LIVES
Swiss National Centre of Competence in Research

FNSNF
Swiss National Science Foundation

Hamberger, K. (2016)

Relational sequence networks as a tool for studying gendered mobility patterns

in G. Ritschard & M. Studer (eds), Proceedings of the International Conference on Sequence Analysis and Related Methods, Lausanne, June 8-10, 2016, pp 367-381.

UNIVERSITÉ DE GENÈVE

FONDATION POUR L'UNIVERSITÉ DE LAUSANNE

UNIVERSITÉ DE GENÈVE
GENEVA SCHOOL OF SOCIAL SCIENCES

UNIL | Université de Lausanne
Institut des sciences sociales

Relational sequence networks as a tool for studying gendered mobility patterns

Klaus Hamberger (Ecole de Hautes Etudes en Sciences Sociales, Paris, klaus.hamberger@ehess.fr)

Paper proposed for the 2nd International Conference on Sequence Analysis and Related Methods, Lausanne, June 8-10, 2016

Abstract

This paper uses relational sequence networks to study the gendered differences of migration biographies. Starting from an integrated model of kinship and migration relations as parts of a single bi-modal network of individuals and events, sequence networks are constructed by classifying mobility events according to the social (kinship or other) relation between the individuals they link together as migrants and hosts. Itineraries thus are conceived of as walks in a space of relational positions.

Using data from 508 migration biographies collected in rural South-east Togo between 2010-2015, we show that male and female trajectories do not so much differ in their degree of mobility as in the topology of the social spaces they traverse and in the structure of the social sequences they trace. While both rest on a basic kinship axis (linking an "internal" parent pole and an "external" extended-kinship pole), male networks tend to evolve through a succession of multiple but structurally isolated non-kinship links, whereas female networks develop into complex and integrated multifocal networks sewn together by marital and affinal ties. Since marital ties are precisely the ties that link male and female networks together, many of the differences between these networks can thus be traced back to their mutual relation (in particular to the fact that women move to and from men but not vice versa). Rather than just confirming the macro-tendencies for male and female mobility patterns stated in the demographic literature, sequence network analysis yields insight into the relational logics that bring these tendencies about.

Data have been analyzed with the open source software Puck 2.2., which implements the model presented in the paper.

Keywords: Social networks, Sequence networks, Gender, Migration, Kinship, West Africa

Extended abstract

Method

The recent applications of network theory to social sequence analysis (Bison 2014; Fitzhugh, Butts, and Pixley 2015; Cornwell et Watkins 2015; Cornwell 2015) have focused on the connections created between individuals through the sharing of similar events, similar sequence motifs or similar sequence network structures. However, events also directly link individuals in a face-to-face relation. The familiar two-mode network linking individuals and events is not just representing an affiliation network, but actually the incidence network where event nodes actually correspond to hyper-edges linking several individuals in complex, polyadic relations. Examples for this type of events are mobility events, where migrants are linked to hosts, co-migrants or financers, but also kinship events, where children are linked to mothers and fathers. In fact, we can conceive of kinship and mobility as two closely related and structurally similar subnetworks within an integrated social space-time made up of individuals and events (Hamberger and Sohler 2014):

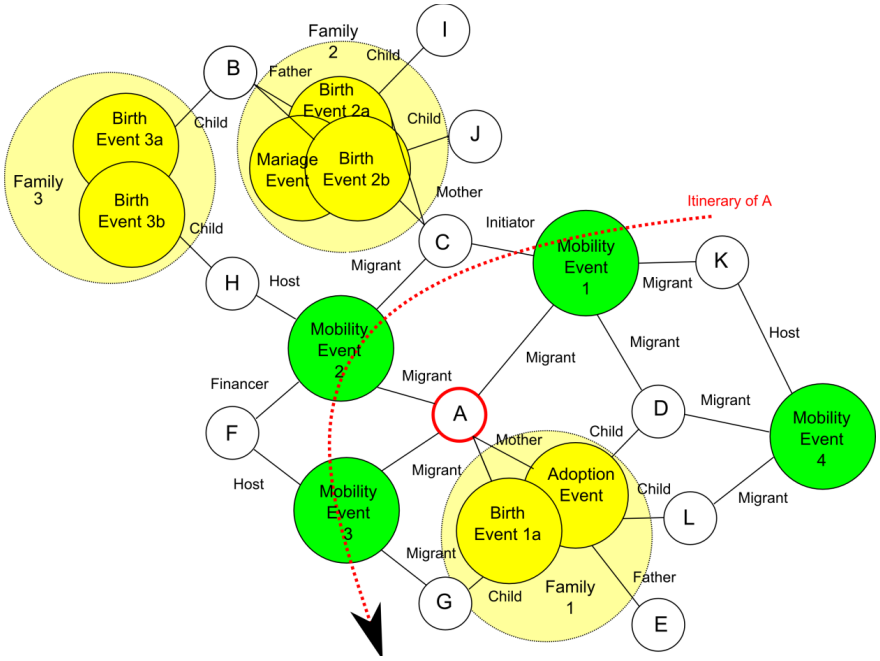

Figure 1: An integrated kinship-mobility network

From this integrated two-mode network are derived the one-mode networks usually studied in migration and life course studies: networks of events linked to each other by the involved individuals, and networks of individuals linked to each other by shared events. For a given individual (ego), we can thus derive both the event sequence that constitutes his or her itinerary, and the personal network that has shaped (or has been shaped by) this itinerary.

Individual itineraries are linear paths unless we merge events into higher-order event classes. This could be done by reference to some attribute (such as the reason for migration, the destination of the move, and so on). Adopting a thoroughly relational approach, we shall, however, derive all attributes characterizing individuals or events from the network itself: thus, individuals that make up ego's migration network will be characterized by the relational (kinship or other) chains that link them to

ego, and the events that constitute his or her itinerary will accordingly be characterized by the chains that link ego to the individuals that play a given role (such as host) in this event. More precisely, we shall characterize both individuals and events according to the type of *relational circuit* (Hamberger 2011) that emerge as the mobility link combines with chains of other links (kinship, friendship, employment, and so) – for example, individuals C and H in figure 1 are linked to each other both as migrant and host (via mobility event 2), but also as brother's wife and husband's sibling (via birth events 3a and 3b and the marriage event 2). As a consequence, mobility event 2 can be characterized as being of the "brother-in-law as host" type.

We will thus partition the ego-network according to the relational circuit types linking ego and alter, and then use the clusters of this partition to classify the events of ego's itinerary. Merging the event nodes of the same cluster then yields a directed network of social relation types linked by temporal adjacency: a relational sequence network.

The morphological similarity of these relational sequence networks (measured by the number of shared arcs rather than that of shared nodes) can then be used to construct a continuous typology of itineraries (represented e.g. by phylogenetic trees), but also to evaluate the extent to which the *similarity* of two given itineraries corresponds to their actual *intersection* in the total event network. Indeed, since one and the same event represents different relational types for the various individuals involved, people who have largely *shared* itineraries not necessarily have *similar* itineraries in relational terms, unless their positons in social space are structurally similar.

By considering the way degree to which ego's itinerary resembles and/or coincides with the itineraries of each of the alters of his or her personal network, we can finally study the way both the similarity and the contiguity between itineraries is related to certain relational positions. Thus, parents and children may have itineraries that are largely coincident but different, friend's itineraries may be similar but show little coincidence, and sibling's itineraries tend to be both similar and coincident, at least at the beginning. Relational sequence network analysis thus constitutes a tool of studying both the similarity and the contiguity relations that events establish between individuals, inasmuch as these relations can be conceived of as relations between sequence networks. In this capacity to analyze the perspectival structure of social space as a network of networks lies the (still largely unexplored) potential of relational sequence network analysis.

Software tools

All analyses used in this paper have been effectuated with the open source software Puck (Hamberger et al. 2014), which can be downloaded at www.kintip.net (source code at http://sourceforge.net/projects/tip-puck/). Initially developed for the study of kinship networks, Puck contains, from its 2.2 version onwards, a package for the study of spatiotemporal networks, including census data and migration biographies.

Visualization has been done with Pajek (Nooy, Mrvar, et Batagelj 2011) from files produced by Puck, and a variant of the software Geneaquilt (Bezerianos et al. 2010) implemented in Puck.

Data

In this paper we analyze the gendered patterns of West-African migration biographies, based on data collected in a field survey from 2010 to 2015 in rural South-east Togo. The zone of inquiry is located in the region of West Africa with the highest intra-regional migrations. The dataset includes extended genealogies and detailed migration biographies of 508 individuals (adults and children) that form part

of the personal networks of 60 inhabitants initially drawn at random from the 2005 population of the rural town Afagnan-Gbléta (about 4800 inhabitants in 2015).

Migration biographies were collected through retrospective semi-directive interviews. We recorded all migratory events leading to a change of residence for more than three months from birth to the present (time of the interview, last update of information in 2015). For each migratory event, the interviewees were asked to describe the context, motive and course of the event. In particular, we collected information (name, relation and contact) on the persons who received ego (*hosts*), accompanied ego (*co-migrants*), initiated the displacement (*initiators*) and financed the journey/means of transport (*financers*). All other persons mentioned in the context of the migration event were equally noted (*others*). This set of names was complemented by a complete list of the person's *parents*, *spouses* and *children*. This dataset is completed by a large genealogical and residential dataset (about 50.000 individuals including the deceased) collected during three subsequent censuses of the village of Afagnan-Gbléta (2005, 2010 and 2015). Most of the remote kinship relations (such as "father's mother's brother's daughter") and mediated non-kinship relations (such as "friend's employer") were thus not (only) directly reported by interviewees but computed from data stemming from numerous different oral sources. The anonymized dataset will be available on the platform www.kinsources.net, where two previous versions (2008 and 2011) can be already accessed.

Since the snowball method leads to the systematic overrepresentation of mobile and connected persons in the total network, most of our analyses are restricted to the initial random sample of 60 itineraries. We thus do use the remaining 448 itineraries to construct the ego-centered social spaces and sequence networks of these 60 independent cases. For the purpose of illustration, four of these cases are considered in more ethnographic detail.

Results

In order to construct the relational circuits that result by linking the participants of a mobility event by a chain of other (non-mobility) links, we have considered seven main types of relations: *genealogical kinship* (chains that can be retraced in the genealogical network), *non-genealogical kinship* (chains were some or all of the kinship links are not retrievable in the genealogy), *friendship*, *apprenticeship*, *initiation*, *employment* (employer-employee) and *rent* (landlord-lodger). Depending on the analysis, kinship relations have be further differentiated into various types of direct (parent, child, sibling, spouse) and remote (agnatic, uterine, cognatic, affinal) relations.

After a general analysis of the frequencies of each of these relation types in male and female itineraries, we consider their structural importance in the personal networks and the relational sequence networks.

Their structural role in ego's personal network is assessed indirectly by considering the relation type of the most central alters, as well as the relation types that dominate in each of the network's connected components. Figure 2 shows four example networks, where relation types are indicated by different colors, central alters have been marked by bold borders, connected components have been encircled.

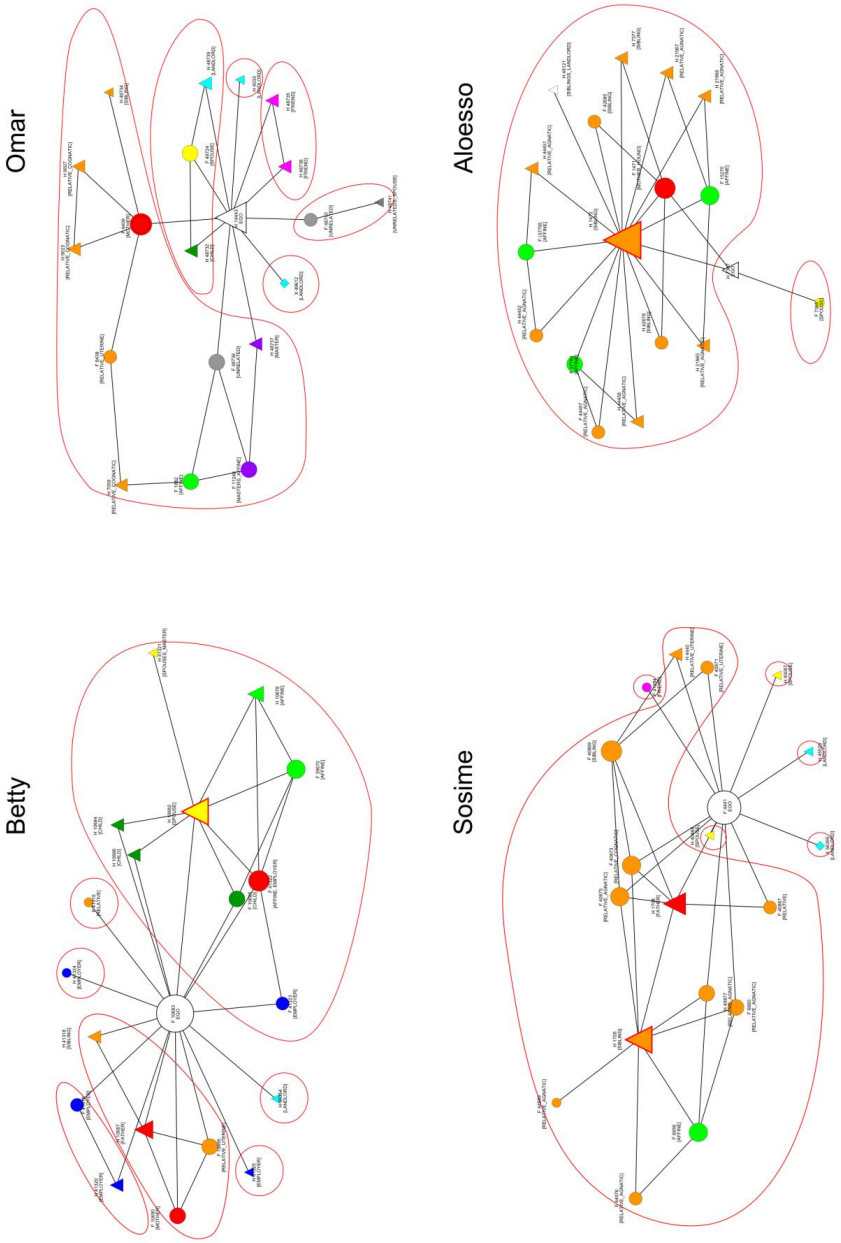

Figure 2: Four case examples – social networks with direct social relations (central alters are highlighted by bold borders, components are encircled). Color code (also valid for figures 5, 6, 7 and 9): red = parents, orange = relative, yellow = spouse, light green = affine, green = child, dark green = own property, grey = unrelated, light blue = rent, blue = public accommodation, marine blue = state, dark blue = employer, violet = master, rose = friend, light red = houno, black = death, white = unknown

A comparison of the 60 personal networks already reveals that relations of different types operate in a different way in organizing ego's social space. While parental ties function as centers and nuclei of large connected components, relations mediated by money tend to form numerous small peripheral components. Between these two extremes, whose co-presence is largely characteristic for the social space of men, we find the intermediary case of marriage relations, which, due to the high matrimonial mobility in this region, give rise to multiple cohesive components of moderate size and centrality which are typical for the social space of women. As a consequence, we find that on average, female networks are more cohesive than male networks, while at the same time, ego's own betweenness centrality is generally lower for women then for men.

After having examined in a synchronic manner the social environments shaped by (and shaping) people's itineraries, we turn to the relational sequence networks that are constructed by successively linking the relational types that characterize ego's relation to his or her host in the adjacent mobility events of his or her itinerary. Figure 3 shows these networks for the four example individuals. Each relational type is now represented by a node (colored according to the same code as the individual nodes in figure 2). We have not numbered the arcs, but each of the four itineraries starts at the position "south pole" of the network, since the "host" of the first "mobility event" (birth) is always the mother.

To visualize the individual and temporal structure of the sequence underlying the network, we have added to the right of each sequence graph the bimodal network of the corresponding individuals and events (ordered by age and time order) in the quilt format developed by Bezerianos et al. (2010). Individuals are listed on the vertical axis, events on the horizontal axis, and dots indicate the involvement of individuals in events. Ego's itinerary can easily be distinguished as a continuous horizontal line of dots.

Figure 4 represents the "aggregate" network that results from projecting all sequence networks of men and women respectively in a single network, where line values represent the numbers of individual itineraries in which a given event sequence occurs.

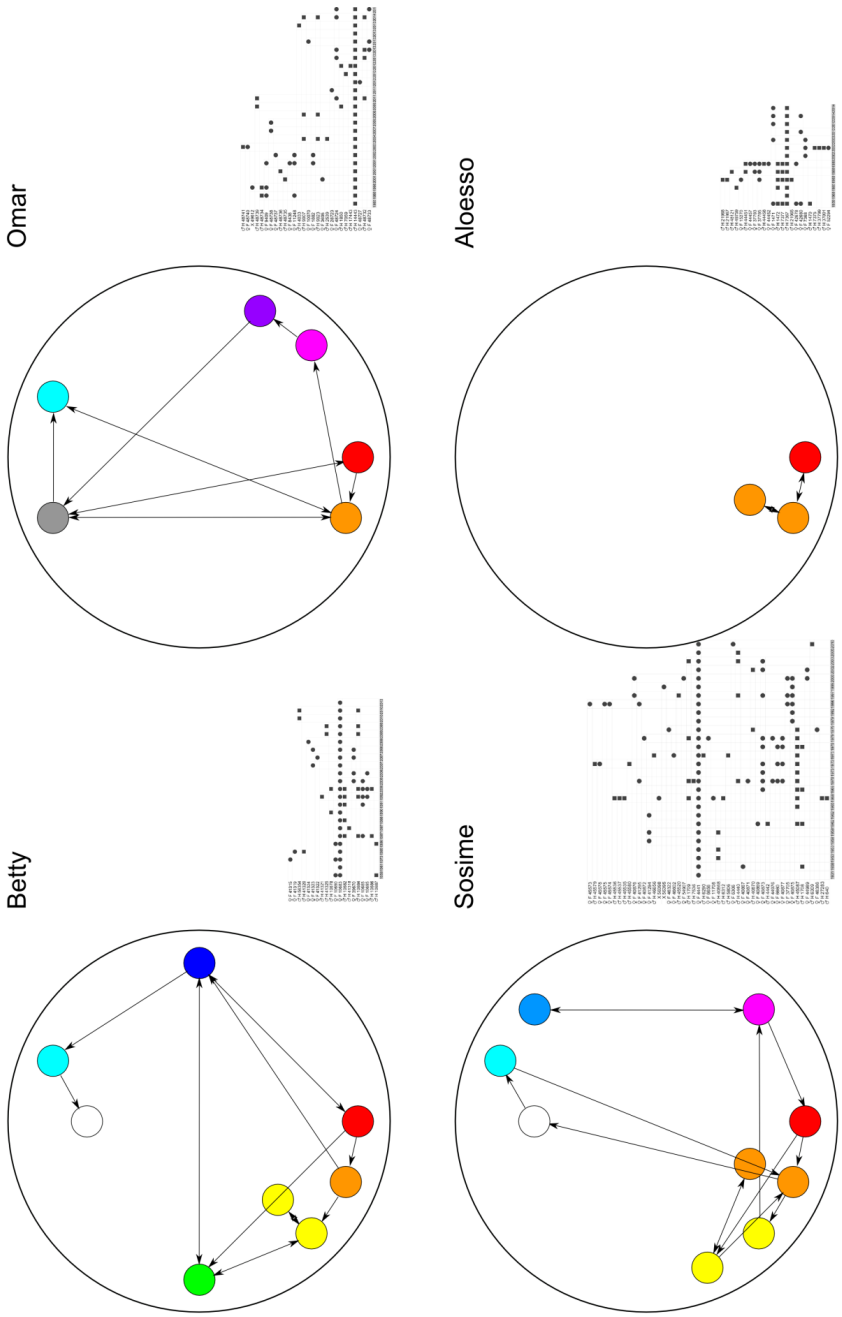

Figure 3: Four case examples - social sequence networks and individual-event networks (in quilt format)

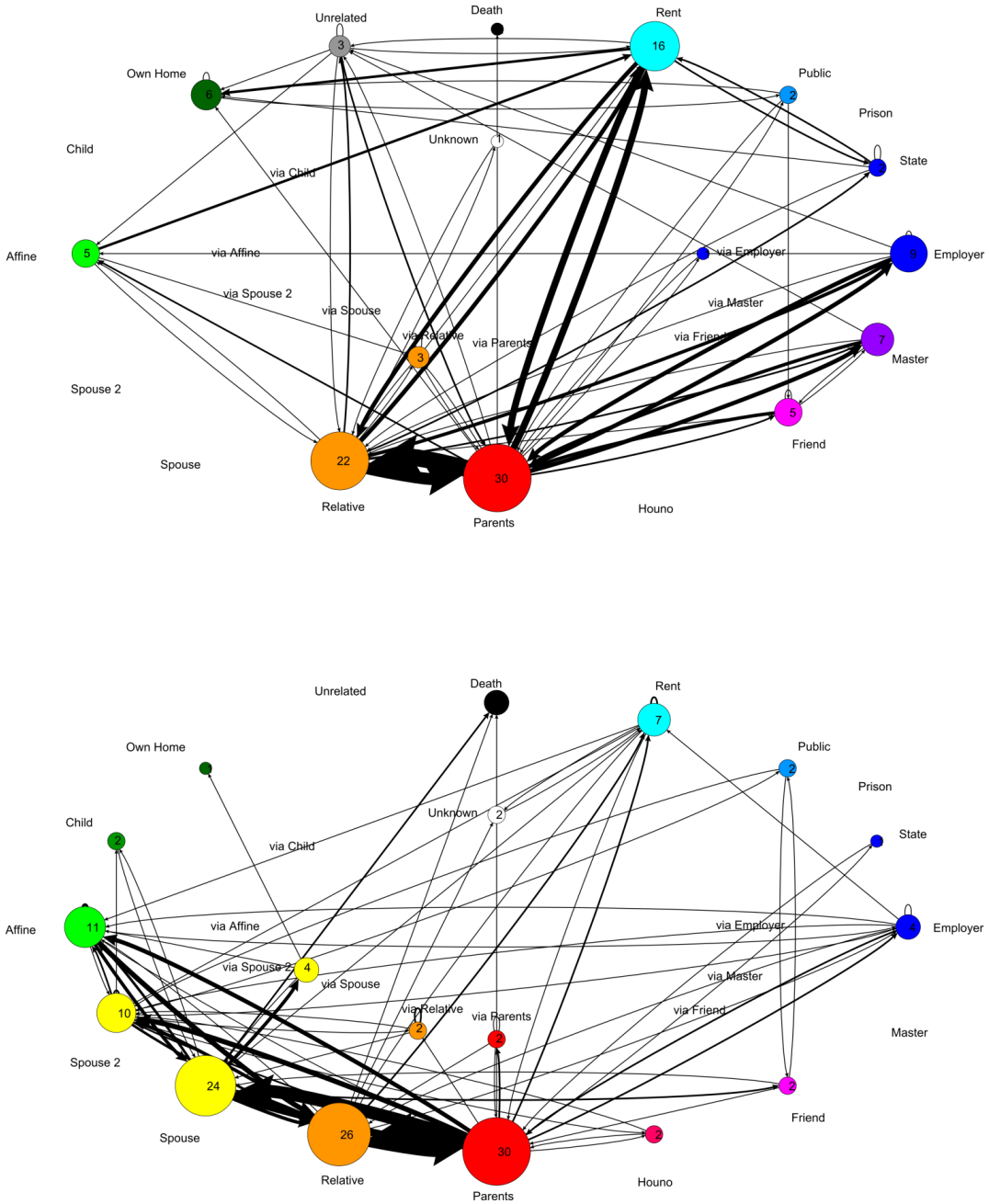

Figure 4: "Aggregate" sequence networks of men and women (initial random sample, n = 60)

As can be seen from fig. 4 as well as from a comparison of node degrees and arc frequencies in male and female aggregate networks, there are marked differences (but also some important similarities) between gendered mobility patterns in terms of social relations. Both male and female networks are centered around a fundamental axis linking parents and non-parental relatives. For both genders, relatives outside the immediate family circle are at least as important as parents in the role of hosts – with a slight preference of male and female for agnatic and uterine relatives, respectively. For women, they are even more important.

However, while men enter two times as frequently into relations with landlords than women, they are five times as frequently to pass from a stay with relatives to a rented apartment. The most significant difference is, of course, the importance of marital and affinal homes for female itineraries, which have no equivalent in their male counterparts. The virilocal orientation of residence is unambiguously brought out (almost all adult women have at least once moved to their husbands or affines, while the reverse is a small minority). While the male network is largely organized around a triangle formed by the parental home, relatives and the residential market, the female network contains in addition a spouse node, which may become the nucleus of an entire marital subnetwork.

The problem with this kind of comparative macro-analysis is, of course, that it already presupposes that gender is a pertinent classification criterion for merging individual sequence networks, instead of deriving the classification criteria from a comparative analysis on the micro-level of individual sequence networks.

This latter perspective characterizes the approach of optimal matching analysis (Abbott 1995) and its more recent network-analytic developments, where sequence matching is replaced by graph similarity (Butts et Pixley 2004; Butts 2008; Fitzhugh, Butts, et Pixley 2015). Since in our relational sequence networks each node type appears, by construction, exactly once in each network (the only quasi-exception being first and subsequent spouses, which we have treated as distinct types), edit distance between networks boils down to the number of differently connected pairs of nodes (that is, the number of different cells in the adjacency matrices of the two graphs, all of which have equivalent node sets). Based on this graph distance matrix, we use the neighbor-joining algorithm (Saitou et Nei 1987) to plot the similarities and differences of the itineraries in form of a phylogenetic tree. Figure 5 shows the tree of the 60 individuals of the initial random sample, where the corresponding individual sequence networks have been plotted into the nodes, and border colors indicate gender (blue for male and red for female).

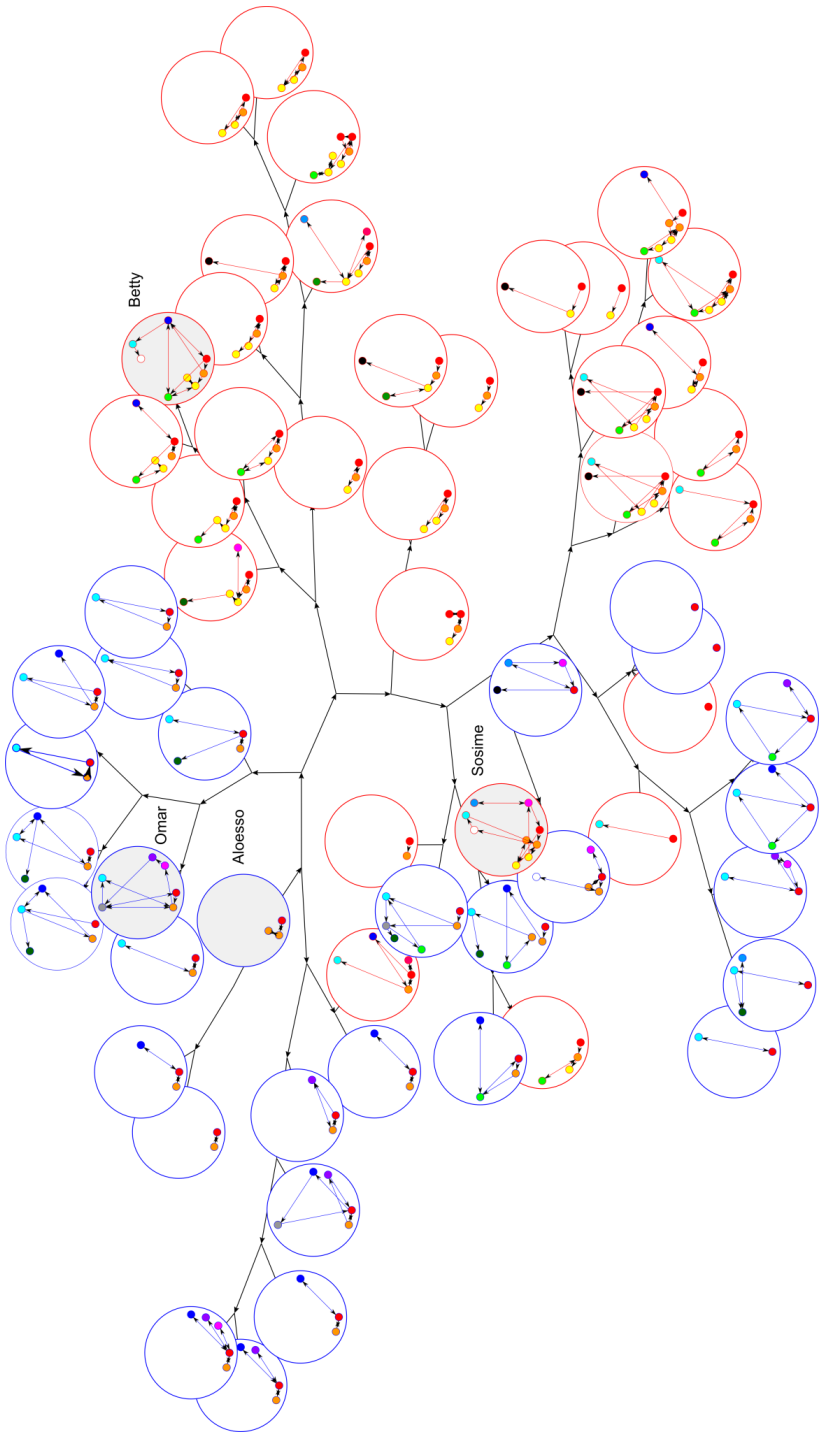

Figure 5: Phylogenetic tree of 60 sequence networks (random seed sample)

While the gender difference is neatly brought out by the graph (roughly speaking, female itineraries constitute the right, male itineraries the left side, with a "mixed" zone of complex itineraries in the middle), a closer look shows that, beyond the great divide introduced by virilocality (the presence of absence of "yellow" marital nodes in the sequence network), both male and female itineraries are differentiated into several branches of the tree.

Apart from the three single-node cases in the middle bottom, the most simple sequence networks, consisting mainly of the parent-relative axis, are located in the upper left, "male" part of the tree. This branch may develop into two more complex forms, as the basic axis combines either with rent (as for the urban migrant workers) or with hosting by the master or employer (as for the rural itinerary masons or woodcutters). A still more complex variant combines rent with lodging by the state, which is the characteristic feature of teachers' itineraries. A quite different version of typically male itineraries is given at the bottom, where the parental node is directly linked to the rent node without passing through a relative's home. This minority pattern is reserved to men who have migrated for professional reasons later in life, and to the few boys whose parents could afford paying them rented apartments for school.

On the "female" side, we find a large group of highly similar sequences completing the parent-relative-axis by one or more marital or affinal nodes, thus giving rise to several distinct groups according to the complexity of the marital subnetwork. This pattern may further evolve by integrating stays with landlords or with employers (mainly for domestic work). By contrast, we almost never find a female pattern without the "relative" node it. Women who leave their parental home directly for a rented apartment are even more rare then men.

The complex patterns in the "mixed" middle of the figure combine "male" and "female" features, such as young men staying with affines (e.g. sisters' husbands) or women leaving for transnational migration with friends.

While the tree of fig. 5 has been constructed from 60 independently drawn examples, the (dis)similarities between individuals' mobility patterns are generally not independent of their mutual interconnections. Indeed, both the similarities and the interconnections between itineraries may be related to their respective roles in the mobility events linking them, as well as to the (kinship or other) relation existing between them, in other words: to the type of relational circuit(s) which ties them together. The logic of these interdependencies is still largely unexplored. We can, however, get an idea of them by linking the individuals that make up a given ego's personal network according to the similarity and intersection of their respective relational sequence networks.

Figures 6 and 7 do so for the four example networks. In figure 6, arc thickness indicates to the degree of intersection of itineraries (measured as the percentage of events which one individual shares with the other). In figure 7, edge thickness indicates the degree of similarity between itineraries (measured as the number equivalently linked or non-linked node-pairs in the respective event sequence networks, normalized by the maximal number of pairs that can occur in either network).

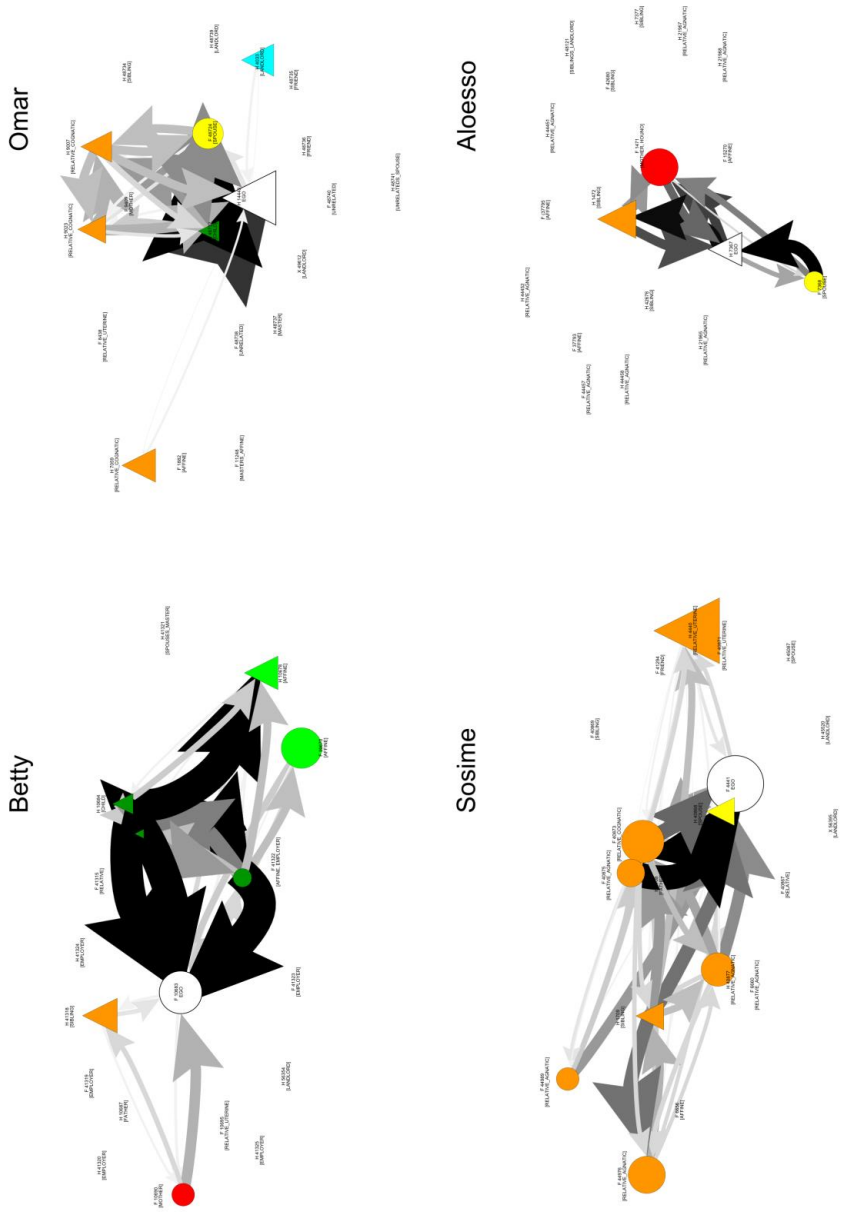

Figure 6: Four case examples – social networks with arc thickness indicating itinerary intersection rates

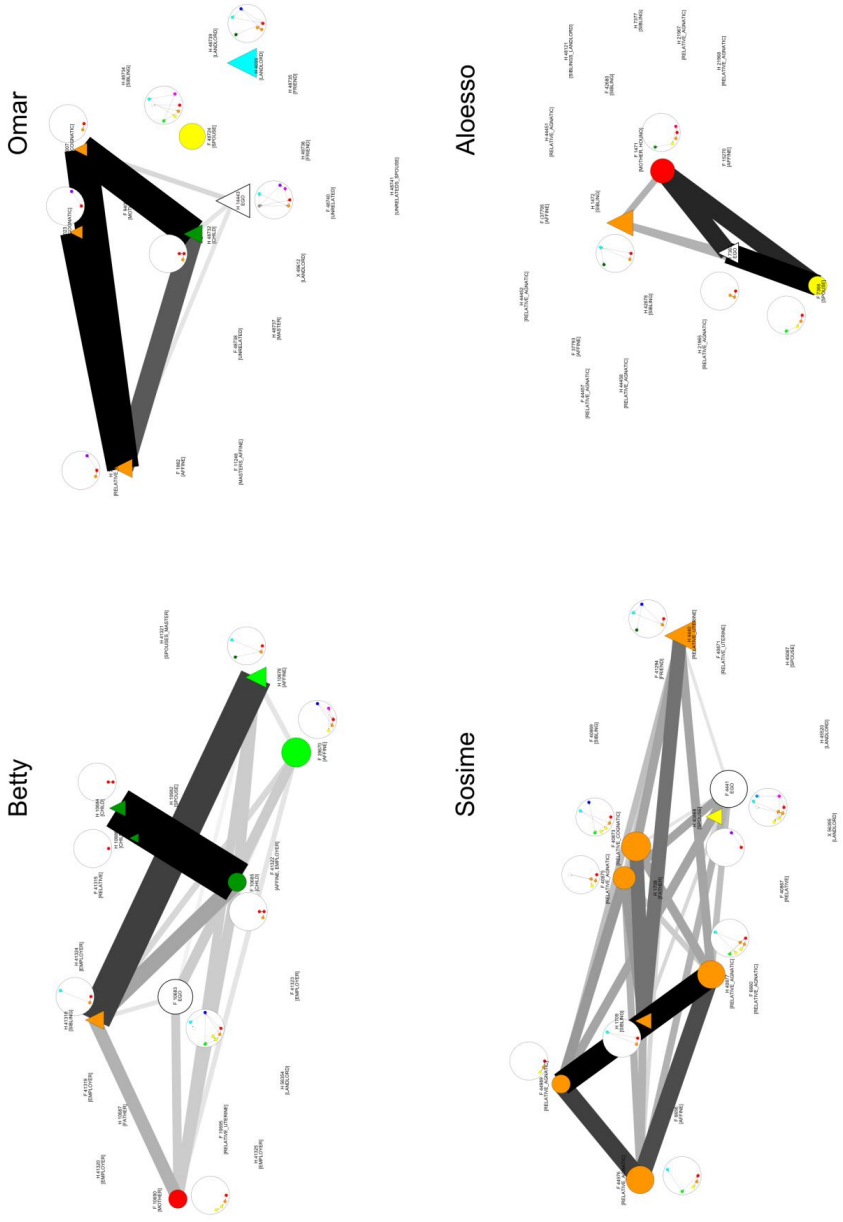

Figure 7: Four case examples – social networks with line thickness indicating itinerary similarity degrees

As one can see, similarity and contiguity structures are as a rule quite different from each other. Thus, the two important male persons in Betty's network – her brother and her father-in-law – have similar itineraries, though they never intersect. To the contrary, the itineraries of Omar and his wife, though overlapping, show no similarity with each other. For itineraries to be both overlapping and similar, it is required that both egos either hold a structurally equivalent position in social space – such as siblings – or have very reduced itineraries – such as children.

The fact that both the intersections and the similarities between two individuals' relational sequence networks are rooted in their mutual relation invites us to reconsider the results of our analysis with a view to a relational conception of the gender difference. Our results show that the topology of both male and female sequence networks rests on a basic kinship axis (linking an "internal" parent pole and an "external" extended-kinship pole). However, while male networks tend to evolve through a succession of multiple but structurally isolated non-kinship links, female networks develop into complex and integrated multifocal networks sewn together by marital and affinal ties. Now, the marital tie is precisely the tie that puts together male and female itineraries. In other words, the central source of difference between the sequence networks of men and women is precisely the relation between them.

Rather than just confirming the macro-tendencies for male and female mobility patterns (as stated in the demographic literature) at the micro-level of individual trajectories, sequence network analysis yields insight into the relational logics that bring these tendencies about. It serves not only to study the differences between gendered social networks, but also to understand the gender relation itself as a relation between networks, that is, not just as an attribute of individuals, but as a structural trait of social space-time. In a more general perspective, the beginning integration of network and sequence analysis may be the first step towards a full-fledged social topology.

Acknowledgements

The paper is part of a larger research conducted since 2009 together with Karin Sohler. Preliminary results have been presented in common presentations at the 1st European conference of Social Network Analysis in Barcelona in 2014 and at the 3rd meeting Réseaux-Histoire in Paris in 2015. Though Karin did not coauthor this (essentially methodological) paper, it remains fundamentally indebted to our cooperative work. I am also grateful to Véronique Hertrich, Ismaël Moya, Sorana Toma and Claire Lemercier for their valuable and encouraging comments and suggestions.

Fieldwork has been supported by the Laboratoire d'Anthropologie Sociale, the EHESS research fund and the Coopération Française au Togo. The 2010/11 fieldwork was carried out in cooperation with Ibitola Tchitou and Kokou Vignikin from the Unité de Recherche Démographique of Lomé University. This work would have been impossible without the competence and dedication of my field collaborators Komi Malou Kakanou and Toussaint Yakobi.

The sequence-network module of Puck has been developed in cooperation with Christian Momon as part of the project "Kinsources" supported by the French National Research Agency ANR (research grant ANR-CORPUS-KINSOURCES).

References

Abbott, Andrew. 1995. « Sequence Analysis: New Methods for Old Ideas ». *Annual Review of*

Sociology 21 (1): 93‑113.

Bezerianos, Anastasia, Pierre Dragicevic, Jean-Daniel Fekete, Juhee Bae, et Ben Watson. 2010. « GeneaQuilts: A System for Exploring Large Genealogies ». *IEEE Transactions on Visualization and Computer Graphics, Institute of Electrical and Electronics Engineers (IEEE)*, 16 (6): 1073‑81.

Bison, Ivano. 2014. « Sequence as network: an attempt to apply network analysis to sequence analysis ». In *Advances in sequence analysis : theory, method, applications*, édité par Philippe Blanchard, Felix Bühlmann, et Jacques-Antoine Gauthier, 231‑48. Cham: Springer.

Butts, Carter T. 2008. « A Relational Event Framework for Social Action ». *Sociological Methodology* 38 (1): 155‑200.

Butts, Carter T., and Joy E. Pixley. 2004. « A Structural Approach to the Representation of Life History Data ». *The Journal of Mathematical Sociology* 28 (2): 81‑124.

Cornwell, Benjamin. 2015. *Social Sequence Analysis: Methods and Applications*. Cambridge: Cambridge University Press.

Cornwell, Benjamin, and Kate Watkins. 2015. « Sequence-Network Analysis: A New Framework for Studying Action in Groups ». In *Advances in Group Processes*, 32:31‑63. Advances in Group Processes 32. Emerald Group Publishing Limited.

Fitzhugh, Sean M., Carter T. Butts, and Joy E. Pixley. 2015. « A life history graph approach to the analysis and comparison of life histories ». *Advances in Life Course Research* 25 (septembre): 16‑34.

Hamberger, Klaus. 2011. « Matrimonial circuits in kinship networks: Calculation, enumeration and census ». *Social Networks* 33 (2): 113‑28.

Hamberger, Klaus, Cyril Grange, Michael Houseman, et Christian Momon. 2014. « Scanning for patterns of relationship: analyzing kinship and marriage networks with Puck 2.0 ». *The History of the Family* 19 (4): 564‑96.

Hamberger, Klaus, and Karin Sohler. 2014. « Integrated kinship-mobility networks. A West African case study ». Paper presented at the 1st European Conference on Social Networks, Barcelona (UAB).

Nooy, Wouter de, Andrej Mrvar, and Vladimir Batagelj. 2011. *Exploratory social network analysis with Pajek*. Royaume-Uni, Royaume-Uni de Grande-Bretagne et d'Irlande du Nord: Cambridge University Press.

Saitou, N., and M. Nei. 1987. « The Neighbor-Joining Method: A New Method for Reconstructing Phylogenetic Trees ». *Molecular Biology and Evolution* 4 (4): 406‑25.