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Spatial and network characteristics of Irish cattle movements

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ABSTRACT

Our aim was to examine, for the first time, the spatial and network characteristics of cattle movements between herds in the Republic of Ireland (ROI), to inform policy and research of relevance to the surveillance and management of disease in Irish cattle. We analysed movements in 2016 as discrete herd to herd pairings (*degree*), herd to herd pairings by date of move (*contacts*) and herd to herd pairings by date and individual animal (*transfers*), and looked at each of these as movements out of a herd (*out degree*, *out contacts*, *out transfers*) and into a herd (*in degree*, *in contacts*, *in transfers*). We found that the frequency distributions, by herd, of these six move types were all heavily right skewed but in the case of the 'out' data types more closely followed a log-normal than the scale free distribution often reported for livestock movement data. For each distinct herd to herd *contact* in a given direction, over 90 % occurred only once, whereas the maximum number of occurrences was 62. Herd-level Spearman rank correlations between inward moves (represented as *in degree*, *in contacts*, *in transfers*) and outward moves (*out degree*, *out contacts*, *out transfers*) were weak or even negative whereas correlations between different measures of outward moves or inward moves (e.g. *out degree* vs. *out contacts*, *in transfers* vs. *in degree*) were stronger. Correlations between these variables and the network measure *betweenness* varied between r = 0.513 and r = 0.587. Some herds took part in a relatively large number of movements whilst also retaining their cattle for long periods (> 100 days) between moves. *In* and *out degree*, *contacts* and *transfers* were mapped across Ireland on a 5 km grid, and additionally normalized per 1000 animals and per herd. We found considerable variation in the number of movements by county. Approximately half of transfers were conducted within a single county, but the number and distance of between county movements varied considerably by county of origin and county of destination, with the proportion of moves completed within a single county correlated with its size. Herds exchanging cattle via a market were generally further apart than when moves were made directly herd to herd. For *contacts*, the distances moved away from the herd were on average greater for origin herds in the west of ROI whereas distances moved to a herd were generally greater for destination herds in the centre-east and the north-west.

1. Introduction

The importance of between-herd movements in the epidemiology of livestock diseases has long been recognised (Bajardi et al., 2011), and many studies have investigated how information on animal movements can be used to understand the transmission and spread of infectious agents or to target surveillance (e.g. Green et al., 2008; Guinat et al., 2016; Nöremark et al., 2011; Ortiz-Pelaez et al., 2006; Vidondo and Voelk, 2018).

Beef and dairy farming are important to the culture and economy of the Republic of Ireland (henceforth ROI), with approximately six and a half million animals in the national herd, compared to a human population of approximately 4.9 million. Most animals are raised outdoors during the summer months and often, but not exclusively, indoors during the winter. Most calving happens in the spring, to take advantage of the availability of grass over the spring and summer. Trade of animals between herds, involving approximately three million animals per year, is often conducted via one of 88 livestock markets, known as 'marts', where animals are typically sold on their day of arrival or, in approximately 7% of cases, return to their original herd unsold (DAFM, 2017). In recent years, a visualisation of Irish cattle movements in 2016 (McGrath et al., 2018) has been disseminated amongst stakeholders in the Irish cattle industry. This had led to a heightened appreciation of the likely role of movements in the spread of

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bovine disease such as bovine TB, BVD and Johne's disease, and a concomitant desire to understand the characteristics of these movements more fully.

Many analyses of livestock trade examine the number and frequency of movements, often employing techniques from network science (e.g. Bajardi et al., 2011; Lentz et al., 2013; Leslie et al., 2015; Robinson et al., 2007; Robinson and Christley, 2007; Schärrer et al., 2015). However, knowledge of the spatial relationships between herds which exchange animals is also important if we are to gain an understanding of how disease may spread across physical space (Brooks-Pollock et al., 2014). For example, an epidemic is likely to spread across a territory more quickly if its hosts engage in long-distance displacements than if they do not, especially where secondary spread to neighbouring herds across farm boundaries may be important. Herds taking part in a large number of long-distance movements into and out of the herd are more likely to be important in disease outbreaks than relatively stable ones which move their animals only short distances, if at all. Surveillance of infection may also need to take account of the spatial characteristics of disease – for example, to concentrate resources in areas or regions of highest risk.

Although data on cattle movements in ROI have been incorporated into a number of studies related to bovine TB (Clegg et al., 2013), BVD (Reardon et al., 2018; Tratalos et al., 2017) and Johne's disease (Sergeant et al., 2019), and summary information is presented in annual reports (e.g. DAFM, 2019), very little has been done to understand the broad characteristics of Irish cattle movements, especially with regard to their spatial and network characteristics. In the light of this, this study will examine a range of spatial and network characteristics of Irish cattle movements, and thereby provide summary information which may be of use in epidemiological investigations as well as highlight avenues where more extensive research would be worthwhile.

It has often been asserted for cattle movement datasets (e.g. Dubé et al., 2011; Mekonnen et al., 2019; Pozo et al., 2018) that measures of the number of movements per herd follow a power law, an even heavier tailed distribution than log-normal (Clauset et al., 2009). This has implications for disease management, as it might indicate that there is an important subset of herds with very many inward and outward cattle movements, which might be important in the spread of infection. However, in recent years, doubt has been cast whether the power law distribution is as widely prevalent, in various fields of study, as previously believed (Stumpf and Porter, 2012; Zwetsloot, 2018).We will investigate the degree to which the Irish cattle movement data show such a heavy tailed distribution, matching or similar to a power law.

Analyses of livestock movements seldom address how different measures of movement are related to each other – for example, whether herds which receive many animals from outside of the herd also tend to sell or otherwise transfer a large number of animals to other herds. This information is important, however, as a herd which might be perceived as risky on one measure but not another. This study will therefore examine how different measures of movement are related to each other.

We will also determine how our measures of number of movements per herd are related to the duration of time that cattle reside in the herd, as, for a given amount of movement into and out of a herd, the longer this period is the more likely livestock are to acquire and/ or transmit infections within it.

To summarise our objectives, they are to examine spatial patterns and variation in Irish cattle movements as well their network characteristics, to examine the degree to which different ways of measuring the number of movements are correlated to one another and to ascertain whether there exist potentially risky herds which engage in a large number of movements whilst at the same time retaining their animals in the herd for long periods.

2. Methods

Data processing was conducted in Microsoft SQL Server 2012 and graphical and statistical outputs produced using Microsoft Excel 2010, SAS 9.3, Python 3 and R. Spatial analysis and mapping was done in the Irish Grid Reference System (TM 75) using the GIS software package ArcGIS 10.6.

Animal-level information for all bovines (henceforth 'cattle' or 'animals') present in ROI during 2016 were drawn from the Department of Agriculture, Food and the Marine (DAFM) Animal Identification and Movement system (AIM) database. These data consisted of registrations of calf births in 2016, cattle movements in 2016, and end-of-year herd profiles for 2015. The end-of-year herd profile lists each animal present in each herd on 31 December of that year. All three data types (births, movements, profile) provide the identification (ID, tag number), sex, breed and date of birth of the animal. Birth records additionally provide the herd of birth of the animal and the ID of its dam. Movement data record the origin and destination of the movement, equivalent to the seller and buyer when an animal is being sold. The origin is a herd in all situations except for imports (where the origin is listed as the exporting country but not the herd) or movements from a market (generally known as 'marts' in ROI). The destination can be a herd, a market, a country in the case of exports, a slaughterhouse, or, when the animal has died in its herd, a knackery, or, in exceptional circumstances, burial on the farm where it died. Summaries of these data can be found in DAFM, 2017.

The coordinates of each herd, in easting and northings of the Irish Grid, was obtained from the DAFM Land Parcels Identification System (LPIS) database (Zimmermann et al., 2016) with the exception of approximately 5% of herds which are not in this database. These herds were mapped by randomly assigning a location within the Electoral Division in which they were located, which can be derived from the herd number. Electoral divisions (EDs) are the smallest legally defined administrative area for which Small Area Population Statistics (SAPS) are published from the Irish Census (N = 3440).

In cases where trade was via a market, these movements were combined into a single movement from the origin herd to the destination herd. All cases where animals returned from the market back to their herd of origin were excluded, as were movements to slaughter, the disposal of dead animals, imports and exports.

The herd profile for 30 June 2016 was calculated, based on the 2015 end of year profile and taking into account cattle movements during 2016 up to 30 June. Herd type (either dairy, beef or mixed) was calculated with reference to whether each herd consisted of 66 % or more of the relevant breed type on that day (see Tratalos et al., 2017).

All movements which resulted in the transport of an animal from one ROI herd to another in 2016 were grouped according to their origin and destination, the date of the movement, and whether the transfer was via a market or a direct movement from farm-to-farm. Moves to slaughterhouses and knackeries were therefore excluded, as they generally do not lead to disease transmission. Foreign imports and exports were also excluded, as information was not available for the origin herd in the case of imports and the destination herd in the case of exports. For each transfer from origin to destination on a given date, the following variables were calculated: the total number of animals moved, whether the move was from a dairy, beef or mixed herd, the Euclidean distance between the origin and destination herd, how long the animal had spent in the origin herd and how long it would spend in the destination herd, and whether it subsequently left its destination herd to move to another herd, to slaughter or export, or had died in the herd.

From these data, three measures of the number of movements were calculated:

i) *Degree*: measuring distinct origin and destination herds
ii) *Contacts*: measuring distinct date, origin and destination herd
iii) *Transfers*: measuring distinct animal, date, origin and destination herd

Henceforth we will use the word '*movements*' as a generic term to

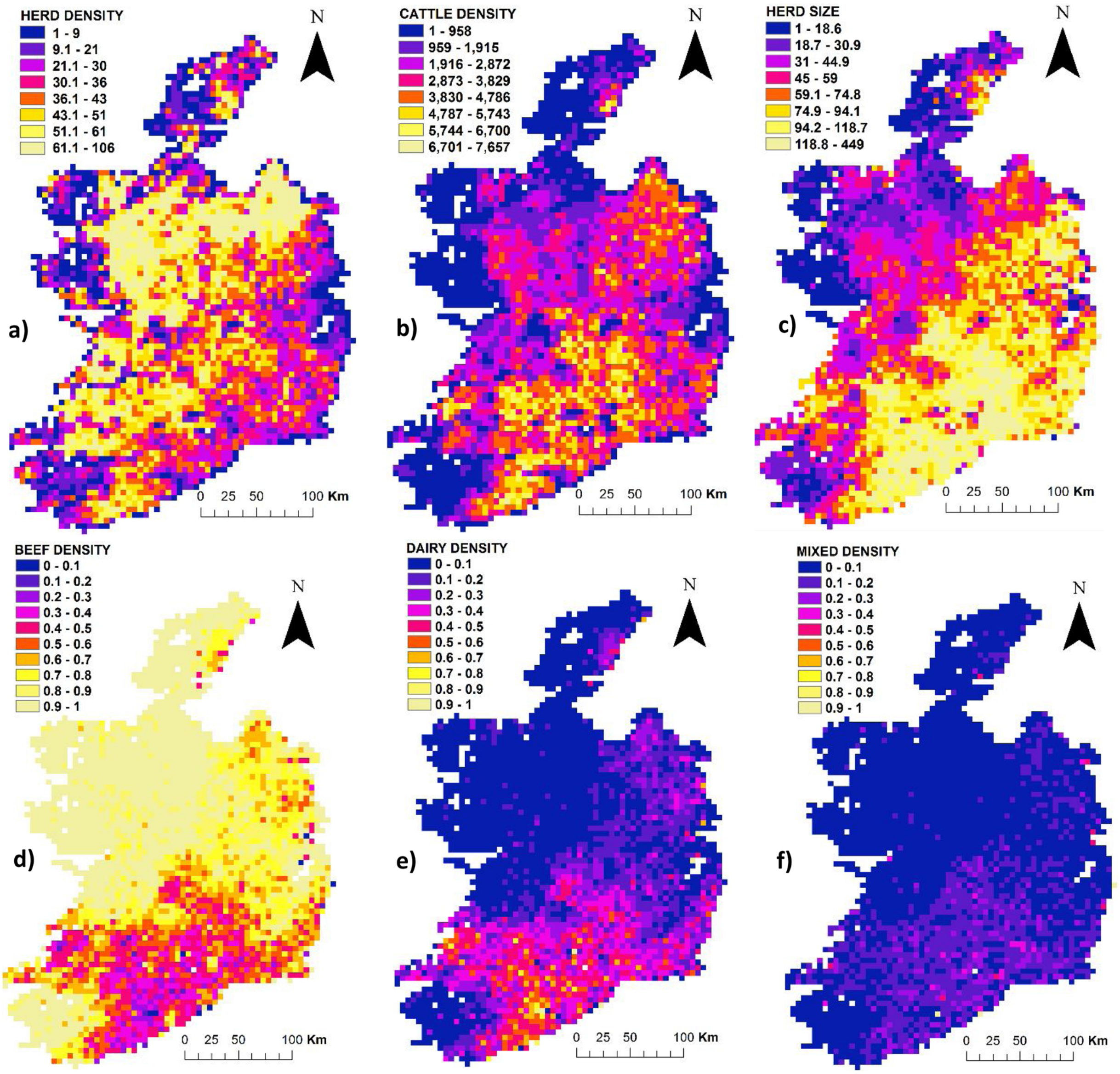

Fig. 1. Six metrics showing the distribution of the cattle population of Ireland, displayed on a 5 km grid: a) the number of herds, b) the number of cattle (all bovines), c) mean herd size, d-f) the proportion of herd consisting of beef, dairy or mixed herd types. Calculated for 30 June 2016.

include any or all of these measures.

In accordance with common practice when describing *degree* in a movement network, for each of these three measures we will describe movements into a herd and out of a herd as follows: *in transfers*, *out transfers, in contacts*, *out contacts*, *in degree*, *out degree*. To illustrate, imagine that herd A were, on two separate occasions (say 1 January and 1 December) to send 4 cattle to each of herds C and D. Imagine also that herd A were to receive, on three separate occasions (say 1 March, 15 March, 31 March), 2 cattle from each of herds E, F and G. In this scenario, movements for herd A could be characterised as follows: *out degree* = 2, *out contacts* = 4, *out transfers* = 16, *in degree* = 3, *in contacts* = 9, *in transfers* = 18.

Using these six measures, we conducted three types of analyses on the 2016 movement data:

2.1. Context

To give context to later results, 6 metrics were mapped on a 5 km grid, including herd and cattle density (the number of herds and bovines per grid square, respectively), mean herd size, the proportion of herds of beef, dairy or mixed type. We also measured the quality of the data by calculating the i) percentage of *transfers* where the animal had been recorded as moving previously, but the previous destination herd did not match the current source herd; ii) the percentage of *transfers* where a subsequent move was recorded for the animal, but the source herd of this subsequent move did not match the destination herd of the current move, and iii) the number of *transfers* where no prior move had been recorded for the animal but the source herd did not match the animal's birth herd.

2.2. Comparison of measures of movement

An examination was made of the distribution of *transfers*, *contacts*, *degree* and *betweenness* across herds (*betweenness* is a measure of the how important each node is likely to be in connecting other nodes (Freeman, 1977)). These were chosen as they are fundamental measures of the movement of animals between herds and have been widely used in other studies of livestock movements and of networks in general (although we are not aware of any previous livestock movement studies which explicitly draw the distinction between the three levels of

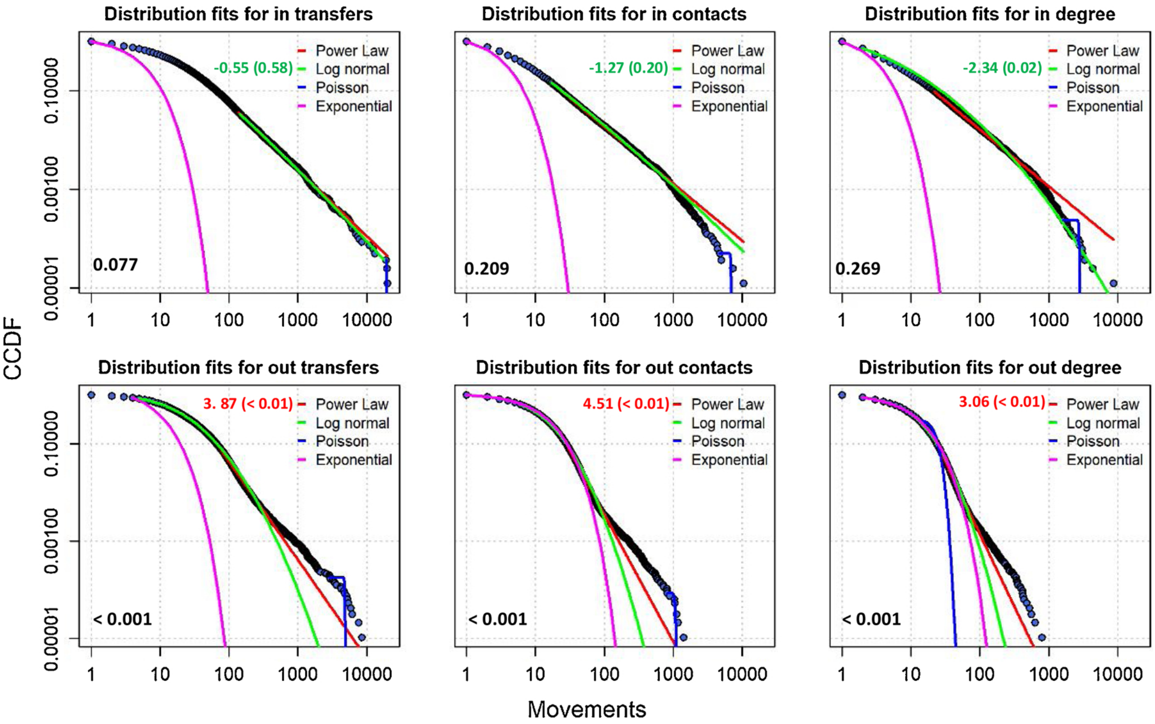

Fig. 2. Complementary Cumulative Distribution Functions (CCDFs) for *in* (top) and *out* (bottom) movements for Irish cattle herds in 2016, measured in terms of *transfers* (distinct origin, destination, date and animal), *contacts* (distinct origin, destination and date), and *degree* (distinct origin and destination). In each case the CCDFs (blue dots) have been plotted alongside lines of best fit for the power law, log normal, Poisson and exponential distributions. A goodness-of-fit test was performed to determine if a power law was a plausible fit by calculating a Kolmogorov-Smirnov statistic and the corresponding p-value is given in the bottom left corner (higher p-values indicate a better power law fit). Additionally, a likelihood ratio test was performed to compare the power law and the log normal distribution for each movement type and this ratio (R) and the p-value for this test is given beside the legend in the top right hand corner, matching its colour (red = power law, green = log normal).

Table 1
Kolgorov Smirnov p-value for goodness of fit to power law distribution, alpha (α) and x-min for the power law distribution calculated, as well as Likelihood Ratio Test Statistic (*R*), and probability based on it, for distinguishing between the goodness of fit of a power law and the log normal distribution. These tests were conducted for *in* and *out* movements for Irish cattle herds in 2016, measured in terms of *transfers* (distinct origin, destination, date and animal), *contacts* (distinct origin, destination and date), and *degree* (distinct origin and destination). For the KS test, the null hypothesis is that the distribution follows a power law, so higher p-values indicate a better fit.

	Goodness of fit test for power law			Likelihood ratio test comparing log-normal and power law fits		
Move Type	α	x-min	p-value	*R*	p-value	Closer fitting distribution
In *Transfer*	2.35	139	0.077	−0.555	0.579	Log Normal
In *Contact*	2.15	21	0.209	−1.272	0.203	Log Normal
In *Degree*	2.15	22	0.269	−2.338	0.019	Log Normal
Out *Transfer*	3.02	71	< 0.001	3.873	< 0.001	Power Law
Out *Contact*	3.61	30	< 0.001	4.508	< 0.001	Power Law
Out *Degree*	3.96	26	< 0.001	3.058	< 0.001	Power Law

aggregation which we refer to as *transfers*, *contacts* and *degree*). Betweenness was calculated using graph-tool (Peixoto, 2014).

This examination included plotting the frequency distribution of *in* and *out transfers*, *contacts*, and *degree*, and investigating whether there was evidence these data might follow a power law (Stumpf and Porter, 2012). A power law distribution is given by:

$$p(x) \propto x^{-\alpha},\ x \geq x_{min,}$$

where x is a unit or event of a particular magnitude, α is a scaling parameter and x_{min} is the magnitude of x beyond which its distribution follows a power law. Following a similar approach to Clauset et al., 2009, for each of the six movement types we estimated α and x_{min}. We then calculated a Kolmogorov-Smirnov (KS) statistic by comparing the distance between the estimated power law fit and the observed distributions to the distance between the estimated power law fit and a large number of simulated datasets drawn from a power law distribution with the parameters α and x_{min}. The p-value is measured as the proportion of the distribution that the KS statistic for the simulated data is larger than for the observed data. However, even in cases where this goodness-of-fit statistic shows that the power law would be a plausible fit, there may be other heavy tailed distributions that fit the data even better. Therefore, for each of the six movement types we compared the power law to three other distributions (log-normal, Poisson and exponential) by overlaying these fits on the original data. We formally compared the power law to the log normal distribution using a likelihood ratio test, *R,* as the log normal is typically seen as the main alternative to power laws due to their many similarities (Zwetsloot, 2018). These analyses were conducted using the poweRlaw package (Gillespie, 2014) in R. We also calculated the number of times each origin and destination herd pairing occurred and calculated the frequency distribution of these data.

Spearman rank correlation coefficients were used to assess the correlation between each of these measures. 5 km grids were produced showing the mean number of *in* and *out transfers*, *contacts* and *degree* per herd, the mean number of *in* and *out transfers* per animal and the mean *in* and *out degree* and *contacts* per herd.

We plotted the relationships between *in degree*, *in contacts* and *in transfers* and the mean of the time each animal involved in movement spent in the herd before its next move (including moves to slaughter or export) or its death in the herd, up to a maximum of 731 days (as data were only available up to 31 December 2018) and the relationship between *out degree, out contacts* and *out transfers* and the time the

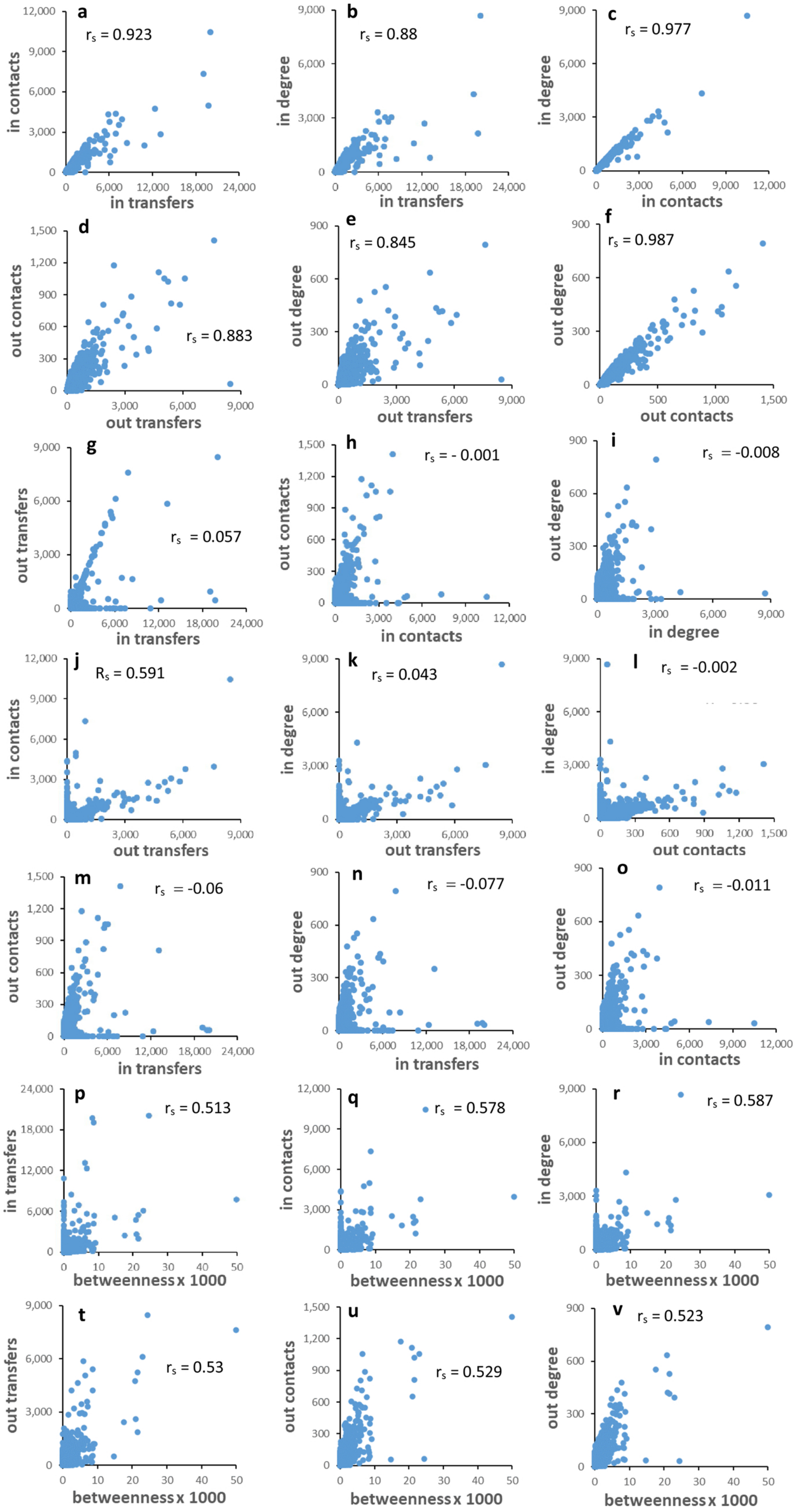

Fig. 3. Scatter plots showing the correlation between seven different measures of movement for Irish cattle in 2016. Spearman Rank Correlation coefficients are denoted by "r_s".

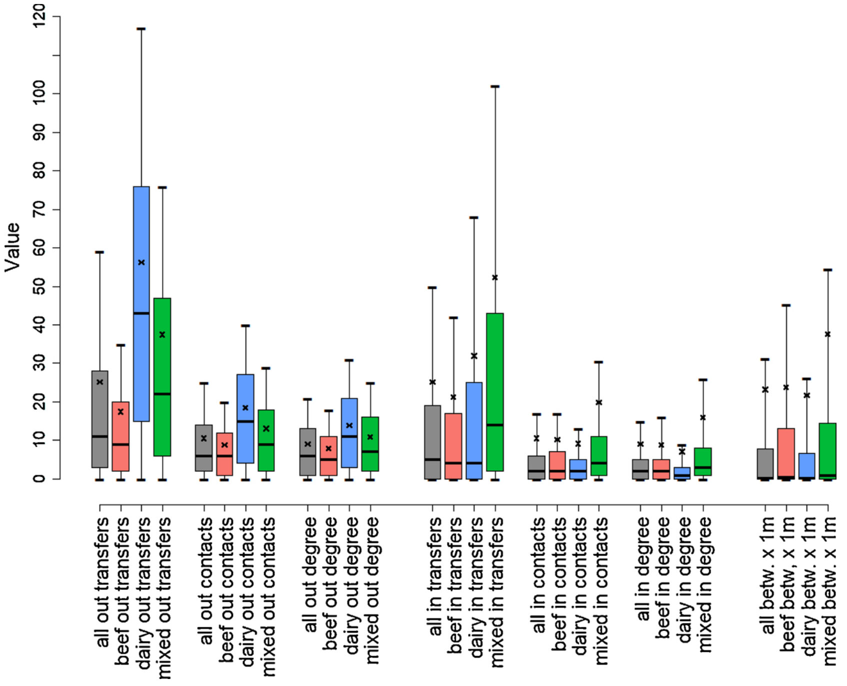

Fig. 4. The number of *in* and *out transfers*, *contacts* and *degree*, as well as *betweenness*, per herd, for all herds and by production type (beef, dairy and mixed). “betw. × 1 m” represents *betweenness* values multiplied by 10^6. Boxes span 25th – 75th percentiles and upper and lower limit of whiskers show 10th and 90th percentile. Mean values are represented by crosses.

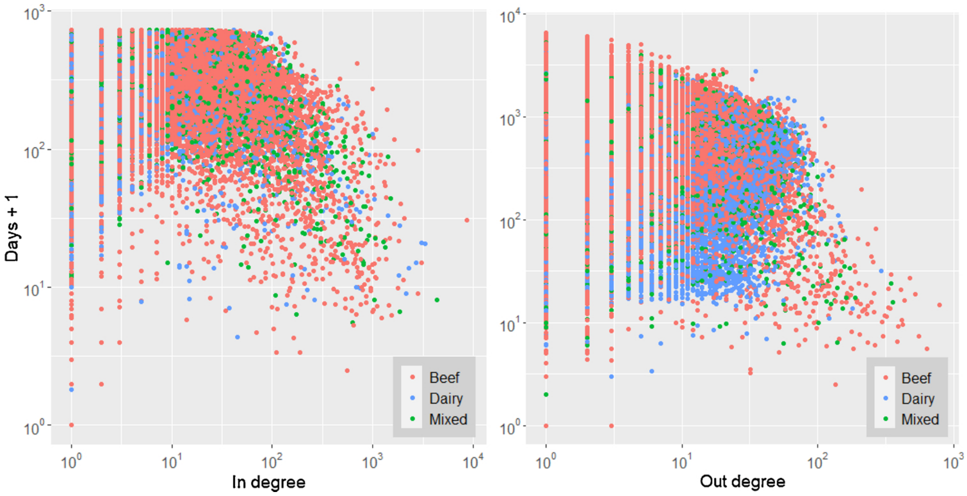

Fig. 5. In *degree* plotted against time till next move and out degree against time since previous move. Time in herd is represented as number of days plus 1, to allow representation of zero values on a log-log scale. Herds were plotted as in beef, dairy or mixed production types, and were drawn in random order (so that herds of one production type do not disproportionately obscure herds of another).

animal had spent in the herd, whether through being born there or moved in previously, up to a maximum of 6210 days (as movement data were only available from 01 January 2000).

2.3. Spatial characteristics of movements

An examination was made of where the origin and destination of between herd movements were located, and the distances covered.

This included mapping the following variables across ROI on a 5 km grid: *in transfers*, *in contacts*, *in degree*, *in transfers* per 1000 animals, *in contacts* per herd, *in degree* per herd, *out transfers*, *out contacts*, *out degree*, *out transfers* per 1000 animals, *out contacts* per herd and *out degree* per herd. We also calculated Moran’s I between herds for all these metrics, to measure the degree of spatial autocorrelation in the data (Moran, 1950). We calculated Moran’s I for all herds, and for beef, dairy and mixed herds separately, and used ESDA, a subpackage of the python library PySAL (Rey and Anselin, 2007), using a neighbourhood of 8 herds.

We also mapped movements at a county level, with reference to the 26 counties of ROI (see Fig1. Of Horner, 2000). For each county, the number of cattle moving out of and into the county (*out transfers* and *in transfers*) were mapped, as well as a further four measures, which calculated *in* and *out degree* according to whether the county was the receiver or sender of the animals. These four measures were as follows: *in degree by destination county* measured the number of herds in the county that animals were entering from other herds in the same county or elsewhere; *in degree by county of origin* measured the number of herds that animals are being moved to, calculated for the county where their herd of origin is located and irrespective of their destination county; out degree by destination county measured the number of herds that animals were coming from into each county, irrespective of the county of their herd of origin; *out degree by county of origin* measured the number of herds in a given county that animals are moved from, into other herds in the same county or elsewhere. Please see the supplementary material (“Explanation of Metrics”) for an illustrated example of how these four metrics were calculated. As well as presenting the raw data, we normalised these maps in the following ways: dividing by the square kilometre land area of the county (denoted as *per sq. km* data), by the number of cattle, x 1000, resident in the county as of 30 June 2016 (*per* 1000 *animals*), and by the number of herds containing cattle resident in

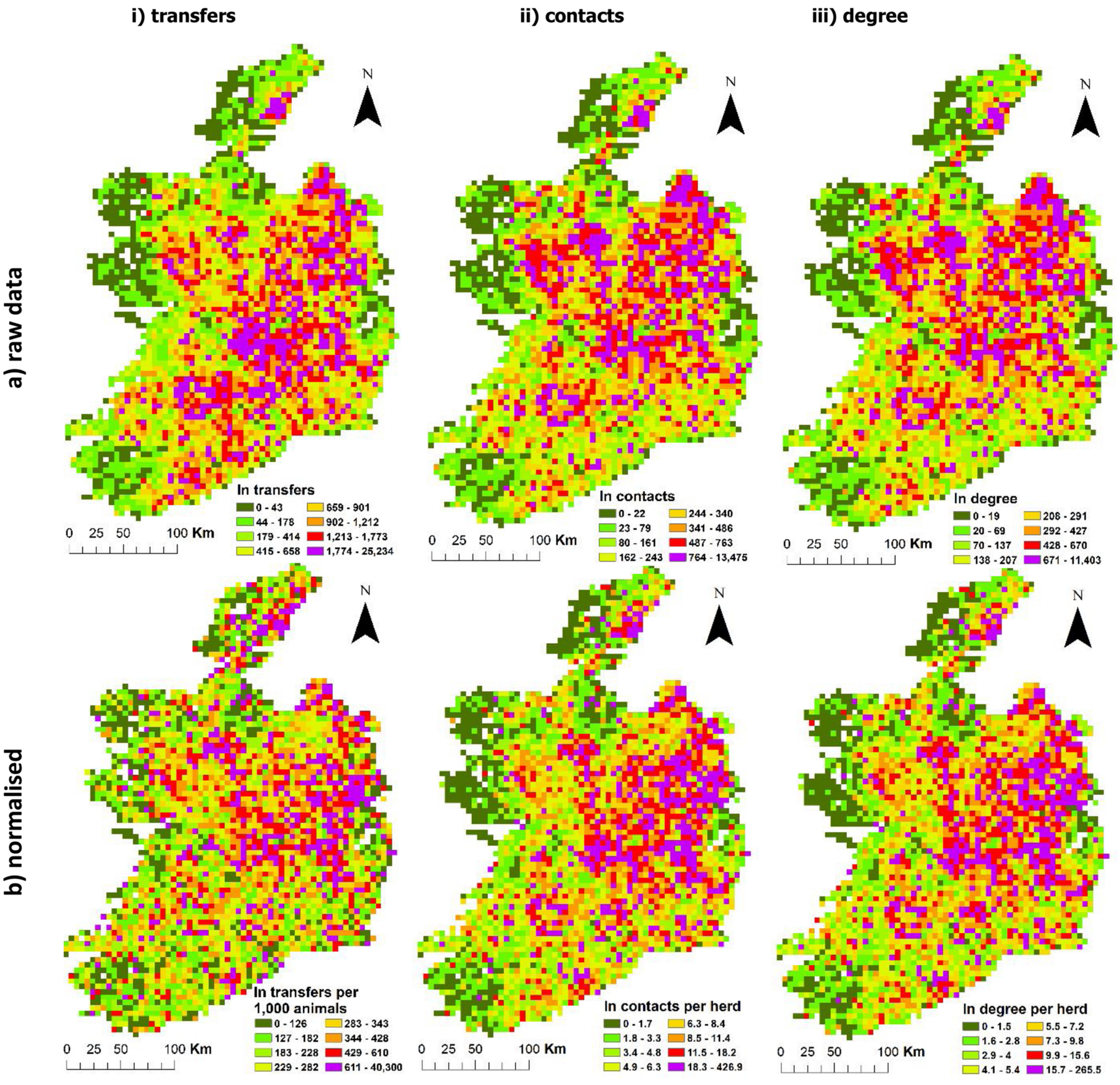

Fig. 6. Total inward *transfers*, *contacts* and *degree* (top row), and the same data divided by the cattle population of the square, in thousands (in the case of *transfers*) and by the number of herds in the square (in the case of *contacts* and *degree*).

the county as of 30 June 2016 (*per herd*). We mapped the number of *transfers* of cattle between pairs of counties: for each county, separate maps were produced showing i) the number of *transfers* from herds in this county to other herds in the same county and to herds in each of the other 25 counties and ii) equivalent data for *transfers* into herds in the county, i.e. the number of *transfers* from other herds within the same county and from herds in each of the other 25 counties.

We mapped the distances of *contacts* between herds as average values in a 5 km grid, as well as using two interpolation methods to produce smoothed 1 km grid surfaces – Ordinary Kriging (using a neighbourhood of 12 herds) and Inverse Distance Weighting (neighbourhood of 10 herds, weighed by distance squared). For each of these three methods we produced separate maps showing 'distance to' and 'distance from' the grid square, mapping the distance at the location (grid square) of the herd of origin for the former and at the location (grid square) of the destination herd for the latter. We calculated Moran's I between herds to examine spatial autocorrelation in the mean distances of *contacts* from and to each herd, for all herds, and between beef, dairy and mixed herds considered separately. We also examined the frequency distribution of these distances in 10 km bands and the extent to which this differed between farm-to-farm *contacts*, where animals were transferred directly between herds, and market *contacts*, where the animals was moved from the origin herd to a market and from there on to the destination herd.

For most of the gridded maps shown in this study, binning of cell values for the figure legends was done using octiles (dividing the data up into 8 groups with an approximately equal number of cells), as opposed to alternative methods such as equal interval or standard deviation, and this should be borne in mind when viewing them. The exception to this was when the proportion of each cell consisting of dairy, beef or mixed herds was mapped – this was done using 10 equal intervals between 0 and 1, which made comparison between the three maps more straightforward than if octiles were used.

3. Results

3.1. Context

On 30 June 2016, there were 110,048 herds in ROI with animals in them. Of these, 83,345 were beef with 3,717,305 animals, 18,647 dairy

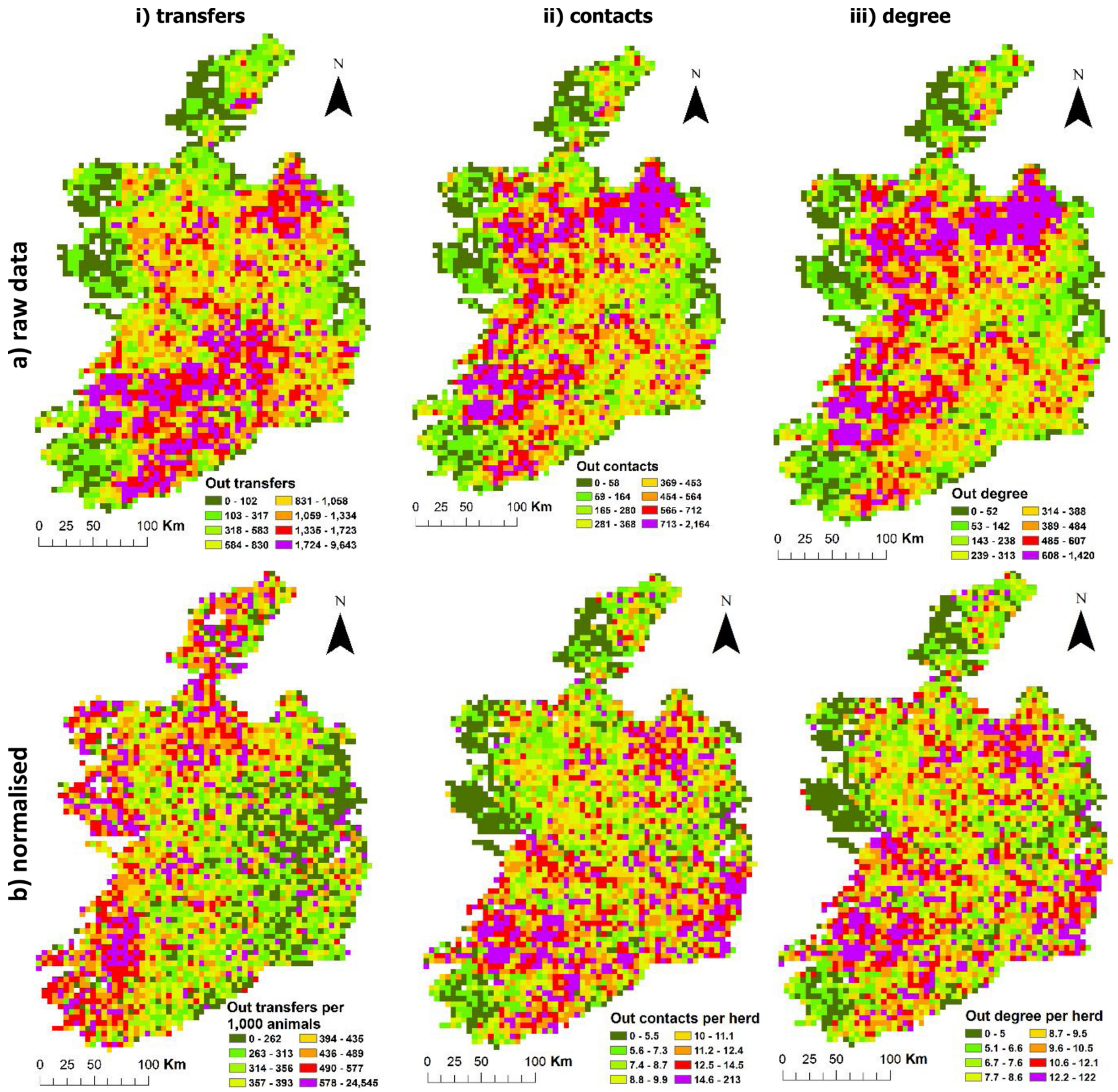

Fig. 7. Total outward *transfers*, *contacts* and *degree* (top row), and (bottom row) the same data divided by the cattle population of the square, in thousands (in the case of transfers) and by the number of herds in the square (in the case of *contacts* and *degree*).

with 2,542,574 animals and 8056 mixed with 907,745 animals. The average size of dairy herds was therefore considerably larger than of beef herds (136.3 > 44.6), with mixed herds between these two extremes but closer in size to dairy herds (112.7). The minimum number for all three production systems was a single individual. 25th percentile, median, 75th percentile, and maximum were as follows: beef: 14; 29; 57; 2430; dairy: 48; 109; 188; 1942; mixed: 38; 87; 157; 1,879. Note that these figures are for the middle of the year and would include young calves born during the spring calving season. The number of herds per unit area (herd density) was generally highest in areas to the north and west of ROI (Fig. 1a). However, this was not the case for the number of cattle per unit area (cattle density), which was often at its highest in the South (Fig. 1b), as was herd size (Fig. 1c). The proportion of beef herds tended to be highest in the North and West of the country (Fig. 1 d), and of dairy and mixed herds in the South (Fig. 1e and 1f respectively).

Our examination of data quality revealed that there were 9278 *transfers* where the current source did not match the previous destination, 4409 where the next source did not match the current destination, and 1759 first *transfers* for an animal where the source herd did not match the birth herd. These represented 0.62 %, 0.31 % and 0.26 % of *transfers*, respectively, which is a small enough percentage to give us confidence that the results of our analyses will not be unduly influenced by errors and omissions in the data.

3.2. Comparison of measures of movement

For each of the three measures (*transfers*, *contacts*, *degree*), the frequency of *in* and *out* movements per herd followed heavy-tailed distributions typical of many contact networks (Fig. 2). However, outward movements per herd contrasted with inward movements at low numbers (n < = 5), as frequencies dropped less sharply in the former as the number of movements increased (Fig. 2). The majority of unique herd to herd *degree* combinations (e.g. herd *x* trading with herd *y*) were represented by only one *contact* during the year (902,397: 89.2 %), with 7.5 % occurring as two *contacts*, 1.8 % as three and 1.5 % as between four and 62 *contacts*.

In the case of the three 'in' measures (*in transfers*, *in contacts*, *in*

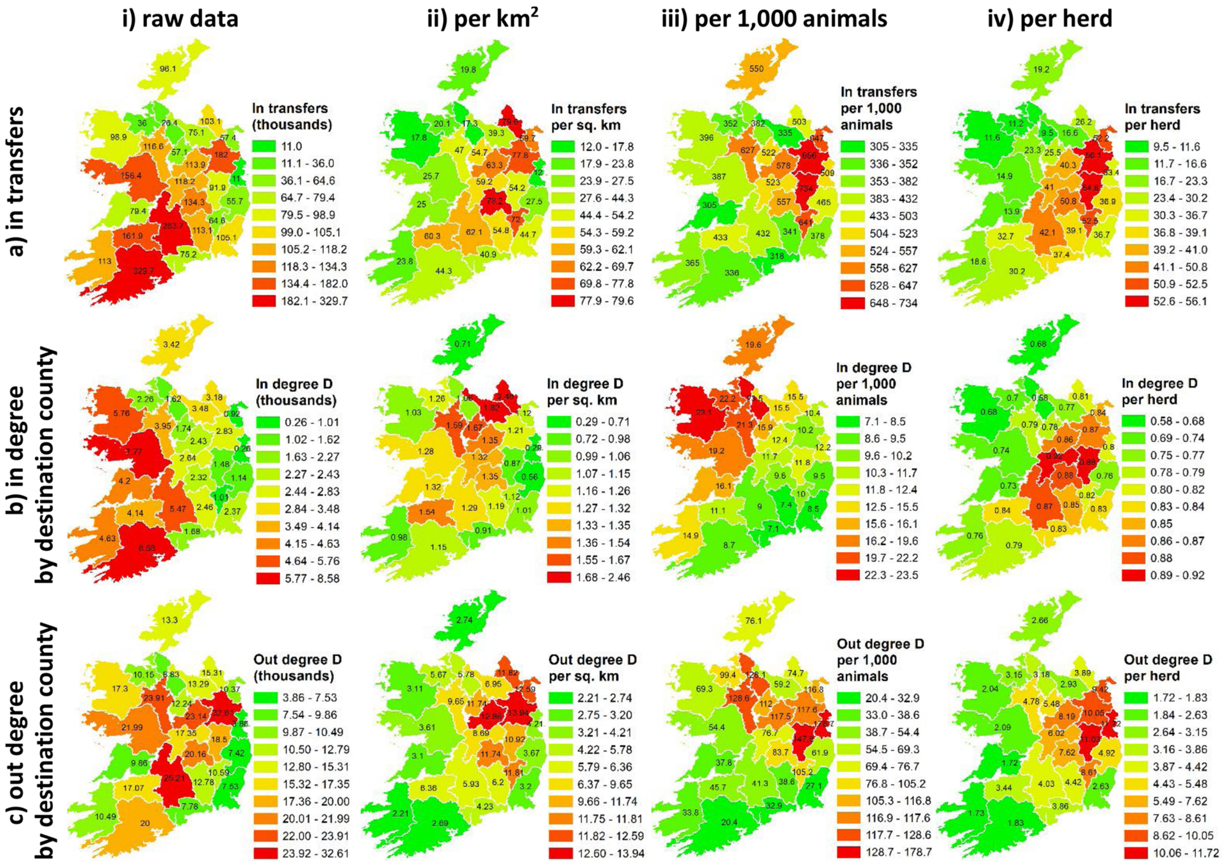

Fig. 8. Measures of movement into counties, shown in terms of number of *transfers* of individual animals (a), as well as in *degree* and out *degree* represented in terms of the destination county (county where the destination herd was located) (b and c respectively). Each of these data types is expressed as raw data (in thousands), per km^2, per 1000 animals and per herd.

degree), KS tests gave some support for the null hypothesis that these follow a power law distribution, with p values to reject this hypothesis of 0.08 for *in transfers*, 0.21 for *in contacts* and 0.27 for *in degree* (Fig. 2 and Table 1). However, for all three of these data sets, log normal was found to offer a better fit, although for both *in transfers* and *in contacts* p values for these comparisons were high, 0.58 and 0.20 respectively, suggesting that the null hypothesis that power law was the correct distribution could not be rejected. KS tests showed that none of the equivalent 'out' measures (*in transfers*, *in contacts*, *in degree*) could plausibly be said to follow a power law (Fig. 2 and Table 1), although it was in each case a better fitting distribution than log normal.

In contacts and *in degree* were very strongly positively correlated (Fig. 3c, Spearman Rank Correlation (r_s) = 0.977), as were *out contacts* and *out degree* (Fig. 3f, r_s = 0987), whereas equivalent correlations between *transfers* and *contacts* and *transfers* and *degree* were weaker (Fig. 3a, b, d, e). *In transfers*, *in degree* and *in contacts* did not show clear relationships with *out transfers*, *out degree* or *out contacts,* and these plots were highly heteroskedastic (Fig. 3g-o). Spearman Rank correlation between *betweenness* and the other measures varied between 0.513 (*in transfers*) and 0.587 (*in degree*) (Fig. 3p-v).

Breaking these data down by production type (beef, dairy and mixed) showed that the distributions of the number of in and out *transfers*, *contacts* and *degree* per herd, as well as betweenness were fairly similar for the different production types ((beef, dairy and mixed) (Fig. 4), but with generally lower values for beef herds when compared with dairy and mixed, and particularly high numbers of out *transfers*, *contacts* and *degree* for dairy cattle. Mean values were generally much higher than the median, consistent with our earlier finding of very high values for a small number of herds.

Plotting *in* and *out degree*, by herd, against the mean time that animals spent in the herd before their next move showed that some herds reported a very high number of distinct trading partners whilst also keeping these animals for a considerable length of time (Fig. 5). For example, of herds with an average stay in the herd > = 100 days, 33 had an *in degree* > = 1000, of which 26 were beef herds, 3 dairy and 4 mixed; 745 had an *in degree* > = 100 (545 beef, 92 dairy, 106 mixed) and 15,928 had an in *degree* > = 10 (12,578 Beef, 1669 dairy, 1611 mixed); 23 had an *out degree* > = 100 (15 beef, 5 dairy, 3 mixed); 37,220 had an *out degree* > = 10 (24, 463 beef, 9367 dairy, 3297 mixed) (a small number of herds could not be classified into a production type as they did not contain any animals on 30 June 2016).

3.3. Spatial characteristics of movements

The total number of *in transfers*, *in contacts* and *in degree* per 5 km grid square tended to be highest around the central areas of ROI, although there was a lot of variability between neighbouring grid squares (Fig. 6a (i-iii)). Normalising these data by the cattle population (in the case of *transfers*) or by the number of herds (for *contacts* and *degree*) did not have a major impact on the overall patterns (Fig. 6 b (i-iii)). Maps of *in contacts* and *in degree* were almost indiscernible from each other both for the raw and normalised data (compare Fig. 6a(ii, iii) with Fig. 6b (ii, iii)).

Out transfers showed a concentration around the south of ROI (Fig. 7a (i)), whereas *out contacts* and *out degree* showed relatively large values toward the west and north of the country (but not Donegal in the extreme north) (Fig. 7a (ii, iii)). However, overall spatial dependence between herds for *in* and *out transfers*, *contacts* and *degree* was weak, with Moran's I values between herds ranging from 0.011 in the case of *in contacts* to 0.024 for *out degree*. Moran's I values were similarly low

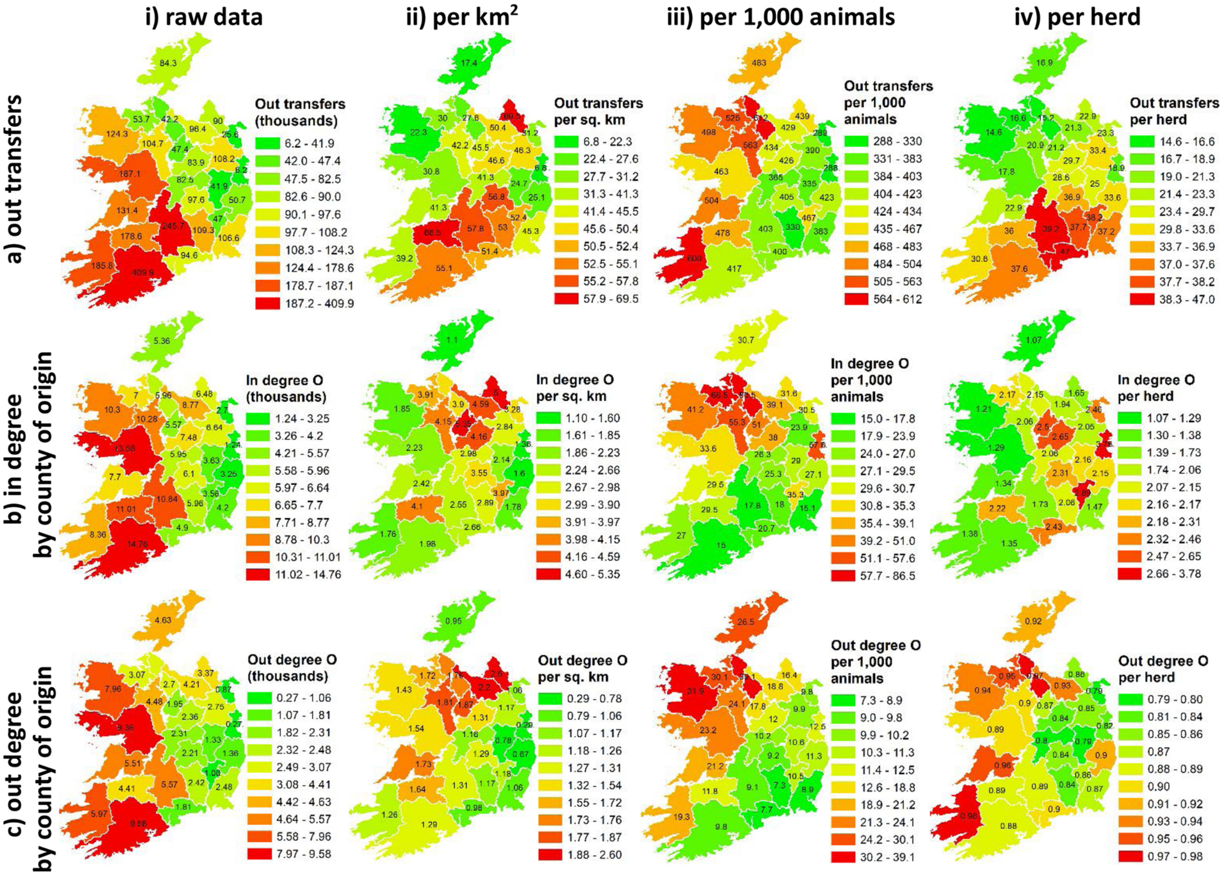

Fig. 9. Measures of movement out of counties, shown in terms of number of *transfers* of individual animals (a), as well as in *degree* and out *degree* represented in terms of the county of origin (county where the origin herd, i.e. the herd where the move originated from, was located) (b and c respectively). Each of these data types is expressed as raw data (in thousands), per km^2, per 1000 animals and per herd.

when analyses were restricted to beef, dairy and mixed herd types, with a low of 0.002 (dairy *in contacts*) and high value of 0.036 (dairy *out degree*). Normalising the *transfers* data by the cattle population produced a northward and westward shift in the areas with the highest values (Fig. 7b (i)), whereas in the case of *contacts* and *degree* there was little impact on the broad geographic trends but the hotspots evident in the raw data were not as pronounced (Fig. 7b (ii, iii)).

The number of animals moving into each county in 2016 ranged from 10,985 (Dublin) to 329,721 (Cork), with counties in the south west of ROI each showing a large number of inward *transfers* (Fig. 8a (i)). However, these counties also tend to be large in size, with a large number of herds and a large number of animals; therefore it was not surprising that normalising the data by county area, the number of animals or the number of herds, revealed different patterns, with counties in the centre and east often showing the highest values (Fig. 8a (ii-iv)). Similar patterns were shown in *out degree by destination county* – a measure of the number of herds that animals were coming from into each county, irrespective of the county of their herd of origin (Fig. 8c), but were somewhat different for *in degree by destination county* – the number of herds in the county that animals were entering, from other herds in the same county or elsewhere (Fig. 8b).

The number of animals moving out of each county ranged from 6218 (Dublin) to 409,904 (Cork) with a distinct concentration of *transfers* from the southern and western counties again evident (Fig. 9a (i)). When data were normalised per 1000 animals, the north western counties of ROI, which generally have very small herd sizes (Fig. 1c) had particularly high values for *out transfers* (Fig. 9a (iii)). *In degree by county of origin* (a measure of the number of herds that animals are being moved to, mapped for the county where their herd of origin is located and irrespective of their destination county) and *out degree by county of origin* (an equivalent measure for the number of herds in a given county that animals are moved from, into other herds in the same county or elsewhere) showed similar patterns to the total number of *out transfers* (Fig. 9a (i), b (i), c (i)). Southern counties showed the highest values for *out transfers* per km^2 and per herd, northern counties (except Donegal) showed the highest values for *in degree by county of origin* per 1000 animals and per km^2, and western counties for *out degree by county of origin* per 1000 animals and per herd (Fig. 9). No strong spatial patterns were evident for *in degree by county of origin* per herd (Fig. 9b iv). County Dublin showed a relatively high *in degree by county of origin* per 1000 animals and per herd, which was not matched in the equivalent data for *out transfers* and *out degree by county of origin* (Fig. 9a-c (iii, iv)).

Fig. 10 presents, for each county, a map of the number of *transfers* to destination herds in the country, with a choropleth showing the percentage of *transfers* each of the counties of origin contributed to the total number of *transfers* into the county. Fig. 11 shows the reverse relationships: for each county, a map of the number of *transfers* originating from herds in this country, with the choropleth showing the proportion of *transfers* each of the destination counties contributed to the total number of *transfers* from the county. The maps in Figs. 10 and 11 are presented individually in the supplementary material to allow closer inspection. For a large proportion of moves, the origin and destination were within the same county (50 % of *transfers*, 44 % of *contacts* and 43 % of *degree*), with the extent to which this was true correlated with the size of the county (Spearman rank correlation; *out transfers*: r = 0.58; *out contacts*; r = 0.59, *out* degree: r = 0.59, *in transfers*: r = 0.81; *in contacts*; r = 0.75, *in degree*: r = 0.76) (Fig. 12). Although in general, in both sets of maps, the relative contribution to *transfers* into and out of a given county tended to dissipate with

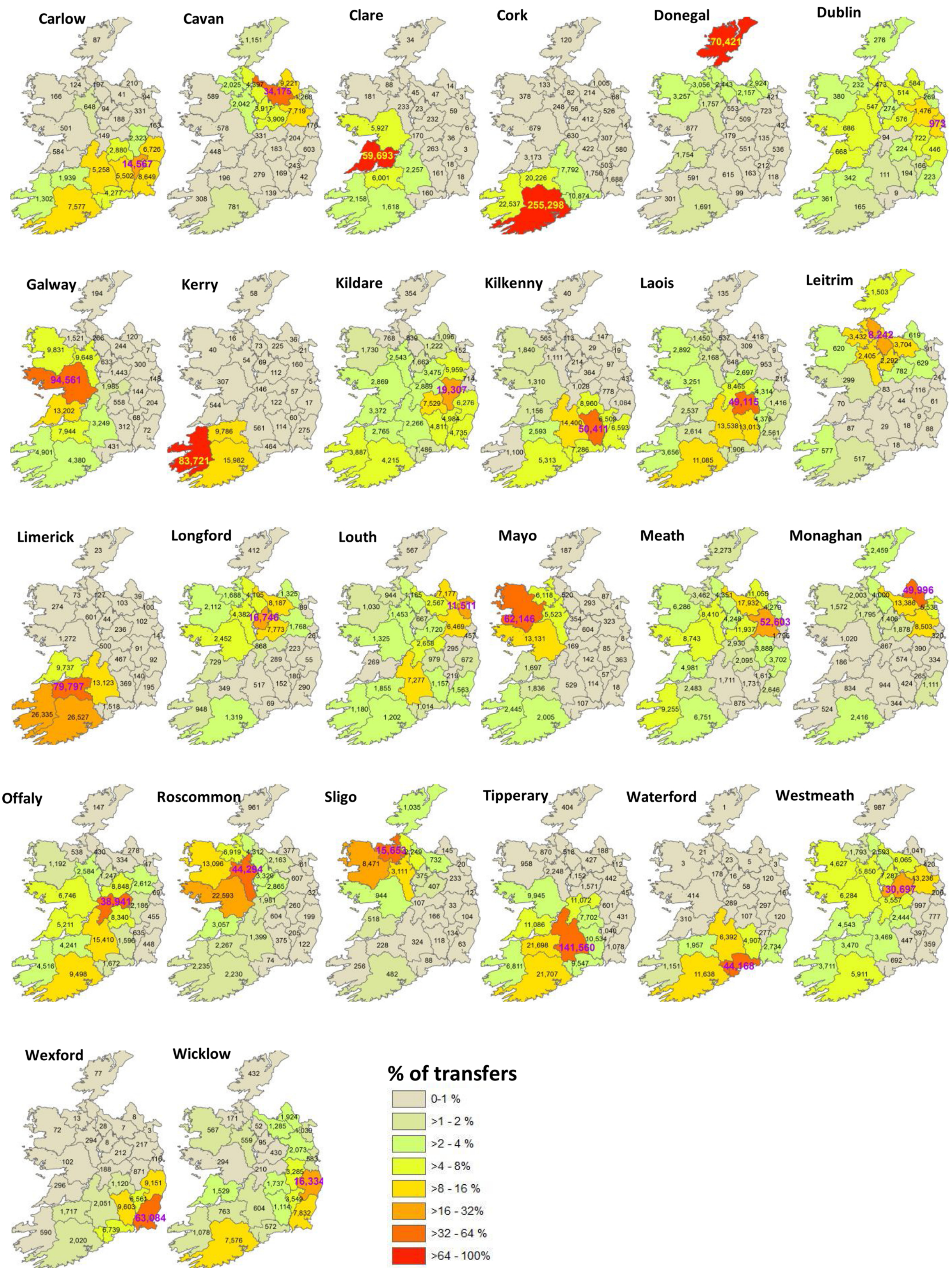

Fig. 10. Total between herd *transfers* in 2016, with a map for each destination county. The numbers displayed show the number of transfers of animals arriving from herds within each county whereas the choropleth legend represents this as a percentage of all transfers into herds in the destination county. To illustrate, considering the county Offaly map, cattle were moved from a total of 6746 herds in county Galway to herds in county Offaly in 2016, representing 2-4% of herd transfers to county Offaly in that year. For each map, the destination county is indicated with a larger, coloured font - purple (if against orange or yellow background) or yellow (if against red background).

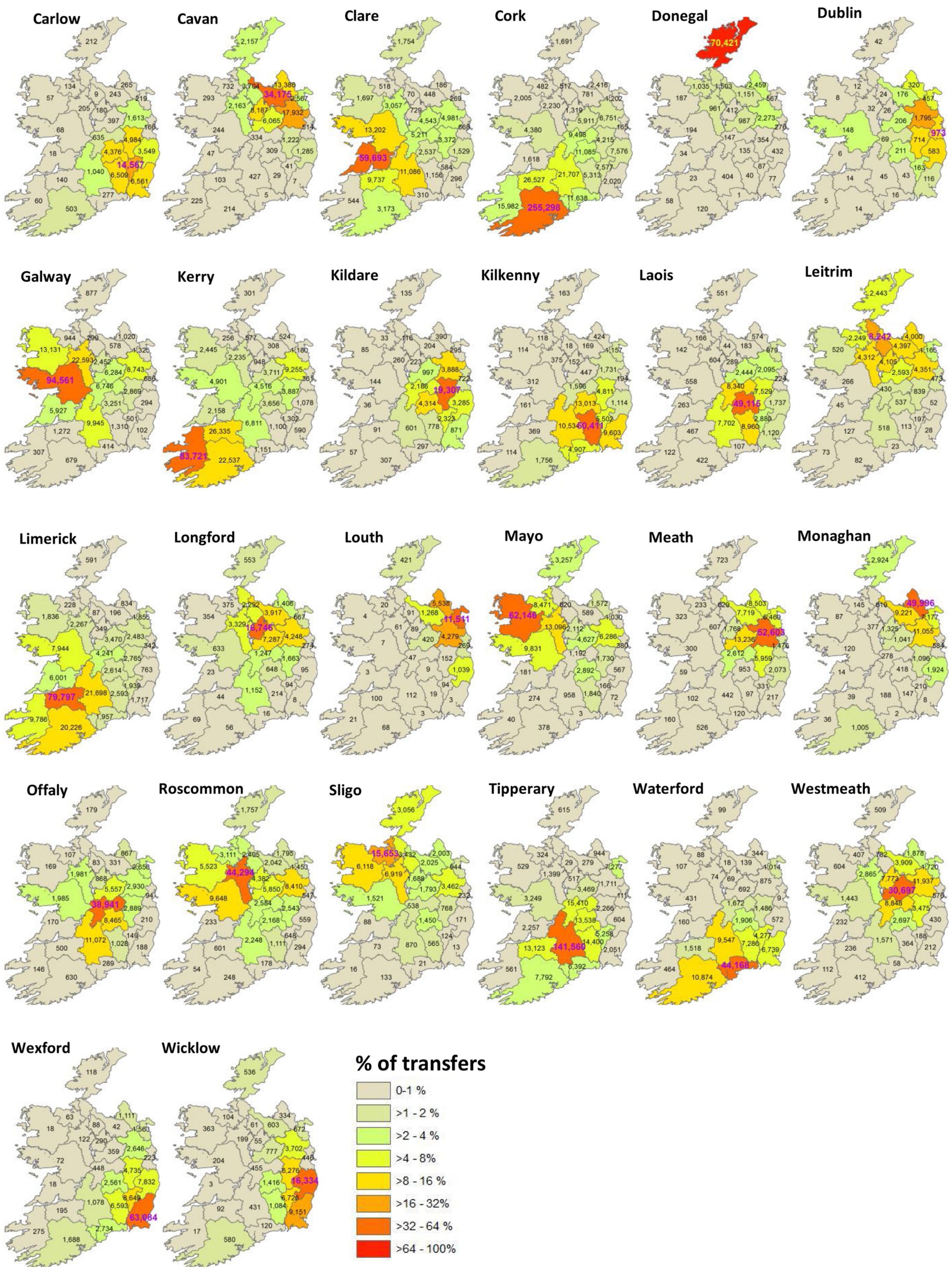

Fig. 11. Total between herd *transfers* of animals in 2016, with a map for each county where the transfer originated. The numbers displayed show the number of transfers of animals to herds within each county whereas the choropleth legend represents this as a percentage of all transfers from herds in the county of origin. To illustrate, considering the county Offaly map, cattle were moved to a total of 1985 herds in county Galway from herds in county Offaly in 2016, representing 2-4% of herd transfers from county Offaly in that year. For each map, the county of origin is indicated with a larger, coloured font - purple (if against orange or yellow background) or yellow (if against red background).

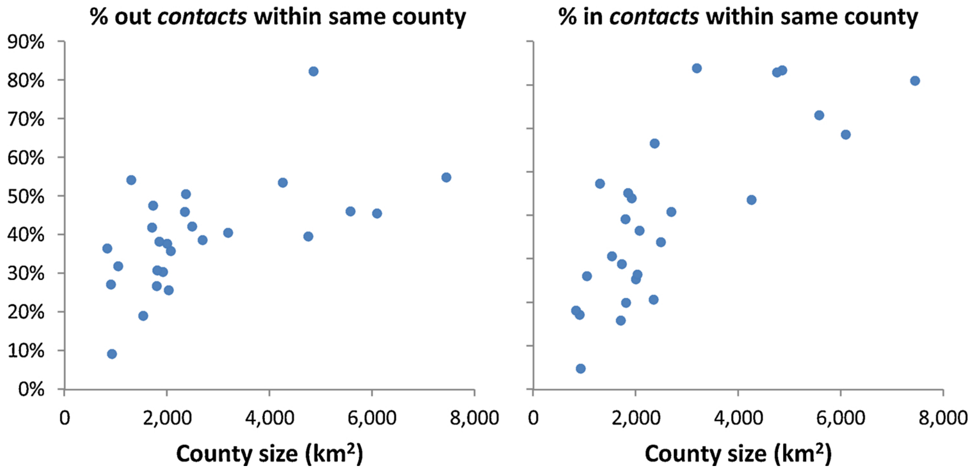

Fig. 12. Percentages of out and in *contacts* which remain in the same county, versus size of county. Plots for out *transfers* and out *degree* (not shown) were similar to that of out *contacts* and those for in *transfers* and in *degree* (not shown) similar to that of in *contacts*.

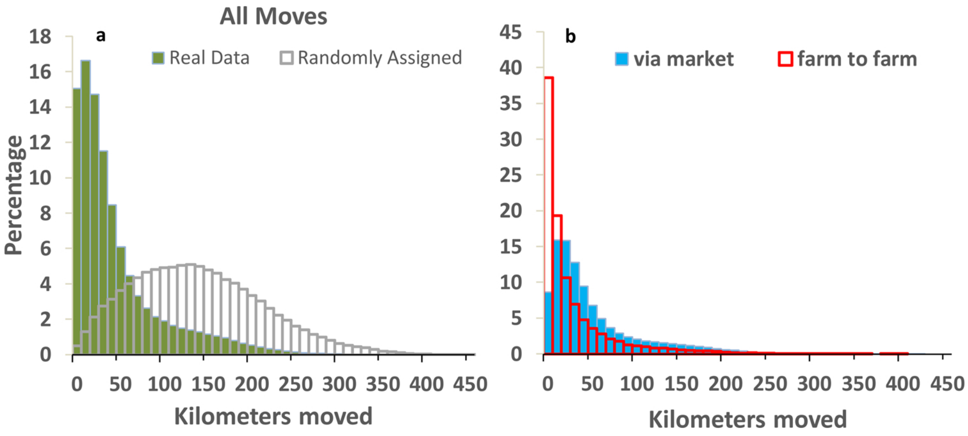

Fig. 13. Percentage of contacts between herds, 2016, by distance in kilometres. Fig. 13a shows all contacts (both farm-to-farm and via a market), with hollow grey bars showing results when destination is randomly assigned to any herd in the same dataset with the same move type (market or farm-to-farm). Fig. 13b shows separate frequency distributions for direct farm-to-farm moves and moves via a market.

distance, the extent to which this was true differed – for example, for *transfers* into County Kerry 96.9 % of *transfers* came from herds within the county or from the two neighbouring counties, whereas for *transfers* into County Dublin only 3.3 % of *transfers* came from herds within County Dublin or the neighbouring three counties.

Approximately two thirds of *contacts* covered a distance of less than 50 km (791, 497 = 66.4 %), with a steady decline in frequency for distances > 20 km. More of these *contacts* were between 10 km and 20 km than for shorter distances (198,219 > 179,418) (Fig. 13a). Randomising the destination herds within these data and overlaying the resulting frequency distribution of distances showed that distances were in general much shorter than would be expected if destination herds were chosen at random (Fig. 13a). Direct farm-to-farm movements tended to be shorter than moves via a market, with over 40 % of farm-to-farm *contacts* closer than 10 km (97,688/242,402), whereas this was the case for only 8.6 % of market *contacts* (80,622/935,313) (Fig. 13b).

The spatial distribution of distance from origin herds to destination herds is displayed in Fig. 14a (i-iii). Fig. 14b (i-iii) shows the same relationships as distances travelled to, as opposed to from, herds. These maps smooth the data in different ways, the mean distance within 5 km grid square is calculated in Fig. 14a (i) and 14b (i); Fig. 14a (ii) and b (ii) used ordinary kriging, with a neighbourhood of 12 herds, whereas Fig. 14a (iii) and b (iii) used inverse distance weighting, using neighbourhoods of 10 herds, and an exponents of 2, respectively. There is a marked tendency for distance travelled *to* herds to be larger in areas close to the capital city of Dublin and also some areas in Donegal around the border with the UK territory of Northern Ireland (Fig. 14a (i-iii)). Conversely, there is a tendency for distance travelled *from* herds to be greater in areas to the extreme West, especially around the South West of ROI (Fig. 14b (i-iii)). There was little difference between different production types in distances travelled in contacts between herds, with median values around 30 km (Figure 15, range = 30.5–34.2) and means around 50 km (Fig. 15, range = 47.3–52.9).

Moran's I was much higher for average distances of contacts from each origin herd (0.275) than average distances to each destination herd (0.003), suggesting a higher level of spatial dependence in the former. This pattern was also evident when these calculations were conducted separately on beef, dairy and mixed herds: for dairy, from origin $I = 0.268$, to destination $I = 0.031$; for beef, from origin $I = 0.29$, to destination = 0.021; for mixed, from origin $I = 0.216$, to destination $I = 0.038$.

4. Discussion

The approach we have adopted in this study is to bring to light the patterns and processes displayed in Irish cattle movements which have not already been touched upon elsewhere, for example in DAFM (2019); McGrath et al. (2018) or Tratalos et al. (2017). Our results offer a variety of insights.

This study is the first to map the distribution of herd types, herd density and cattle density at a detailed scale across the Republic of Ireland (Fig. 1) (the distribution of dairy and suckling cows have previously been mapped at a county level, INRA, 2018). We show that there is a distinct spatial pattern in the distribution of dairy and beef

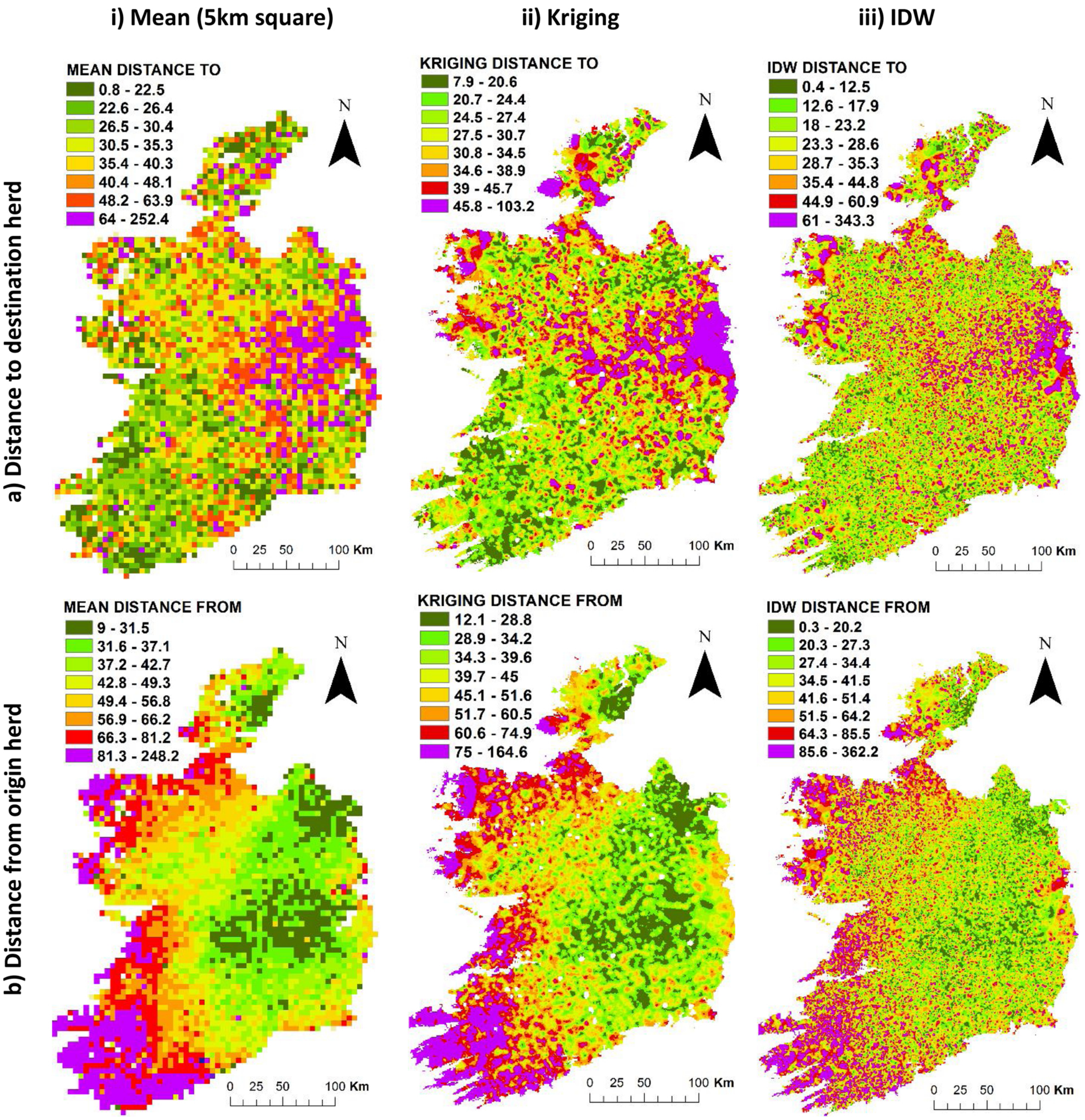

Fig. 14. Spatial distribution in *contacts* during 2016, using 3 different methods to demonstrate spatial variation. Fig. 14a (i-iii) map the distance travelled according to the grid square of the destination herd whereas b i-iii due this for the grid square that the herd where the *contact* originated. Fig. 14a (i) and b (i) show the mean distance travelled using a 5 km grid; a (ii) and b (ii) show the results of ordinary Kriging, using 12 neighbours; a (iii) and b (iii) used inverse distance weighting, with 10 neighbours and an exponent of 2.

production types, with dairy herds in the south and beef herds in the north and west (Fig. 1d–f). The typically smaller sizes of beef herds are in turn revealed in lower animal densities relative to herd densities in areas which a high proportion of beef production (Fig. 1a-c.). Much of the variability in the spatial patterns observed in the data (Figs. 6,7,8–11,14) are likely due to the existence within the same territory of two distinct production systems (dairy and beef). It is known that within these systems there is also a considerable amount of variability. Individual herds vary considerably in size within both production types, from a single individual to more than one thousand cattle. Furthermore, there are many distinct types of cattle production systems within both dairy and beef farming in Ireland. Some dairy herds raise most of their replacement stock and keep unwanted animals for fattening, whereas others introduce new heifers or cows from outside the herd, or sell on stock not wanted for milk production. Contract rearing of dairy heifers, where they are raised in herds different to their birth herd and then returned to it prior to first calving, has become increasingly common in recent years, and approximately 5 % of dairy herds used this approach in 2015 (Kinsella et al., 2017). There are a number of different models of beef production including the home-rearing of animals born from beef dams, the fattening of young calves purchased from dairy farms (the 'calf to beef' system), the purchase of animals as weanlings for subsequent fattening and sale, or the operation of finishing herds where animals are purchased at a relatively mature age (12–18 months) for fattening and slaughter. Further analysis of these data may reveal how different production systems contribute to the overall picture.

We also show that there are a small number of herds which are the origin or destination for a very large number of movements (Fig. 2–4), so-called high-volume herds. However, there was limited support for

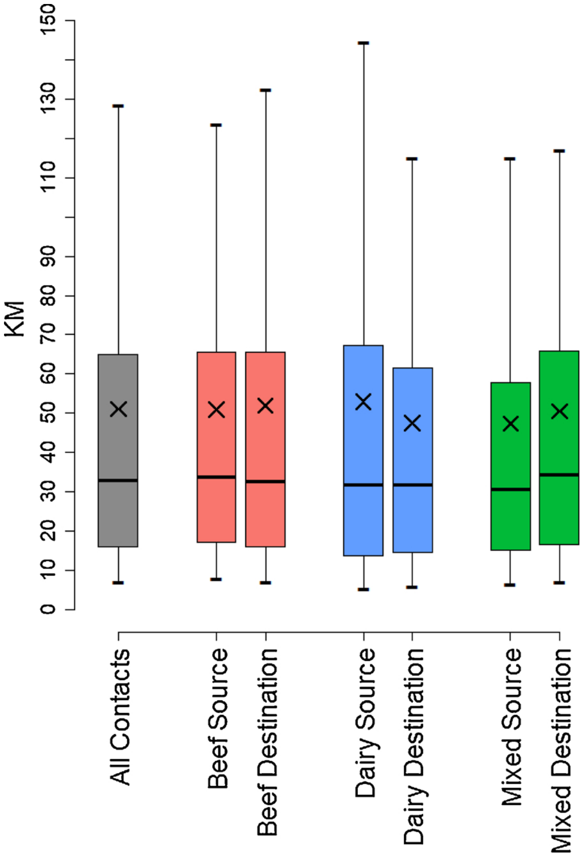

Fig. 15. Distances covered by *contacts*, for all contacts and by production type (beef, dairy and mixed) for source and destination herds. Boxes span 25th – 75th percentiles and the upper and lower limit of whiskers show 10th and 90th percentile. Mean values are represented by crosses.

the hypothesis that the data would follow a power law distribution, in contrast to claims made for similar data elsewhere (e.g. Bigras-Poulin et al., 2006, Büttner et al., 2013, Dubé et al., 2011; Mekonnen et al., 2019; Natale et al., 2009; Nöremark et al., 2011; Pozo et al., 2018). For all of the 6 movement measures, a scale free distribution was either rejected or a better fitting distribution (log normal) was found. Fig. 2 shows that although the three 'in' movement measures ('*in* transfers', '*in* contacts', '*in* degree') are less heavy tailed than if they followed a power law (though only marginally so in the case of *in* transfers), the equivalent three 'out' movement measures all followed an even heavier tailed distribution. Networks such as this, where small number of high-volume nodes are responsible for relatively high proportion of connections, are vulnerable to disruption when these nodes are removed. In contrast, these networks are relatively immune to disruption if nodes are removed at random (Büttner et al. 2013). This suggests that more work should be done to understand where these high-volume herds reside and how monitoring them more closely can be used to control disease.

Some of these high-volume herds were found to retain their animals for long periods (Fig. 5). For example, we found that there were some herds that had sent animals to over 100 other herds after keeping them for, on average, over 100 days, although it should be borne in mind that these animals may have been born in the high-volume herd, rather than entered as a result of movement. Similarly, there were some herds that received animals from over 100 herds and these animals remained in these high-volume herds for, on average, over 100 days. Likewise, it should be borne in mind that some of these animals may die in the high-volume herd or be sold for slaughter rather than move to another herd. Notwithstanding these caveats that some animals in these high-volume nodes have not entered the herd from elsewhere or, conversely, may never enter another herd, these high-volume, long duration herds, in which a large number of animals are involved in movements and are potentially mixing with a large number of others for a long period of time while in the herd, are likely to be especially important in the transmission of infection. Further analysis of how such herds operate is likely to shed more light on their epidemiological role.

We also measured distance between origin and destination herds, where it should be noted that we chose to measure these as Euclidean distance as opposed to the shortest or quickest distance by road. We also ignored the location of markets which might have formed an intermediate stopping point for such moves. We did this because we were primarily interested in the role that long distance moves might have had in spreading infection across a territory. It is clear that there is considerable variability in the distances moved where animals are traded, with some moves > 400 km in distance but the majority within 40 km and/or the same county, and direct farm-to-farm movements typically shorter than moves mediated via markets (Figs. 10–14). It was particularly notable that moves away from herds were on average much further in many areas in the west and south of ROI than they were elsewhere and that, conversely, moves into herds were furthest for herds in the east around County Dublin, and some areas of the north west. Examination of the county to county transfers maps (Figs. 10 and 11), show this to some degree explained by the movements of animals from areas in the south west (e.g. county Kerry) to those in the north west (e.g. Galway and Mayo) and centre and east (e.g. Dublin, Kildare, Meath). Closer examination of these data will shed light on the drivers of these differences, although explanations include the movements of animals born in herd in the west of Ireland for fattening in more productive grazing areas and feedlots in the east, as well as movements to herds in the east and north of ROI prior to export.

We found that no single measure adequately captured movement for an individual herd, whether we looked at this using *in* or *out* moves measured as *degree*, *contacts* or *transfers*. There will be some herds which have the same *in* or *out degree* but very different *in* or *out contacts* and *transfers* – e.g. a dairy herd which moves a single bull in for breeding purposes will have the same *in degree* (i.e. 1) as one that moves in a large number of in-calf heifers every year. We did find that there was generally a very close correspondence between *degree* and *contacts*, which matches our finding that movements between a given destination and source herd tended to occur only once during the year. Particularly notable was that measures of movement into herds were poorly correlated with movements out. This should be born in mind when conducting analyses on the role of connectivity in the spread of infectious agents. Where possible in our analyses we have tried to show all three types of movement measure (*degree*, *contacts* or *transfers*) but in some cases we have only shown data for a specific type, where this appeared to us to be the most informative approach and/or there was little difference in results between the three types. For example, in Fig. 5 we showed *degree*, in Figs. 8 and 9 *transfers* and Figs. 12–14 *contacts*. The use of weighted networks would have been an alternative to our approach based on these three different levels of aggregation, with, for example, the number of *transfers* of individual animals in a given *contact* or *degree* used as a weighting factor. For example, our calculation of *betweenness* could have used this approach.

We have had to limit both the scope and depth of this study on Irish cattle movements so that it could be described in a single manuscript which would both readable and intelligible. Our primary aim was to broadly cover spatial and network aspects of the Irish cattle industry, both to enable better understanding of these phenomena in an Irish setting, but also to suggest areas where further, more in depth work could be carried out. There is therefore much scope for further work. One aspect which we have not addressed is the temporal aspect of movements. Irish cattle movements undergo distinct temporal patterns over the course of a year (DAFM, 2017, 2019) and these are likely to be pertinent to the way in which infection can spread throughout the network. Similarly, different diseases are infectious at different rates, which means that consideration must be given to the frequency of moves between herds and its role in maintaining infection. However, it should be noted that many of the cattle diseases of economic importance in Ireland, such as Bovine TB, BVD and paratuberculosis, are maintained in the host for long periods, and therefore this issue is of lesser importance than for diseases such as foot and mouth disease, which are highly infectious but generally for a limited time (Kitching et al., 2005). It would also be interesting to examine how the vulnerability of the entire network to infection is evolving over time, through an examination of metrics such as the size of strongly and weakly connected components (Robinson et al., 2007), or the epidemic threshold (Robinson et al., 2007), or through the use of dynamic SEIR models (Duncan et al., 2012).

In our analysis of distances between herds covered by markets, we found that market-mediated moves on average resulted in greater between herd displacements than did direct farm to farm sales, and it is known that market moves also account for a larger number of moves in total (McGrath et al., 2018; DAFM, 2017, 2019). Much existing work on cattle movement networks does not distinguish between markets and herds, and considers them both simply as nodes in a network, even though animals typically only reside in markets for a day or so, and are typically restricted to a small pen with a few other individuals. For this reason, we were careful to restrict our analyses to cattle herds, where disease transmission characteristics are very different, so that the patterns we observed were clearly understandable within this context. However, useful insights might be offered in a study of the role of the network and spatial characteristics of cattle markets in Ireland, especially with regard to their potential role in the spread of highly infectious diseases, such as foot and mouth disease, which could be transmitted to a large number of animals with minimal direct contact between them.

Further work could extend the analysis of the network characteristics of Irish cattle movements touched on here. For example, we restricted our analysis of centrality measures to *in* and *out degree*, *contacts* and *transfers*, as well as betweenness. Other measures of centrality such as the in and out going infection chain, in and out closeness, and Eigenvector Centrality could also be explored as a means to capturing the likely role of an individual herd in spreading infection (Büttner et al. 2013, Nöremark et al., 2011). Perhaps an index based on the mean rank across a number of movement-related variables would be a useful approach. Further work on networks could consider the temporal evolution of the whole network (as distinct from the node-level analysis conducted here), investigating the extent to which the network has changed over time and whether the situation is becoming more or less risky in respect to the likelihood of disease outbreaks.

Examination of those herds which are potentially most important in the spread of infection, such as those with a large number of *contacts*, where animals remain in the herd for long periods before moving on, and where long distance movements are common, would reveal the type of trade they are engaged in, where they are sending their animals and where their animals are coming from. It is also hoped that these further studies will allow analyses of the relationship between the movement characteristics of cattle herds and the likelihood that they will have tested positive for diseases such as bovine TB, BVD and paratuberculosis, which will in turn enable a better understanding of how surveillance and disease management can be better targeted in disease control.

Declaration of Competing Interest

None.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.prevetmed.2020.105095.

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