Supplementary Materials to

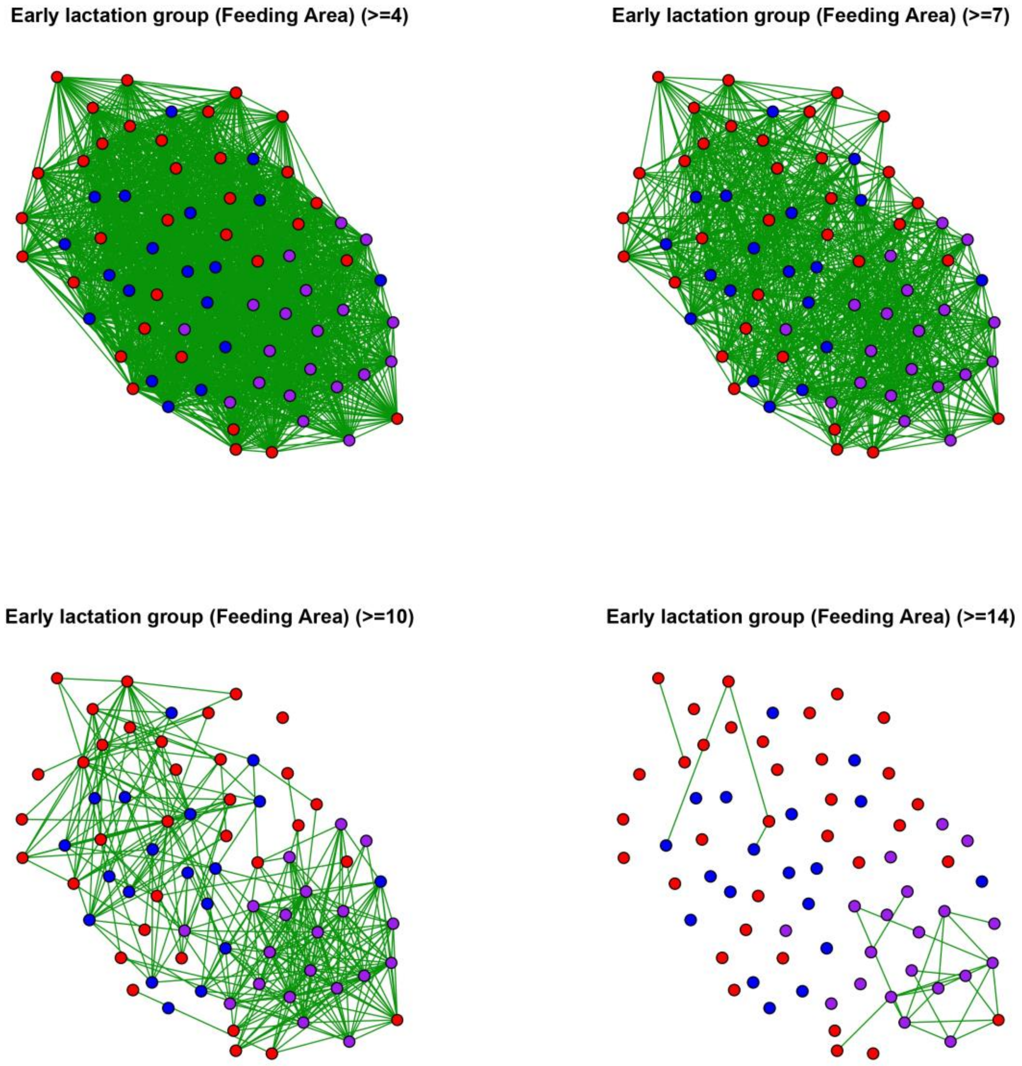
New insight into social relationships in dairy cows, and how time of birth, parity and relatedness affect spatial interactions later in life. *Journal of Dairy Science*

H. Marina,[1*] K. Ren,[1] I. Hansson,[1] F. Fikse, [2] P. P. Nielsen, [3] and L. Rönnegård[1,4,5]

[1] Department of Animal Breeding and Genetics, Swedish University of Agricultural Sciences, Box 7023, SE-750 07 Uppsala, Sweden.
[2] Växa, Swedish University of Agricultural Sciences, Ulls väg 26, SE-756 51 Uppsala, Sweden.
[3] RISE Research Institute of Sweden, Division of Bioeconomy and Health, Department of Agriculture and Food, RISE Ideon, SE-223 70 Lund, Sweden.
[4] School of Technology and Business Studies, Dalarna University, SE-791 88 Falun, Sweden.
[5] The Beijer Laboratory for Animal Science, Swedish University of Agricultural Sciences, Box 7024, SE-750 07 Uppsala, Sweden

[*]Corresponding author: hector.marina@slu.se

Supplemental Figure S1 (A). The sociograms represent the cumulative number of contacts during the 14 days of the study within the feeding (green edges) and resting (blue edges) areas for the early and late lactation groups filtered by different thresholds (whether the cumulative number of contacts was four, seven, ten, and fourteen days). The colors of the nodes represent the parity number: red (1), blue (2) and purple (3+).



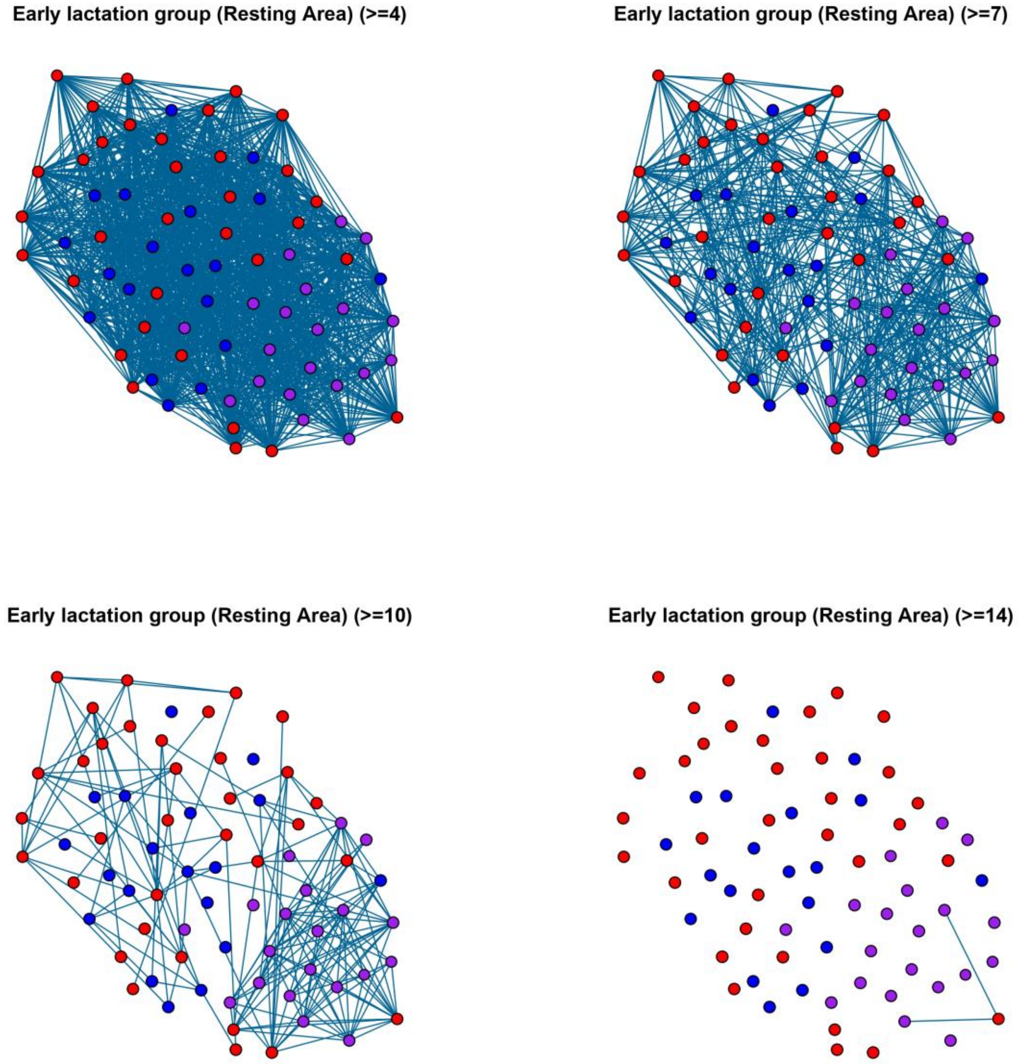
Early lactation group (Feeding Area) (>=4)

Early lactation group (Feeding Area) (>=7)

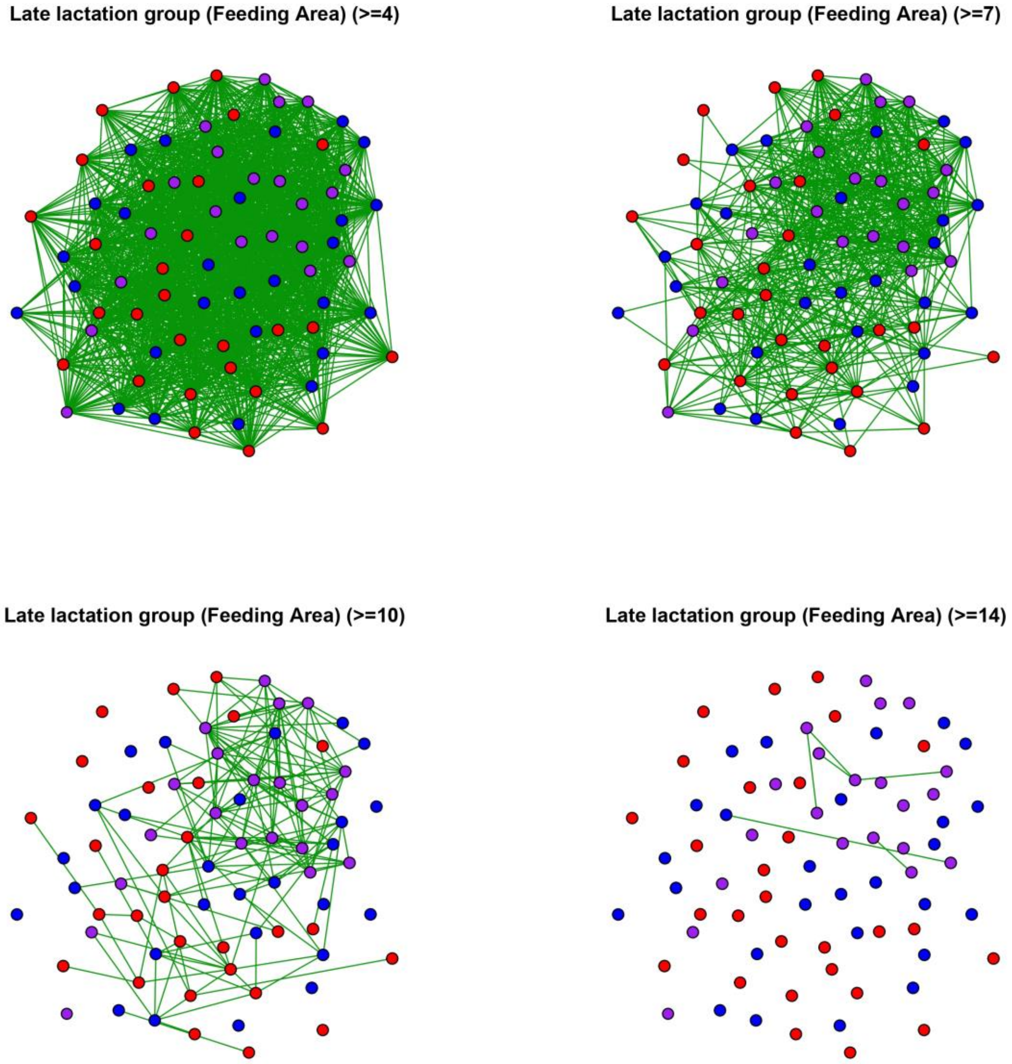
Early lactation group (Feeding Area) (>=10)

Early lactation group (Feeding Area) (>=14)

Supplemental Figure S1 (B). The sociograms represent the cumulative number of contacts during the 14 days of the study within the feeding (green edges) and resting (blue edges) areas for the early and late lactation groups filtered by different thresholds (whether the cumulative number of contacts was four, seven, ten, and fourteen days). The colors of the nodes represent the parity number: red (1), blue (2) and purple (3+).



Supplemental Figure S1 (C). The sociograms represent the cumulative number of contacts during the 14 days of the study within the feeding (green edges) and resting (blue edges) areas for the early and late lactation groups filtered by different thresholds (whether the cumulative number of contacts was four, seven, ten, and fourteen days). The colors of the nodes represent the parity number: red (1), blue (2) and purple (3+).



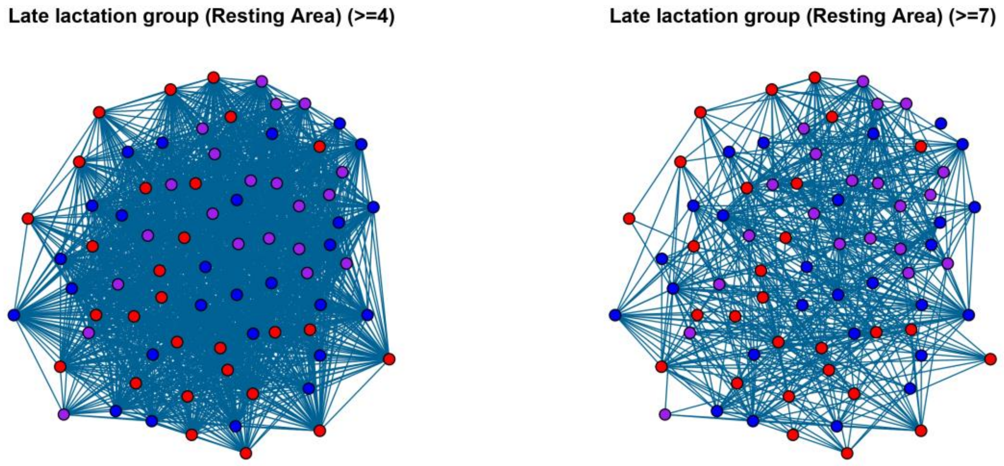
Late lactation group (Feeding Area) (>=4)

Late lactation group (Feeding Area) (>=7)

Late lactation group (Feeding Area) (>=10)

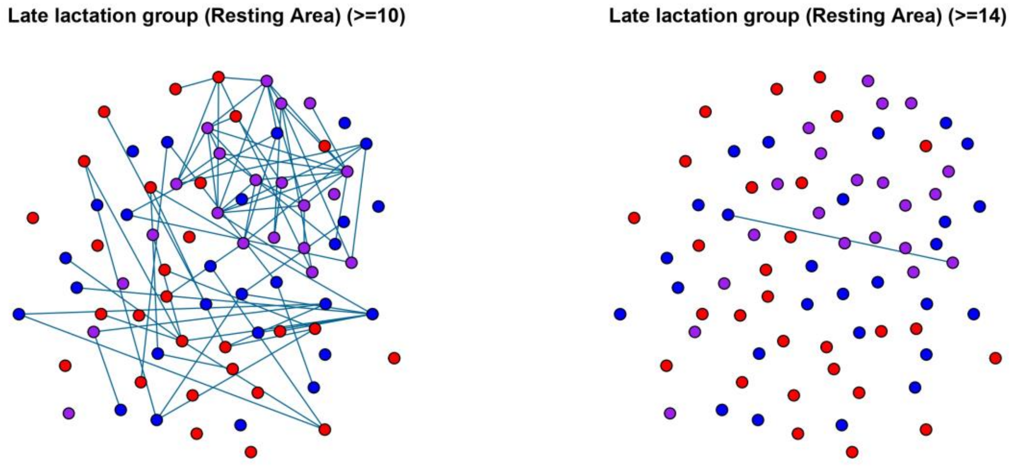
Late lactation group (Feeding Area) (>=14)

Supplemental Figure S1 (D). The sociograms represent the cumulative number of contacts during the 14 days of the study within the feeding (green edges) and resting (blue edges) areas for the early and late lactation groups filtered by different thresholds (whether the cumulative number of contacts was four, seven, ten, and fourteen days). The colors of the nodes represent the parity number: red (1), blue (2) and purple (3+).



Late lactation group (Resting Area) (>=4)

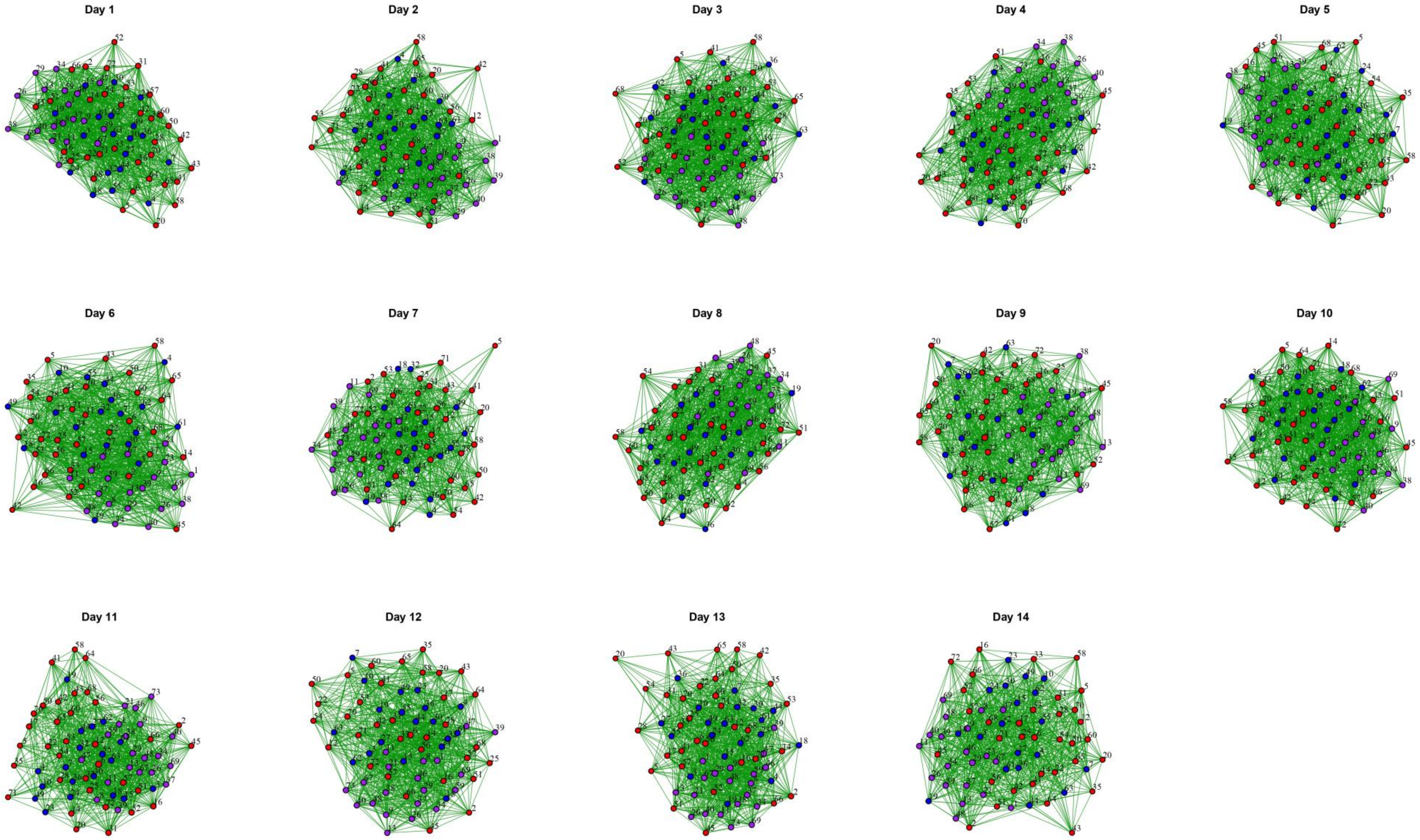
Late lactation group (Resting Area) (>=7)



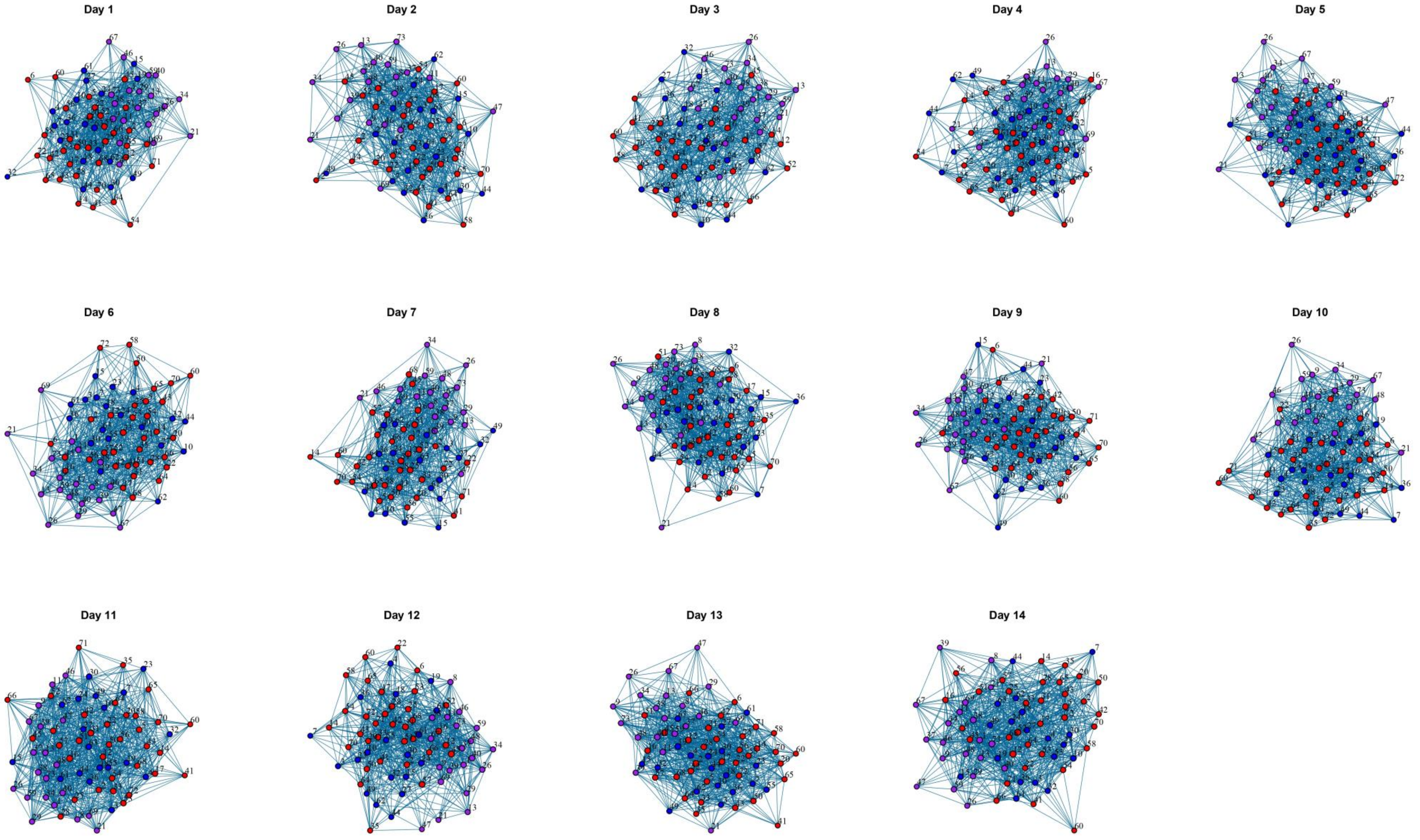
Late lactation group (Resting Area) (>=10)

Late lactation group (Resting Area) (>=14)

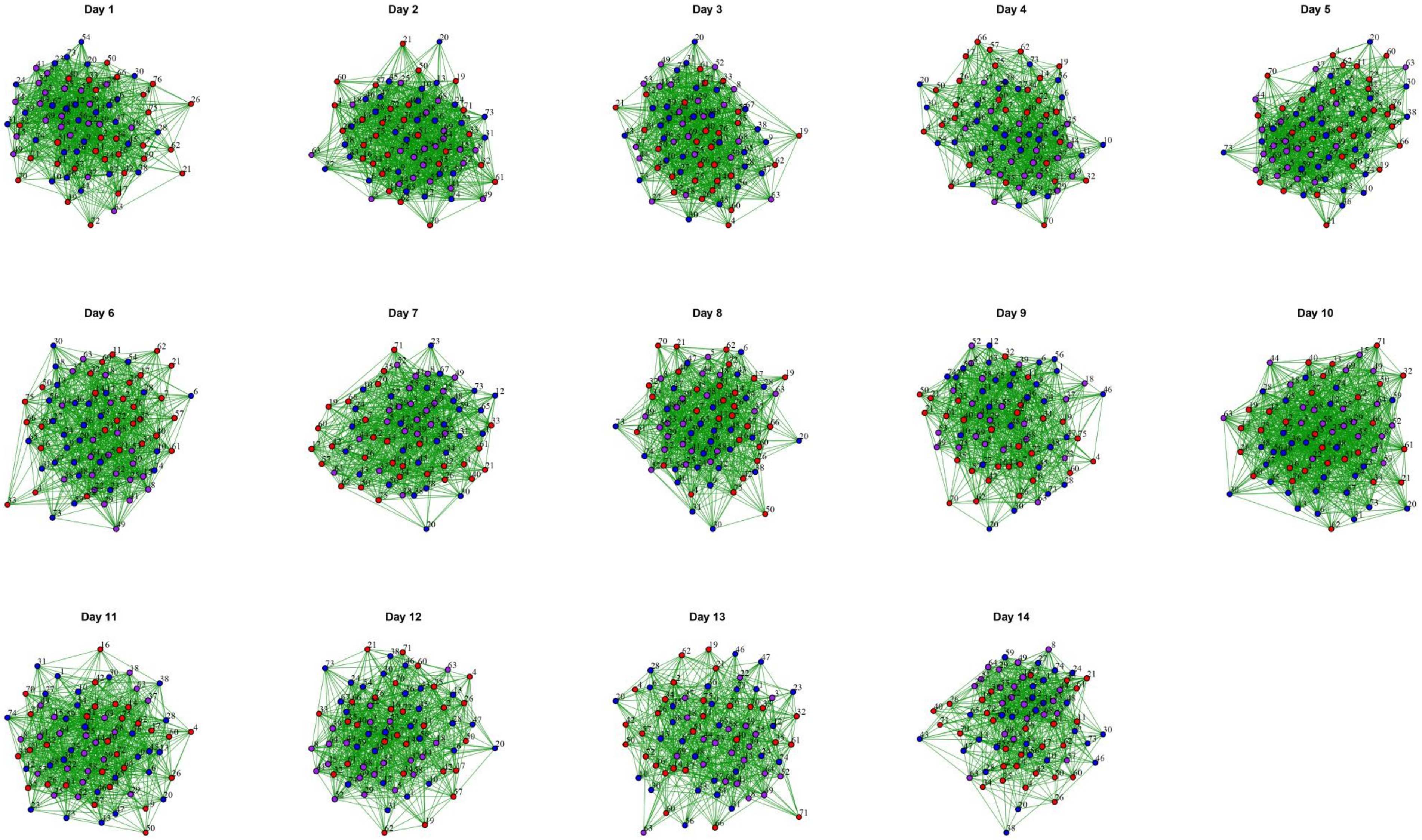
Supplemental Figure S2. Graphical representation of the changes in the sociograms throughout the 14 days considered in this study in the feeding area for the early lactation group. The nodes represent each dairy cow considered in the study and the bars represent whether the nodes have been in contact or not. The colors of the nodes represent the parity number: red (1), blue (2) and purple (3+).



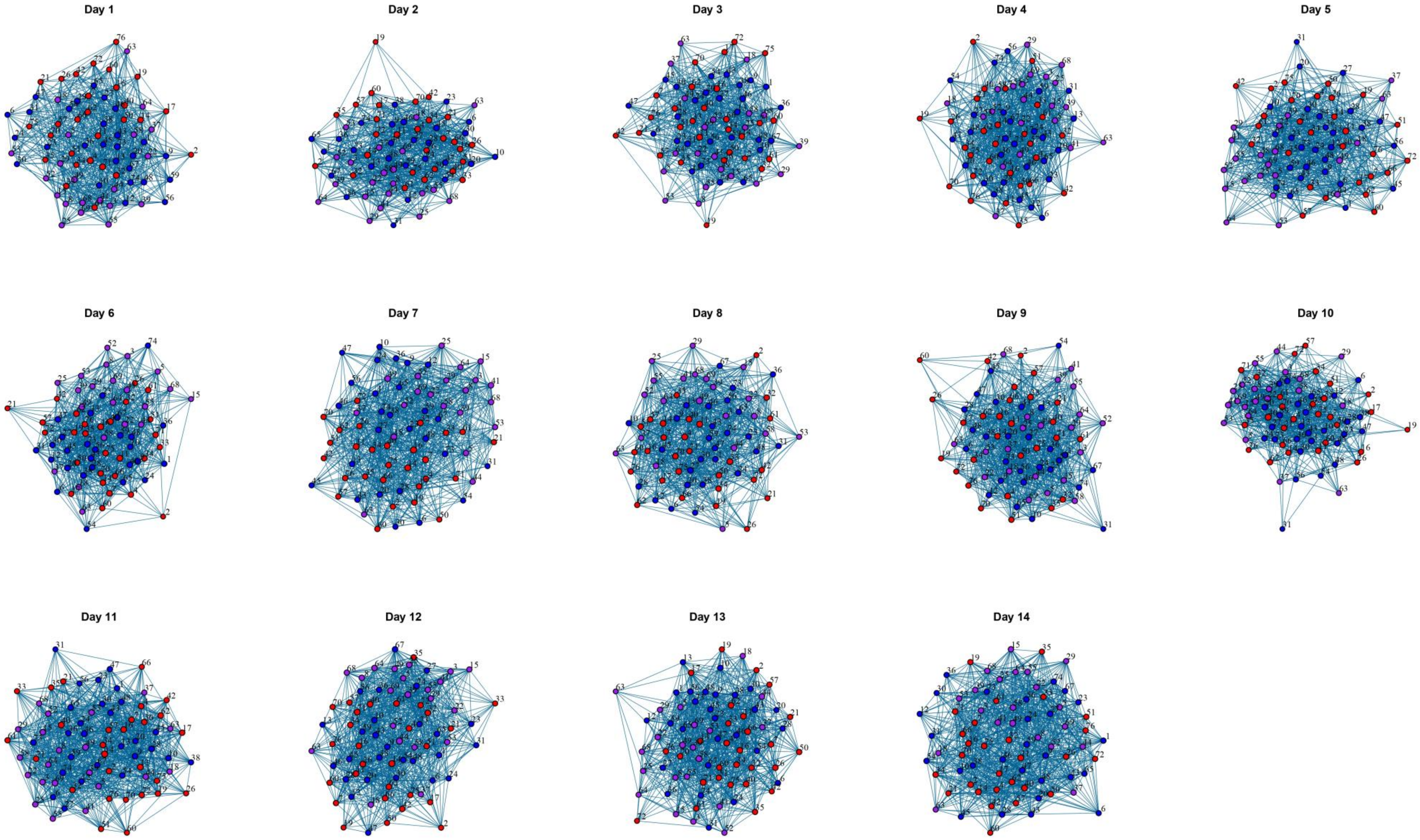
Supplemental Figure S3. Graphical representation of the changes in the sociograms throughout the 14 days considered in this study in the resting area for the early lactation group. The nodes represent each dairy cow considered in the study and the bars represent whether the nodes have been in contact or not. The colors of the nodes represent the parity number: red (1), blue (2) and purple (3+).



Supplemental Figure S4. Graphical representation of the changes in the sociograms throughout the 14 days considered in this study in the feeding area for the late lactation group. The nodes represent each dairy cow considered in the study and the bars represent whether the nodes have been in contact or not. The colors of the nodes represent the parity number: red (1), blue (2) and purple (3+).



Supplemental Figure S5. Graphical representation of the changes in the sociograms throughout the 14 days considered in this study in the resting area for the late lactation group. The nodes represent each dairy cow considered in the study and the bars represent whether the nodes have been in contact or not. The colors of the nodes represent the parity number: red (1), blue (2) and purple (3+).



Day 1

Day 2

Day 3

Day 4

Day 5

Day 6

Day 7

Day 8

Day 9

Day 10

Day 11

Day 12

Day 13

Day 14

Supplemental Table S1. Variance inflation factor results of the complete and filtered models for early and late lactation groups of dairy cows.

	Early lactation group		**Late lactation group**	
	First model	**Second model**	**First model**	**Second model**
Age	1.95	-	2.27	-
Breed	1.10	1.06	1.11	1.09
Claw health	1.04	1.02	1.11	1.10
DIM	2.18	-	1.50	-
Lactation stage	1.47	1.15	1.43	1.11
Parity	1.40	1.11	1.57	1.12
Pregnant	1.28	1.17	1.14	1.09
Time in area	1.23	1.16	1.22	1.12

Supplemental Table S2. Formation and persistence estimates obtained through the STERGM implementation considering different time thresholds for the feeding area (10, 20 and 30 minutes) and for the resting area (10, 20, 30 and 60 minutes).

		Early lactation group							Late lactation group						
		Feeding area			Resting area				Feeding area			Resting area			
		10 minutes	20 minutes	30 minutes	10 minutes	20 minutes	30 minutes	60 minutes	10 minutes	20 minutes	30 minutes	10 minutes	20 minutes	30 minutes	60 minutes
Formation	edges	-1.43 (0.20)***	-2.89 (0.22)***	-4.65 (0.28)***	0.33 (0.20)	0.28 (0.21)	0.26 (0.22)	0.34 (0.26)	-2.82 (0.17)***	-4.56 (0.20)***	-6.26 (0.29)***	-0.51 (0.16)**	-0.39 (0.17)*	-0.35 (0.17)*	-0.64 (0.21)**
	factor(Parity: 2)	0.14 (0.03)***	-0.06 (0.03)	-0.18 (0.04)***	0.20 (0.03)***	0.17 (0.03)***	0.14 (0.03)***	0.06 (0.04)	-0.05 (0.03)	-0.08 (0.03)*	-0.13 (0.05)**	0.02 (0.03)	-0.02 (0.03)	-0.05 (0.03)	-0.04 (0.04)
	factor(Parity: 3+)	-0.17 (0.04)***	-0.31 (0.04)***	-0.44 (0.04)***	0.06 (0.03)	0.01 (0.03)	-0.02 (0.03)	-0.11 (0.04)**	-0.03 (0.03)	-0.03 (0.03)	-0.04 (0.05)	0.01 (0.03)	-0.02 (0.03)	-0.03 (0.03)	-0.01 (0.04)
	match(Parity)	0.41 (0.04)***	0.51 (0.04)***	0.59 (0.04)***	0.51 (0.03)***	0.53 (0.03)***	0.58 (0.04)***	0.58 (0.04)***	0.18 (0.03)***	0.29 (0.04)***	0.41 (0.05)***	0.13 (0.03)***	0.17 (0.03)***	0.19 (0.03)***	0.21 (0.04)***
	factor(Pregnancy status: Pregnant)	0.07 (0.06)	0.19 (0.06)**	0.47 (0.08)***	-0.22 (0.06)***	-0.13 (0.06)*	-0.10 (0.06)	-0.08 (0.08)	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
	match(Pregnancy status)	-0.07 (0.04)	0.03 (0.04)	0.17 (0.05)**	-0.07 (0.04)	-0.03 (0.04)	0.00 (0.04)	0.03 (0.05)	0.09 (0.04)*	0.19 (0.04)***	0.28 (0.06)***	0.01 (0.04)	0.01 (0.04)	-0.03 (0.04)	0.02 (0.05)
	factor(DIM: Late)	-0.00 (0.04)	0.02 (0.05)	0.17 (0.06)**	0.02 (0.04)	0.06 (0.04)	0.05 (0.05)	0.01 (0.06)	0.01 (0.05)	0.06 (0.05)	0.23 (0.07)***	0.05 (0.04)	0.04 (0.05)	0.03 (0.05)	0.08 (0.06)
	factor(DIM: Middle)	0.06 (0.03)*	0.05 (0.03)	-0.02 (0.03)	-0.06 (0.03)*	-0.11 (0.03)***	-0.11 (0.03)***	-0.15 (0.03)***	0.10 (0.04)**	0.07 (0.05)	0.11 (0.07)	0.12 (0.04)**	0.09 (0.04)*	0.09 (0.04)*	0.07 (0.05)
	match(DIM)	0.04 (0.03)	0.07 (0.03)*	0.04 (0.04)	-0.03 (0.03)	-0.04 (0.03)	-0.02 (0.03)	0.00 (0.04)	-0.02 (0.04)	0.10 (0.06)	0.19 (0.08)*	-0.04 (0.04)	-0.00 (0.04)	-0.02 (0.05)	0.04 (0.06)
	factor(Breed: Holstein)	-0.05 (0.03)	-0.04 (0.03)	-0.11 (0.04)**	0.03 (0.03)	0.01 (0.03)	-0.01 (0.03)	0.03 (0.04)	-0.06 (0.03)*	-0.05 (0.04)	-0.02 (0.05)	-0.07 (0.03)*	-0.06 (0.03)*	-0.05 (0.03)	0.04 (0.04)
	factor(Breed: Red dairy cattle)	0.02 (0.03)	-0.02 (0.03)	-0.11 (0.04)**	-0.05 (0.03)	-0.06 (0.03)	-0.06 (0.03)	-0.06 (0.04)	-0.25 (0.03)***	-0.25 (0.03)***	-0.19 (0.05)***	-0.04 (0.03)	-0.05 (0.03)	-0.04 (0.03)	0.00 (0.04)
	match(Breed)	0.09 (0.03)**	0.07 (0.04)*	0.04 (0.05)	0.05 (0.03)	0.04 (0.03)	0.05 (0.04)	0.03 (0.04)	-0.03 (0.03)	-0.05 (0.04)	-0.10 (0.06)	-0.03 (0.03)	-0.06 (0.03)	-0.03 (0.04)	0.04 (0.04)
	factor(Claw health: Remark)	0.06 (0.03)	-0.01 (0.03)	0.02 (0.04)	-0.05 (0.03)	-0.05 (0.03)	-0.03 (0.03)	-0.08 (0.04)	-0.04 (0.03)	0.08 (0.03)*	0.19 (0.04)***	-0.10 (0.03)***	-0.12 (0.03)***	-0.17 (0.03)***	-0.18 (0.04)***
	match(Claw health)	0.04 (0.04)	0.05 (0.04)	0.08 (0.05)	0.03 (0.04)	0.02 (0.04)	0.09 (0.04)*	0.04 (0.05)	0.02 (0.03)	0.04 (0.04)	0.11 (0.05)*	0.06 (0.03)*	0.03 (0.03)	-0.00 (0.04)	0.01 (0.05)
	covariable(Time in area)	0.71 (0.17)***	1.48 (0.18)***	2.51 (0.23)***	-1.83 (0.17)***	-2.08 (0.18)***	-2.44 (0.19)***	-3.13 (0.23)***	2.33 (0.16)***	2.91 (0.19)***	3.25 (0.27)***	-0.82 (0.15)***	-1.21 (0.16)***	-1.47 (0.17)***	-2.19 (0.20)***
	edge covariable(Agecont)	0.14 (0.18)	0.29 (0.14)*	0.33 (0.15)*	0.46 (0.15)**	0.33 (0.14)*	0.28 (0.14)*	0.27 (0.16)	0.80 (0.16)***	0.50 (0.15)***	0.55 (0.17)**	0.65 (0.14)***	0.49 (0.14)***	0.55 (0.14)***	0.46 (0.16)**
	edge covariable(DIMcont)	0.10 (0.06)	0.14 (0.06)*	0.06 (0.08)	-0.05 (0.06)	-0.03 (0.06)	-0.04 (0.06)	0.03 (0.07)	0.07 (0.07)	0.14 (0.08)	0.17 (0.10)	0.01 (0.07)	0.07 (0.07)	0.12 (0.07)	0.11 (0.09)
	edge covariable(Relationship matrix)	0.78 (0.34)*	0.42 (0.36)	0.30 (0.46)	0.95 (0.34)**	1.02 (0.35)**	1.20 (0.35)***	0.57 (0.44)	0.97 (0.37)**	1.12 (0.42)**	0.84 (0.56)	1.20 (0.35)***	0.97 (0.36)**	1.16 (0.36)**	0.65 (0.44)
Persistance	edges	-2.49 (0.23)***	-3.63 (0.36)***	-4.70 (0.64)***	0.72 (0.27)**	0.71 (0.31)*	0.87 (0.36)*	1.00 (0.57)	-2.90 (0.22)***	-3.18 (0.41)***	-4.43 (0.78)***	0.01 (0.22)	0.20 (0.27)	-0.21 (0.31)	0.07 (0.52)
	factor(Parity: 2)	-0.19 (0.03)***	-0.27 (0.05)***	-0.36 (0.08)***	-0.12 (0.04)**	-0.19 (0.05)***	-0.26 (0.05)***	-0.38 (0.09)***	-0.13 (0.04)***	-0.14 (0.06)*	-0.13 (0.12)	-0.13 (0.04)**	-0.15 (0.05)**	-0.11 (0.05)*	-0.10 (0.09)
	factor(Parity: 3+)	-0.32 (0.03)***	-0.38 (0.05)***	-0.42 (0.09)***	-0.10 (0.04)**	-0.12 (0.04)**	-0.13 (0.05)*	-0.17 (0.08)*	-0.10 (0.04)**	-0.20 (0.06)**	-0.14 (0.12)	-0.15 (0.04)***	-0.14 (0.05)**	-0.14 (0.05)**	-0.19 (0.09)*
	match(Parity)	0.49 (0.04)***	0.49 (0.05)***	0.59 (0.10)***	0.36 (0.04)***	0.27 (0.05)***	0.19 (0.06)**	0.18 (0.10)	0.35 (0.04)***	0.42 (0.07)***	0.38 (0.14)**	0.32 (0.04)***	0.28 (0.05)***	0.36 (0.06)***	0.19 (0.09)*
	factor(Pregnancy status: Pregnant)	0.17 (0.07)*	0.08 (0.11)	0.24 (0.20)	-0.08 (0.08)	-0.22 (0.10)*	-0.11 (0.11)	-0.14 (0.19)	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.	n.a.
	match(Pregnancy status)	0.13 (0.04)**	0.17 (0.07)**	0.22 (0.12)	0.19 (0.05)***	0.19 (0.06)**	0.12 (0.08)	0.17 (0.13)	0.16 (0.05)***	0.32 (0.07)***	0.34 (0.11)**	0.04 (0.05)	0.03 (0.06)	0.14 (0.07)*	0.15 (0.11)
	factor(DIM: Late)	0.19 (0.05)***	0.31 (0.08)***	0.46 (0.14)***	0.07 (0.06)	0.01 (0.07)	0.10 (0.09)	0.16 (0.15)	0.10 (0.06)	0.32 (0.09)***	0.59 (0.16)***	0.10 (0.06)	0.08 (0.07)	0.25 (0.08)**	0.33 (0.14)*
	factor(DIM: Middle)	-0.02 (0.03)	-0.06 (0.04)	-0.14 (0.07)	-0.15 (0.03)***	-0.15 (0.04)***	-0.19 (0.05)***	-0.22 (0.07)**	0.11 (0.06)*	0.12 (0.11)	-0.38 (0.16)*	-0.06 (0.05)	-0.11 (0.06)	-0.10 (0.07)	-0.13 (0.10)
	match(DIM)	0.02 (0.04)	0.05 (0.05)	0.01 (0.09)	-0.01 (0.04)	-0.05 (0.05)	-0.08 (0.06)	-0.14 (0.09)	-0.01 (0.06)	0.13 (0.12)	0.50 (0.21)*	0.09 (0.06)	0.10 (0.07)	0.17 (0.08)*	0.25 (0.13)*
	factor(Breed: Holstein)	0.01 (0.03)	-0.01 (0.05)	-0.02 (0.08)	0.12 (0.04)**	0.11 (0.04)*	0.15 (0.05)**	0.09 (0.08)	0.01 (0.04)	-0.06 (0.07)	0.16 (0.13)	0.02 (0.04)	0.00 (0.05)	0.00 (0.05)	-0.15 (0.09)
	factor(Breed: Red dairy cattle)	-0.03 (0.03)	-0.13 (0.05)*	-0.16 (0.09)	0.02 (0.04)	0.01 (0.04)	0.01 (0.05)	-0.15 (0.09)	-0.15 (0.04)***	-0.15 (0.07)*	0.02 (0.14)	-0.03 (0.04)	-0.03 (0.05)	-0.02 (0.05)	-0.03 (0.09)
	match(Breed)	-0.02 (0.04)	0.02 (0.06)	0.01 (0.10)	0.10 (0.04)*	0.08 (0.05)	0.04 (0.06)	-0.16 (0.10)	-0.08 (0.04)	-0.09 (0.08)	0.00 (0.15)	0.01 (0.05)	0.04 (0.05)	0.04 (0.06)	-0.16 (0.11)
	factor(Claw health: Remark)	-0.02 (0.04)	0.00 (0.06)	0.07 (0.09)	-0.07 (0.04)	-0.07 (0.05)	-0.08 (0.06)	-0.01 (0.08)	0.07 (0.03)*	0.14 (0.06)*	0.16 (0.10)	-0.04 (0.04)	-0.06 (0.05)	-0.03 (0.06)	0.03 (0.09)
	match(Claw health)	0.03 (0.05)	0.12 (0.07)	0.19 (0.12)	-0.00 (0.05)	0.02 (0.06)	-0.04 (0.07)	0.08 (0.11)	0.04 (0.04)	0.05 (0.07)	0.06 (0.13)	0.04 (0.05)	0.00 (0.06)	0.03 (0.07)	0.15 (0.11)
	covariable(Time in area)	2.76 (0.19)***	2.99 (0.29)***	3.20 (0.51)***	-1.51 (0.23)***	-1.68 (0.28)***	-1.89 (0.32)***	-2.76 (0.53)***	2.69 (0.21)***	1.47 (0.40)***	2.26 (0.78)**	-0.53 (0.21)*	-0.99 (0.26)***	-1.22 (0.30)***	-2.46 (0.51)***
	edge covariable(Agecont)	0.36 (0.15)*	0.06 (0.17)	0.14 (0.22)	0.31 (0.15)*	0.33 (0.17)	0.53 (0.19)**	0.70 (0.25)**	0.56 (0.14)***	0.65 (0.20)**	1.00 (0.28)***	0.37 (0.15)*	0.48 (0.17)**	0.48 (0.19)**	0.43 (0.31)
	edge covariable(DIMcont)	0.01 (0.07)	-0.06 (0.09)	0.03 (0.15)	-0.16 (0.08)*	-0.13 (0.09)	-0.18 (0.11)	-0.01 (0.16)	0.13 (0.08)	0.14 (0.14)	-0.18 (0.25)	0.14 (0.09)	0.09 (0.10)	0.02 (0.12)	0.12 (0.20)
	edge covariable(Relationship matrix)	0.00 (0.40)	0.37 (0.58)	-0.09 (0.99)	-0.07 (0.44)	0.02 (0.51)	-0.36 (0.60)	0.62 (0.91)	0.92 (0.45)*	0.68 (0.68)	-0.29 (1.44)	-0.26 (0.47)	-0.07 (0.55)	-0.20 (0.63)	1.14 (0.90)

* $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; n.a.: not available. Estimates can be interpreted as conditional log-odds ratios. The standard error is shown between brackets. The model included the following terms: i) *factor*: sum of the node values for all existing edges in the network; ii) *match*: number of edges in which the value between the nodes (i, j) is the equivalent; iii) covariable: sum of the node value for all existing edges in the network; iv) *edge covariable*: value for each edge appearing in the network. Agecont represents pairs of animals born within 7 days of each other. DIMcont corresponds to pairs of animals calved within 7 days of each other. REL stands for the relationship matrix based on pedigree records.

Supplemental Material S1. A general description of the separable temporal exponential random graph model (STERGM).

The separable temporal exponential random graph model (STERGM), described by Krivitsky and Handcock (2010)**,** extends the exponential random graph model (ERGM) to temporal data. The ERGM is a model applied on social network data. Social networks consist of nodes and edges. In our application, each cow is a node and every contact between two cows, say *i* and *j*, is an edge. In ERGMs, the edges are fitted as a binary outcome y_{ij} where $y_{ij} = 1$ if there is an edge between node *i* and *j*, and $y_{ij} = 0$ if there is no edge between node *i* and *j*. In its simplest formulation, an ERGM is fitted using logistic regression assuming that the existence of an edge between node *i* and *j* is independent of an edge between node *i* and *k*, where $j \neq k$. Hence, the probability of an edge $\mathrm{P}(Y_{ij} = 1)$ is modelled as

$$\mathrm{logitP}(Y_{ij} = 1) = \mu + \beta x_{ij}$$

Here the model is specified for a single covariate x but an ERGM may include several covariates of different types. The most common types of explanatory variables in ERGMs are referred to as node factor, node match, or edge covariate. The value of a *node factor* for an edge between node *i* and *j* is given by the characteristics of the two nodes. For instance, in our application on cows suppose there are two breeds, say Red and Black, and we choose the Red breed as the reference, then the node factor x_{nf} is coded as 0, 1 or 2 depending on how many of the two cows belong to the Red breed.

A *node match,* x_{nm}, is coded as 0 or 1. Continuing the same example as above, $x_{nm} = 1$ if the two cows belong to the same breed and $x_{nm} = 0$ if they belong to different breeds.

An *edge covariate*, is given by the value specific to an edge between nodes *i* and *j*. An *edge covariate*, x_{edge} ,could for instance be how related two cows are. Suppose cow *i* and *j* are half-sibs such that their additive genetic relationship coefficient is 0.25 then $x_{edge,ij} = 0.25$, and for any additive relationship coefficient a_{ij} we have $x_{edge,ij} = a_{ij}$.

STERGMs extends the ERGM to temporal data by including the observed edges from the previous time point in the model.

$$\mathrm{logitP}(Y_{ij,t+1} = 1 \middle| Y_{ij,t} = y_{ij,t}) = \mu_f(1 - y_{ij,t}) + \beta_f x_{ij}(1 - y_{ij,t}) + \mu_p y_{ij,t} + \beta_p x_{ij} y_{ij,t}$$

where $\mathrm{y}_{\mathrm{ij,t}} = 0$ if the edge did not exist in the previous time point t and $\mathrm{y}_{\mathrm{ij,t}} = 1$ if the edge did exist in the previous time point. The intercept for the formation effect is given by μ_f and the formation effect for the covariate x is given by the regression term β_f. Similarly, the intercept and slope for the persistence is given by μ_p and β_p, respectively. An equivalent, but computationally faster, model producing the same results can be fitted by splitting the data into two for $y_{ij,t} = 0$ and $y_{ij,t} = 1$, and by subsequently fitting

$$\mathrm{logitP}\left(Y_{ij,t+1} = 1 \middle| Y_{ij,t} = 0\right) = \mu_f + \beta_f x_{ij}$$

and

$$\mathrm{logitP}\left(Y_{ij,t+1} = 1 \middle| Y_{ij,t} = 1\right) = \mu_p + \beta_p x_{ij}$$

This is the conditional maximum likelihood estimation procedure for STERGMs (Krivitsky and Handcock, 2010) that we applied in our paper. The model can also be interpreted as a Markov chain model. In a Markov chain, the transition probabilities between states are modelled. In the STERGM, the two states are existence and non-existence of an edge, and the four fitted transition probabilities are

$$\mathrm{P}\left(Y_{ij,t+1} = 1 \middle| Y_{ij,t} = 0\right) = \exp\left(\hat{\mu}_f + \hat{\beta}_f x_{ij}\right) / (1 + \exp\left(\hat{\mu}_f + \hat{\beta}_f x_{ij}\right))$$

$$\mathrm{P}\left(Y_{ij,t+1} = 1 \middle| Y_{ij,t} = 1\right) = \exp\left(\hat{\mu}_p + \hat{\beta}_p x_{ij}\right) / (1 + \exp\left(\hat{\mu}_p + \hat{\beta}_p x_{ij}\right))$$

$$\mathrm{P}\left(Y_{ij,t+1} = 0 \middle| Y_{ij,t} = 0\right) = 1 - \mathrm{P}\left(Y_{ij,t+1} = 1 \middle| Y_{ij,t} = 0\right)$$

$$\mathrm{P}\left(Y_{ij,t+1} = 0 \middle| Y_{ij,t} = 1\right) = 1 - \mathrm{P}\left(Y_{ij,t+1} = 1 \middle| Y_{ij,t} = 1\right)$$