, whereby identified genosoils and phenosoils become genoforms and phenoforms.
Phenoform	Persistent variants of a genoform with sufficient physical or chemical differences to substantially affect soil functions	Degree of change in soil physical and chemical properties that would affect soil functions		
Genosoil	Soil mapping units that were least disturbed by human activities	Soil mapping units generated by digital soil mapping	When detailed soil survey map (e.g. soil series map) is not available and the users want to understand the changes in soil properties/conditions/capacities relative to different soil mapping units.	
Phenosoil	Soil mapping subunits with different levels of changes of soil physical and chemical properties	Degree of change in soil physical and chemical properties, which can be computed using a reference soil database (e.g. comprehensive soil classification system)		

within each current soil class that are least disturbed will be considered as the genosoils while the remaining soils are named as different phenosoils according to the degree of human disturbance. Therefore, the concepts of genosoil and phenosoil can be applied to improve the existing studies on the effects of land use change on soil physical and chemical properties that did not take soil types into consideration (e.g. Giertz et al., 2005; Khresat et al., 2008; Biro et al., 2013).

Thirdly, large parts of the world do not have soil series mapping. The genoform and phenoform concepts of Droogers and Bouma (1997) and revisited two decades later by Rossiter and Bouma (2018) – an indication of the precociousness of the original paper – are defined and designed for areas where soil series mapping exist. Here we have defined a more general approach which can be used more widely, but includes where soil series mapping occurs. Consider our approach in the case where there is soil series mapping – what we're suggesting is overlaying the soil series by land use change and looking at the effects on soil properties – functional and factual. So in this sense, we have a way of operationalising the genoform-phenoform concepts for analysing anthropic soil change (Tugel et al., 2005; Robinson et al., 2012).

Last and perhaps the most important aspect of this paper is that it maps out the anthropogenic effect objectively – and we see that in modern landscapes this effect is large. Our current classification systems still largely attempt to mask this effect and place it at the margins. Humanity has profoundly changed the soil landscape and that change is ongoing. The genosoil-phenosoil approach allows us to define reference states against which soil change can be gauged – these reference states are not 'one size fit all' but are locally defined. We argue in the soil security concept (McBratney et al., 2014; McBratney and Field, 2015) that that condition should be separated from capability by gauging phenosoils against genosoils.

4. Conclusions

- A spatial genosoil-phenosoil analysis was developed which presented the soil landscape highlighting anthropogenic factors as the principal agent of soil change. It showed potential in detecting areas with soil changes due to human activities.
- The approach was developed using a combination of digital soil mapping and pedogenic landscape understanding.
- The approach successfully mapped the spatial distribution of least-disturbed Pre-European genosoils and phenosoils and identified the shifts between present phenosoils at the district scale.
- The distance between the present genosoils and phenosoils was calculated in a principal component space created using a recently published comprehensive soil classification system enabling several present phenosoils of a genosoil to be redefined as new genosoils.
- Future work is required to separate the seasonal fluctuations in NDVI from the long-term variations and improve the land use classification using remote sensing data.
- The concepts of genosoils and phenosoils can be applied in areas with long-term human activities where remnant vegetation is not dominant, which requires generating a current soil class map using a digital soil mapping approach.

Acknowledgments

The authors acknowledge Professor Johan Bouma (formerly of Wageningen University) and Professor David G. Rossiter (Cornell University, ISRIC) and one anonymous reviewer for the valuable comments on the manuscript.

References

Amundson, R., Jenny, H., 1991. The place of humans in the state factor theory of ecosystems and their soils. Soil Sci. 151, 99–106.
Arrouays, D., Marchant, B.P., Saby, N.P.A., Meersmans, J., Orton, T.G., Martin, M.P., ...

Kibblewhite, M., 2012. Generic issues on broad-scale soil monitoring schemes: a review. Pedosphere 22, 456–469.
Biro, K., Pradhan, B., Buchroithner, M., Makeschin, F., 2013. Land use/land cover change analysis and its impact on soil properties in the northern part of Gadarif region, Sudan. Land Degrad. Dev. 24, 90–102.
Bishop, T.F.A., McBratney, A.B., Laslett, G.M., 1999. Modelling soil attribute depth functions with equal-area quadratic smoothing splines. Geoderma 91, 27–45.
Bonfante, A., Bouma, J., 2015. The role of soil series in quantitative land evaluation when expressing effects of climate change and crop breeding on future land use. Geoderma 259, 187–195.
Bureau of Meteorology, 2017. Climate statistics for Australian locations. http://www.bom.gov.au/climate/averages/tables/cw_055024.shtml.
Chauveau, D., Saby, N.P., Orton, T.G., Lemercier, B., Walter, C., Arrouays, D., 2014. Large-scale simultaneous hypothesis testing in monitoring carbon content from French soil database — a semi-parametric mixture approach. Geoderma 219, 117–124.
Core Team, R., 2017. R Language Definition. R Foundation for Statistical Computing, Vienna, Austria.
De Groot, R.S., Wilson, M.A., Boumans, R.M., 2002. A typology for the classification, description and valuation of ecosystem functions, goods and services. Ecol. Econ. 41, 393–408.
Droogers, P., Bouma, J., 1997. Soil survey input in exploratory modeling of sustainable soil management practices. Soil Sci. Soc. Am. J. 61, 1704–1710.
Gallant, J.C., Dowling, T.I., 2003. A multiresolution index of valley bottom flatness for mapping depositional areas. Water Resour. Res. 39.
Geeves, G.W., Cresswell, H.P., Murphy, B.W., Gessler, P.E., Chartres, C.J., Little, I.P., Bowman, G.M., 1995. The Physical, Chemical and Morphological Properties of Soils in the Wheat-belt of Southern New South Wales and Northern Victoria. NSW Department of Conservation and Land Management.
Giertz, S., Junge, B., Diekkrüger, B., 2005. Assessing the effects of land use change on soil physical properties and hydrological processes in the sub-humid tropical environment of West Africa. Phys. Chem. Earth 30, 485–496.
Gong, Z.T., Lei, W.J., Chen, Z.C., Gao, Y.X., Zeng, S.G., Zhang, G.L., Xiao, D.N., Li, S.G., 2001. Chinese Soil Taxonomy. Science Press, Beijing.
Gorelick, N., Hancher, M., Dixon, M., Ilyushchenko, S., Thau, D., Moore, R., 2017. Google earth engine: planetary-scale geospatial analysis for everyone. Remote Sens. Environ. 202, 18–27.
Hawley, S.P., Glen, R.A., Baker, C.J., 1995. Newcastle Coalfield Regional Geology 1:100 000, 1st Edition. Geological Survey of New South Wales, Sydney, Australia.
Hern'andez, L.A., Galbraith, J.M., 1997. Soil Survey of South Latourette Park, Staten Island, New York City, NY. USDA Natural Resources Conservation Service.
Homer, C., Dewitz, J., Yang, L., Jin, S., Danielson, P., Xian, G., ... Megown, K., 2015. Completion of the 2011 National Land Cover Database for the conterminous United States–representing a decade of land cover change information. Photogramm. Eng. Remote Sens. 81, 345–354.
Hoyle, J., Brooks, A., Brierley, G., Fryirs, K., Lander, J., 2008. Spatial variability in the timing, nature and extent of channel response to typical human disturbance along the upper Hunter River, new South Wales, Australia. Earth Surf. Process. Landf. 33, 868–889.
Hughes, P., McBratney, A., Huang, J., Minasny, B., Hempel, J., Palmer, D.J., Micheli, E., 2017. Creating a novel comprehensive soil classification system by sequentially adding taxa from existing systems. Geoderma Reg. 11, 123–140.
Isbell, R., 2002. The Australian Soil Classification. CSIRO Publishing, Melbourne.
Jandl, R., Rodeghiero, M., Martinez, C., Cotrufo, M.F., Bampa, F., van Wesemael, B., ... Lorenz, K., 2014. Current status, uncertainty and future needs in soil organic carbon monitoring. Sci. Total Environ. 468, 376–383.
Khresat, S.E., Al-Bakri, J., Al-Tahhan, R., 2008. Impacts of land use/cover change on soil properties in the Mediterranean region of northwestern Jordan. Land Degrad. Dev. 19, 397–407.
Kidd, D., Field, D., McBratney, A.B., Webb, M., 2018. A preliminary spatial quantification of the soil security dimensions for Tasmania. Geoderma 322, 184–200.
Lal, R., 2010. Beyond Copenhagen: mitigating climate change and achieving food security through soil carbon sequestration. Glob. Food Sec. 2, 169–177.
Lavelle, P., Spain, A.V., 2001. Soil Ecology. Springer Science & Business Media.
Li, S., Shi, Z., Chen, S., Ji, W., Zhou, L., Yu, W., Webster, R., 2015. In situ measurements of organic carbon in soil profiles using vis-NIR spectroscopy on the Qinghai–Tibet plateau. Environ. Sci. Technol. 49, 4980–4987.
Liaw, A., Wiener, M., 2002. Classification and regression by randomForest. R News 2, 18–22.
Malone, B.P., Hughes, P., McBratney, A.B., Minasny, B., 2014. A model for the identification of terrons in the Lower Hunter Valley, Australia. Geoderma Reg. 1, 31–47.
Malone, B.P., McBratney, A.B., Minasny, B., 2018. Description and spatial inference of soil drainage using matrix soil colours in the Lower Hunter Valley, New South Wales, Australia. PeerJ 6, e4659.
McBratney, A., Field, D., 2015. Securing our soil. Soil Sci. Plant Nutr. 61, 587–591.
McBratney, A.B., Santos, M.M., Minasny, B., 2003. On digital soil mapping. Geoderma 117, 3–52.
McBratney, A., Field, D.J., Koch, A., 2014. The dimensions of soil security. Geoderma 213, 203–213.
Morvan, X., Saby, N.P.A., Arrouays, D., Le Bas, C., Jones, R.J.A., Verheijen, F.G.A., ... Kibblewhite, M.G., 2008. Soil monitoring in Europe: a review of existing systems and requirements for harmonisation. Sci. Total Environ. 391, 1–12.
Odgers, N.P., McBratney, A.B., Minasny, B., 2011. Bottom-up digital soil mapping. II. Soil series classes. Geoderma 163, 30–37.
Pulleman, M.M., Bouma, J., Van Essen, E.A., Meijles, E.W., 2000. Soil organic matter content as a function of different land use history. Soil Sci. Soc. Am. J. 64, 689–693.
Quinn, P.F., Beven, K.J., Lamb, R., 1995. The in (a/tan/β) index: how to calculate it and how to use it within the topmodel framework. Hydrol. Process. 9, 161–182.
Robinson, D.A., Hockley, N., Dominati, E., Lebron, I., Scow, K.M., Reynolds, B., Emmett, B.A., Keith, A.M., de Jonge, L.W., Schjønning, P., Moldrup, P., Jones, S.B., Tuller, M., 2012. Natural capital, ecosystem services, and soil change: why soil science must embrace an ecosystems approach. Vadose Zone J. 11 (1).
Rossiter, D.G., 2007. Classification of urban and industrial soils in the world reference base for soil resources. J. Soils Sediments 7, 96–100.
Rossiter, D.G., Bouma, J., 2018. A new look at soil phenoforms – definition, identification, mapping. Geoderma 314, 113–121.
Schloss, P.D., Handelsman, J., 2005. Introducing DOTUR, a computer program for defining operational taxonomic units and estimating species richness. Appl. Environ. Microbiol. 71, 1501–1506.
Shi, X.Z., Yu, D.S., Warner, E.D., Pan, X.Z., Petersen, G.W., Gong, Z.G., Weindorf, D.C., 2004. Soil database of 1: 1,000,000 digital soil survey and reference system of the Chinese genetic soil classification system. Soil Horizons 45, 129–136.
Smith, G.D., Ahmad, N., 1986. The Guy Smith interviews: Rationale for concepts in soil taxonomy (Vol. 11). Soil Management Support Services, Soil Conservation Service, US Department of Agriculture.
Stockmann, U., Malone, B.P., McBratney, A.B., Minasny, B., 2015. Landscape-scale exploratory radiometric mapping using proximal soil sensing. Geoderma 239, 115–129.
Stockmann, U., Huang, J., Minasny, B., Triantafilis, J., 2017. Utilizing a DUALEM-421 and inversion modelling to map baseline soil salinity along toposequences in the Hunter Valley Wine district. Soil Use Manag. 33, 413–424.
Tugel, A.J., Herrick, J.E., Brown, J.R., Mausbach, M.J., Puckett, W., Hipple, K., 2005. Soil change, soil survey, and natural resources decision making. Soil Sci. Soc. Am. J. 69, 738–747.
Wang, X., Gong, Z., 1998. Assessment and analysis of soil quality changes after eleven years of reclamation in subtropical China. Geoderma 81, 339–355.
Zhu, Z., Woodcock, C.E., 2014. Continuous change detection and classification of land cover using all available Landsat data. Remote Sens. Environ. 144, 152–171.