Cultural and Demic Diffusion of First Farmers, Herders, and their Innovations Across Eurasia

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Abstract. Was the spread of agropastoralism from the Eurasian founder regions dominated by demic or by cultural diffusion? This study employs a mathematical model of regional sociocultural development that includes different diffusion processes, local innovation and societal adaptation. Simulations hindcast the emergence and expansion of agropastoral life style in 294 regions of Eurasia and North Africa. Different scenarios for demic and diffusive exchange processes between adjacent regions are contrasted and the spatiotemporal pattern of diffusive events is evaluated. This study supports from a modeling perspective the hypothesis that there is no simple or exclusive demic or cultural diffusion, but that in most regions of Eurasia a combination of demic and cultural processes were important. Furthermore, we demonstrate the strong spatial and temporal variability in the balance of spread processes. Each region shows sometimes more demic, and at other times more cultural diffusion. Only few, possibly environmentally marginal, areas show a dominance of demic diffusion. This study affirms that diffusion processes should be investigated in a diachronic fashion and not from a time-integrated perspective.
Keywords: Cultural diffusion; demic diffusion; modeling; Neolithic; Eurasia

1. Introduction

The transition to agriculture and pastoralism, termed the “Neolithic revolution” by Childe (1925) has fundamentally changed social systems and the relationship of people and their environments. However revolutionary - even termed “traumatic” (Rowley-Conwy 2004) - this transition was locally, the more gradual it appears on the continental scale, spanning almost 10000 years of human prehistory and history (e.g. Barker 2006).

The spatial diffusion of the new agropastoral and animal husbandry innovations, technologies, and life styles played a major part in the abandonment of a foraging life style following local innovations in very few places worldwide that are associated with the domestication of plants and animals (Fuller et al. 2014). From these few founder regions, the new domesticates, their cultivation knowledge and the idea of farming and herding itself spread to all but the most secluded or marginal regions of the world; not only these cultural traits spread, but also people, who carried along their “hitchiking” traits (Ackland et al. 2007).

The spatiotemporal pattern of dated Neolithic sites consequently radiates outward from the founder regions. For different cultural and individual traits, the apparent rates of spreading can be determined (Edmonson 1961, Bocquet-Appel et al. 2012), but it is unclear from the spatiotemporal analysis of dated sites, what process dominated the expansion (Lemmen, Gronenborn, and Wirtz 2011): Within a broad spectrum of diffusion mechanisms that include, e.g., also leapfrog migration and elite replacement (Zvelebil 1998) demic diffusion and cultural diffusion represent two contrasting views that have received widespread attention in the literature. The demic diffusion hypothesis suggests the introduction of the new agropastoral technologies through movements of people - migrations of any form; the cultural diffusion hypothesis suggests a technology shift through indigenous adaptations and inventions fostered by culture contact - information dispersal of any form.

Demic diffusion, i.e. the spread of agropastoralism by migration of people has been put forward as one of the earliest hypotheses for explaining the spatiotemporal pattern of Neolithic arrival dates in Europe (Clark 1965); evidence for demic diffusions is accumulating with modern mtDNA and Y-chromosomal analyses revealing matrilinear and patrilinear relationships in space and time (Chikhi et al. 2002, Déguitloux et al. 2012, Fu et al. 2012) (although contrasting views have been presented by Battaglia et al. 2008 and Haak et al. 2010), and with earlier linguistic work (Renfrew 1987).

Cultural diffusion is the spread of agropastoralism by information and material transmission in the absence of migrations. As both maternal and paternal genetic lines are continuous from the Founder regions into Europe, approval for the cultural diffusion hypothesis depends on a temporal mismatch between the expansion of traits and knowledge and the expansion of people. Already Ammerman and Cavalli-Sforza (1973) suggested that both demic and diffusive spread are active and that it is the relative contribution of each that needs to be investigated rather than deciding on either demic or cultural diffusion. Furthermore, cultural diffusion theories have also been put forward as a reaction against processual diffusionist views and emphasize the agency and innovativity of local populations (Hodder 1990) (but refuted again by e.g., Rowley-Conwy 2004)).

Mathematical models on the spread of agropastoralism have a long tradition in Europe and can be traced back to Childe (1925)’s observations on the spatio-temporal distribution gradient of ceramics from Southeastern to Northwestern Europe. This pattern was replicated from Neolithic radiocarbon dates by Clark (1965), and subsequently mathematically formulated by Ammerman and Cavalli-Sforza (1973) as the “wave of advance” model on which many subsequent formulations have been built (Ackland et al. 2007, Galleta et al. 2011, Davison, Dolukhanov, and Sarsøn 2009)).

A common feature of diffusion models is a concentric expansion from one or multiple centers of supposed origins, with modifications introduced to account for geographic bottlenecks, terrain, or rivers (Davison et al. 2006, Patterson et al. 2010, Silva 2014a). Fort (2012) and Fort (2015) attempted to disentangle demic and cultural diffusion both from a modeling as well as a data perspective. In a diffusion model, they found that both demic and cultural diffusion are important, with demic diffusion responsible for 60% (vs. 40% for cultural) of the spreading process. Similarly, our own investigation (Lemmen, Gronenborn, and Wirtz 2011) concluded that a mixed model produces a pattern of Neolithization best representing the data.

Much less numerical studies have been performed for Eurasian regions outside Europe. The best investigated test case is probably South Asia and the Indian subcontinent. For this region Ackland et al. (2007) investigated the transition to agriculture as a diffusion process that emanates from a single founder region in Southwest Asia; in contrast, Patterson et al. (2010) reported on a simulation of the Neolithic transition in India expanding from two centers, representing Chinese and Harappan migration streams. Our own simulations for the Indian subcontinent showed that the connection from the Indus region to the Levante...
was only established after the transition to agropastoralism (Lemmen and Khan 2012), consistent with the wheat/rice barrier identified by (Barker 2006). The demic–cultural debate has not been investigated for greater Eurasia yet.

In the current study, I demonstrate with numerical simulations how the different assumptions about the diffusion process -interpreted as demic diffusion and cultural diffusion or a mixture thereof- may have played different roles in the spread of agropastoralism through Eurasia. Emanating from founder regions in North and South China, Central Asia, and the Levant about 9000 years ago, the entire continent (except Northern Eurasia) transitions to agropastoral life styles by 3000 BC drawing a complex picture of cultural and demic diffusion.

The goal of this study is to investigate qualitatively the spatial and temporal predominance of either cultural or demic diffusion processes within Eurasia, and to provide a novel visualization of the complexity of the interplay between these processes at a continental scale.

2. Methods

I employ the Global Land Use and technological Evolution Simulator (GLUES, Lemmen, Gronenborn, and Wirtz 2011)—a numerical model of prehistoric innovation, demography, and subsistence economy—to hindcast the regional transitions to agropastoralism and the diffusion of people and innovations across Eurasia for the period 7500–3500 BC.

Figure 1: Geographic setting of 294 Eurasian and North African simulation regions in the Global Land Use and technological Evolution Simulator. This is a subset of the full (global) simulation comprising 685 world regions.

The model operates on 294 (country-like) spatial units within the domain -15° E to 135° E and 10° N to 60° N (Figure 1). These regions represent ecozones that have been derived to represent homogenous net primary productivity (NPP) clusters based on a 3000 BC 1° x 1° palaeoproduction estimate (Wirtz and Lemmen 2003); this estimate was derived from a dynamic palaeovegetation simulation (Brovkin, Ganopolski, and Sivirezhev 1997) scaled down with the New et al. (2001) climatology. By using NPP, many of the environmental factors taken into account by other expansion or predictive models, such as altitude, latitude, rainfall, or temperature (e.g. Silva2014b, Arikan2014).

Within each region, a trait-based adaptive model describes regional societies with three characteristics: intrinsic innovations (technology), extrinsic (economic diversity), and subsistence style (Lemmen, Gronenborn, and Wirtz 2011). The evolution of these characteristic traits is interdependent and drives the growth of a regional population according to the gradient adaptive dynamics approach formulated by Wirtz and Eckhardt (1996) for ecological systems. In his approach, the rate of change of the mean of each characteristic trait is calculated as the product of the trait’s variability and its marginal growth benefit, i.e. the derivative of population growth rate with respect to the trait, evaluated at the mean growth rate. In Wirtz and Lemmen (2003), we adopted this mathematical approach for social systems; as the approach is an aggregate formulation operating on the statistical moments of traits and growth rate, it requires large populations, and thus larger geographic areas. For further details on the trait-based model formulation, see Lemmen, Gronenborn, and Wirtz (2011) (their supplementary online material).

Exchange of characteristic traits and migration of people between regions is formulated with a diffusion-like approach, i.e., the flow of a quantity (technology, economic diversity, subsistence style) is directed from a region with higher influence (i.e. product of technology and population) to a region with lesser influence. The speed of the spread is proportional to the interregional difference of the respective quantity and of influence, is proportional to the influential region’s technology, and proportional to common boundary length divided by interregional distance. Migration is furthermore dependent on acceptable living conditions (positive growth rate) in the influenced region. Equations for interregional interchange are given in the appendix. The size of the simulation regions (on average 300000 km²) is insufficient for detailed local analyses, but appropriate for subcontinental and continental-scale simulations and necessary to allow for parameter space exploration.

We performed three different simulations, one with mixed diffusion, one with exclusively demic diffusion and one with exclusively cultural diffusion (see appendix for the different formulations). The global simulations (in total 685 regions) are started at 8500 BC, assuming equal initial conditions for all societies in all regions; we use the same set of parameters that have been used by Lemmen, Gronenborn, and Wirtz (2011): for the three diffusion scenarios, we obtained the diffusion coefficients by tuning each model...
to optimally represent the European arrival dates. Simulations were performed with GLUES version 1.1.20a; this version can be obtained as free and open source from

Despite tuning all scenarios to the radiocarbon record used in Lemmen, Gronenborn, and Wirtz (2011), the highest correlation could only be obtained with the mixed (base) scenario. To disentangle cultural and demic diffusion processes, we compared the demic and cultural diffusion scenarios with each other after normalization with the mixed scenario. Where the demic scenario predicted at least a 10% greater share of agropastoral life style, we diagnosed a predominantly demic diffusion. Where the cultural scenario predicted a greater share, we diagnosed a predominantly cultural diffusion. To estimate the overall influence of demic versus cultural diffusion, we averaged for each region the relative predominance of demic over cultural diffusion processes over time.

3. Results

The timing of the arrival of agropastoralism (Figure 2) reveals its multicentric origin and spatiotemporal expansion, including the typical radiation from founder regions seen in all diffusive models.

By 6600 BC, the transition to agropastoralism has occurred in five founder regions: (1) Northern coastal China, (2) Southern tropical inland China, (3) Northern Indus region, (4) West Anatolia and Greece, and (5) Zagros mountains. At this time, emerging agropastoralism connects the Chinese regions with each other (Figure 2). By 6300 BC, agropastoralism is the dominant life style in all founder regions; it has expanded west to the Balkans and Italy, and east to Korea. A broad band of agriculturalists is visible across China.

By 6100 BC, the Levante and Anatolian founder regions connect and expand north and eastward, likewise the Chinese regions. The Indus regions extends towards the Ganges. These emerging life styles consolidate in the ensuing centuries. By 5500 BC, the western Eurasian center has continued to expand in all directions, reaching around the Black Sea and to the Caspian Sea. All of China has transitioned Emerging agropastoralism connects the Indus to the Chinese region. By 5100 BC, North African pastoralism emerges. There is now one large Asian agropastoralist region, also with emergent transitions throughout India.

By 4700 the Western and Eastern Eurasian center connect. Agropastoralism emerges in Southeast Asia and Western Europe. By 4000 BC, one large belt of agropastoral life style connects the Mediterranean with West Asia, South Asia, and East Asia.

Multiple, intermittent, and recurrent predominantly

demic or cultural diffusion processes are seen throughout the simulation for all regions. For example, exchange processes around the Central Asian plateau are dominated by demic diffusion at all times. At most times, North African and Southwest European exchange processes are domi-
nated by demic diffusion. Cultural diffusion, on the other hand, is at all times dominant within east and south China, and in Southeast Asia. It is at most times dominant on the Indian subcontinent.

A more complex pattern of demic and cultural diffusion in space and time is observed in Western Asia and Southeast Europe. Diffusion from the Fertile Crescent is predominantly demic before 4900 BC, and cultural thereafter. Just east of the Red Sea, it is demic until 4200 BC, and cultural from 4000 BC. The expansion of Southeastern and Anatolian agropastoralism northward is predominantly cultural at 5500 BC, and predominantly demic 500 years later. At 5000 BC, it is demic west of the Black Sea and cultural east of the Black Sea. The, at 4500 BC, demic processes again take over part of the eastern Black Sea northward expansion.

![Diagram showing demic and cultural diffusion](image)

Figure 3: Time integrated contribution of predominantly demic (red) and cultural (green) diffusion represented geographically (top panel) and as a histogram (bottom panel). For most regions, no predominance (grey) of either mechanism is found.

Integrated over time, both demic and diffusive processes are equally relevant for most regions. No region, however, shows a demic contribution of less than 30%, and all regions have at least a cultural contribution of more than 15%. 90% of all regions show no dominance of either demic or cultural diffusion (Figure 3). A dominance of demic diffusion is evident in the Sahara, and the Hindukush and other regions around the Central Asian Plateau. Cultural diffusion is persistent on the Arabian pensinsual, South and Southeast Asia, and a several regions in southern Siberia and north of the Aral Sea.

4. Discussion

During each regional transition, both cultural and demic processes play a role, often even contribute sequentially to a regional agropastoral transition. In only very few regions, the simulated transition is best explained by either demic or cultural diffusion processes. Previous attempts to prove either demic or diffusion processes as solely responsible for regional agropastoral conditions seem too short-ferred, when the spatial and temporal interference of cultural and diffusive processes might have left a complex imprint on the genetic, linguistic and artifactual record.

In this respect, we confirm Ammerman and Cavalli-Sforza (1973)’s suggestion and Fort (2012)’s analysis of a probably mixed process underlying the expansion of agropastoralism and herding. The new finding here is that for most regions within Eurasia both processes are active, often contemporaneously, or subsequently, and that a time integrated view (such as population genetic or linguistic analyses) only picks out the few regions where either process dominates. For most regions, however, all of the complex interplay between cultural and demic diffusion is hidden in a time-integrated view.

This time-integrated view is, however, the only information that is accessible from radiocarbon arrival date compilations and most model simulations. Fort (2015), e.g., analysed the variations in diffusion speeds and attributed these to predominant cultural, demic, or mixed diffusion for slow, intermediate, and fast apparent diffusion rates, respectively (Fort 2015). Theirs and our analysis indicate potentially more demic exchange within Iberia and Northern Italy separated by predominant cultural or mixed exchange in Southern France; at the coarse scale of the model regions, however, this comparison should not be expected to yield conclusive insights.

Based on this time-integrated view, ancient DNA work (e.g. Bramanti et al. 2009), infers a demic signal throughout Europe. As time control is difficult in this record, the demic signal might have occured before the expansion of agropastoralists by migrations of Mesolithic hunter-gatherers or horticulturalists, or even later. The Y-chromosomal and the mitochondrial DNA data show different expansion patterns and can be attributed to multiple migration events, including pre-Neolithic and post-Neolithic demic events (Szécsényi-Nagy et al. 2014), although most of the introduced variability in the European gene pool was well established by the Bronze Age (Ricaut 2012).

Migration might have to be functionally disconnected from the spread of agropastoralism (Gronenborn 2011). Our simulations show that it is not necessarily only one migration wave and another cultural diffusion event that...
shaped the expansion of agropastoralism, but a multitude of combined events, sometimes more demic, some times more culturally dominated. This two-faceted expansion process then explains both archaeogenetic data as well as cultural diffusion evidence, without requiring distinct migratory processes before the expansion of agropastoralism.

In GLUES, I did not consider maritime migration, because the Iberian arrival dates could largely be reconstructed without explicitly including this process in the model because a secondary wave of advance enters Iberia from Gibraltar (there are artificial land bridges connecting across the strait of Gibraltar, Bosporus and the English Channel to compensate for the lack of maritime transport), which possibly emulates the fast leap-frog maritime that has been proposed for that region [Battalia2008]. For the purpose of investigating intracontinental diffusion processes in a compact land mass like Eurasia, the addition of a coastal or sea-mediated additional spread is not required.

The diachronic view of exchange processes presented here may help to identify individual migration and cultural exchange processes better than a time-integrated view. Thus, evidence of trade and exchange between two cultural layers with genetic continuity does not necessarily exclude demic diffusion during the entire period of interest, nor does a different genetic signal imply that cultural diffusion did not take place, or did not take place at other times.

Where do we see preferential cultural or demic diffusion in this study? Very roughly, mountaneous regions seem to favour demic diffusion in the model simulation when integrated over time (Figure 3). This is especially visible for the Central Asian plateau and its ridges. The Alps, the Pyrenees, the Iranian Plateau fit this pattern. Other important mountain regions, such as Anatolia or the Indian Ghats do not exhibit preferential demic diffusion.

Together with the apparent preferred demic diffusion is the western Sahara this possibly gives a hint that a lack of local adoption (due to environmental contraints) could be possible reason for slower or lesser cultural diffusion. This does not explain, however, the preferential cultural diffusion in the (also environmentally marginal) Arabian peninsula. Clearly, more work both in situ and in silico has to be done to explore the possibility of an environmental constraint selecting for a specific diffusion process.

These simulations have been performed without being confronted with sufficient regional archaeological data for most parts of Eurasia, and the parameters values have been tuned to best reproducing the origin locations and times of agropastoralism. Only European radiocarbon dates were used to estimate the diffusion coefficients for the demic, cultural and mixed diffusion scenarios (see appendix). One Eurasian region tested for model skill is the Indus region (Lemmen and Khan 2012), and there the model appears slightly too fast compared to the (often very uncertain) dates; In a non-Eurasian study (Lemmen 2013) found that radiocarbon dates for the transitory period 1000 BC–AD 1000 in Eastern North America were successfully simulated, again with a small model bias towards earlier dates.

The overall simulation for Eurasia is thus realistic in the sense of providing a consistent spatio-temporal view of one expectation of prehistoric developments (from a Eurocentric view) at a large scale. The results are not real in the sense that they provide the exact historical trajectory that has been found at the local scale (cmp Ackland et al. 2007). The great challenge and promise arising from the simulation is thus to confront the expectation from the model with the realization in the archaeological record: only when both disagree can we learn that either the model is not performing well enough, or that there is a process that is emancipated from the environmental and cultural context: then we have quantified human agency. The individual or society-level decision to migrate or to communicate should be expected to be at least as rich and complex as the cultural-demic diffusion picture appearing from a simulation.

5. Conclusion

I presented a numerical simulation study on the diffusion processes during the Neolithization in Eurasia, using an adaptive model of prehistoric societies in their environmental context that is able to resolve local innovation, cultural diffusion and demic diffusion. Although a mixed diffusion process had been suggested already long ago, the analysis of simulations with either cultural or demic diffusion, and with mixed diffusion, reveals an even more complex spatio-temporal pattern of the expansion of agropastoralism throughout Eurasia than has previously been found: demic and cultural processes occur contemporaneously, or multiple times iteratively or intermittently in most regions of Eurasia. There is no simple demic or cultural explanation, but a very complex and rich interplay of both processes in time and space. The polarized debate of either demic or cultural diffusion should give way to acknowledging again this more complex picture and to study and appreciate the richness of mechanisms.

6. Appendix

The diffusion process between a region $i$ another region in its neighbourhood $j \in \mathcal{N}$ is realized with three diffusion equations, representing communication, trade, and migration. Diffusion depends on the influence difference (Renfrew and Level 1979), where influence is defined as
the product of population density $P$ and technology $T$. The diffusion flux $f$ is proportional to the influence difference relative to the average influence of regions $i, j$ times geographically determined conductance between the two regions.

The entries for $c_{i,j}$ in the conductance matrix $C$ between two regions $i, j$ are constructed from the common boundary length $L_{i,j}$ divided by the mean area of the regions $\sqrt{A_i A_j}$. As in Etten and Hijmans (2010), geographically not connected regions have zero conductance; to connect across the Strait of Gibraltar, the English Channel, and the Bosporus, the respective entries in $C$ were calculated as if a narrow land bridge connected them.

No additional account is made for increased connectivity along rivers (Davison et al. (2006), Silva and Steele (2014)), as the regional setup of the model is biased (through the use of net primary productivity (NPP) similarity clusters) toward elongating regions in the direction of rivers. Altitude and latitude effects are likewise implicitly accounted for by the NPP clustering in the region generation.

Finally, if the flux between $i, j$ is negative, it is directed inward from $j$ to $i$, else outward from $i$ to $j$.

$$f_{i,j} = c_{i,j}\left(\frac{(P_i T_i A_i + P_j T_j A_j)}{A_i + A_j} - P_j T_j\right).$$

(1)

**Trade/information exchange:** Trait value differences in all traits $X$ between $i$ and all its neighbours $j$ are summed and added to region $i$’s trait value.

$$\frac{dX_i}{dt}_{\text{trade}} = \sigma_{\text{trade}} \sum_{j \in \mathcal{N}_i, f_{ij} > 0} f_{ij} \cdot (X_j - X_i)$$

(2)

The parameter $\sigma_{\text{trade}}$ needs to be estimated (see below); trade is not mass-conserving.

**Migration** is composed of immigration or emigration, depending on the sign of the diffusion flux $f$.

$$\frac{dP_i}{dt}_{\text{demic}} = \sigma_{\text{demic}} \sum_{j \in \mathcal{N}_i, f_{ij} > 0} f_{ij} P_j \frac{A_j}{A_i} - \sum_{j \in \mathcal{N}_i, f_{ij} < 0} f_{ij} P_i.$$  

(3)

The free parameter $\sigma_{\text{demic}}$ can be chosen to adjust the speed of migration (see below). Population is redistributed by scaling with region area $A$, thus, migration is mass-conserving.

**Hitchhiking traits:** Whenever people move in a demic process, they carry along their traits to the receiving region:

$$\frac{dX_i}{dt}_{\text{demic}} = \sigma_{\text{demic}} \sum_{j \in \mathcal{N}_i, f_{ij} > 0} f_{ij} X_j \frac{P_j A_j}{P_i A_i}.$$  

(4)

### 6.1. Spread parameter estimation

Suitable values for the spread parameters are assessed after all other model parameters have been fixed (for the equations and parameters not directly relevant to the demic/diffusive analysis, see the supporting online material provided as a supplement to Lemmen, Gronenborn, and Wirtz (2011)).

We initially assume that information travels two orders of magnitude faster than people, based on the typical size of exchange networks (1000 km, Mauvilly, Jeunesse, and Doppler (2008), Gronenborn (1999)), the average active life time of a tradesperson (order 10 years), and the comparison with the typical demic front speed of the order 1 km per year (Ammerman and Cavalli-Sforza (1973)). Starting with this fixed relation between $\sigma_{\text{trade}}$ and $\sigma_{\text{demic}}$, we vary both parameters such the we get the highest correlation with the dataset by Pinhasi, Fort, and Ammerman (2005) on European sites; with $\sigma_{\text{trade}} = 0.2$ and $\sigma_{\text{trade}} = 0.002$ the highest correlation achieved is $r^2 = 0.61$ ($n = 631$, $p < 0.01$). Analysis of the simulation confirms that this is a parameterisation that describes mixed diffusion (Lemmen, Gronenborn, and Wirtz (2011), their figure 6).

For a purely **demic diffusion** model, trade was switched off ($\sigma_{\text{trade}} = 0$) and $\sigma_{\text{demic}}$ was varied (systematically increased) to again obtain the best correlation with the data. The estimated parameter value is $\sigma_{\text{demic}} = 0.008$. The respective procedure was applied to estimate the parameter $\sigma_{\text{trade}}$ for a purely **cultural diffusion** best-fitting model; its value was determined to be 0.3.

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