Master Thesis, Institute of Computer Science, Freie Universität Berlin

Biorobotics Lab, Intelligent Systems and Robotics

# Temporal Analysis of Honeybee Interaction Networks

**based on Spatial Proximity**


*Alexa Schlegel*

Matriculation number: 4292909

alexa.schlegel@fu-berlin.de


Supervisor: Prof. Dr. Tim Landgraf

Second Supervisor: Prof. Dr. ???

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Berlin, den March 19, 2017

Alexa Schlegel

Everything we hear is an opinion, not a fact.
Everything we see is a perspective, not the truth.

— Marcus Aurelius

Dedicated to my parents and my sister.

## Abstract

some abstract in english

## Zusammenfassung

ein abstract auf deutsch

# Contents

# Chapter 1

# Introduction

Social insect societies are formed by thousands of individuals, which continuously move and interact with each other inside a dark nest. Honey bee colonies are thus organized complex and dynamical systems, which form a collective intelligence. Observing individual honey bees is, therefore, vital for understanding collective behavior, decision making, and organization of tasks within the colony.

Within the BeesBook[1] project of the Biorobotics Lab of Freie Universität Berlin Wario et al. [28] developed technologies to automatically track all individuals of a honey bee (Apis mellifera) colony. Shortly after birth, each bee has been marked on their thorax using circular 12-bit tags (figure 1.1) and then added to the colony. The comb is observed by four cameras over a period of nine weeks and each picture is evaluated automatically. The resulting data set contains the position of each bee and its decoded id.

In this thesis, temporal worker-worker interaction networks, based on spatial proximity, are derived from the described data set. Each node in the network is a bee and a link between two individuals is created if they share a position close to each other. The temproal networks are aggregated for several points in time. Social network analysis methods are applied to determine the usefulness and the characteristics of the resulting networks and its communities.

Until now, social network analysis has been applied to only a subset of a honey bee colonies live, simply because the data were not available to this extent and quality so far.

## 1.1 Motivation

Most of the studies in the field of animal social network analysis, especially when analyzing the behaviour of social insects colonies, only include a reduced subset of the colonies life, due to a large number of individuals. Usually, the reduction is carried out on three levels (1) time and resolution, (2) space, and (3) number of individuals.

Labeling only a subset of the colonies individuals, a short observation period, low res-

[1] `http://beesbook.mi.fu-berlin.de/wordpress/`; Last accessed: 16.03.2016, 12:05 p.m.

**Figure 1.1:** Tagged bees inside the hive.

olution and manually extracting information from photos or videos is very common in behavioral sciences [19, 25].

Baracchi and Cini [3] observed 300 bees out of a colony with 4000 individuals over a period of ten hours. One of the two sides of the hive was observed by taking a photo each minute. Coloured numbered discs were used for individually marking bees. The analysis of a weighted und undirected worker-worker interaction network revealed a highly compartmentalized structure inside the honey bee colony. Depending on the age, bees occupy different areas of the comb and correspond to different tasks. Also, the contact is limited within groups. Blonder and Dornhaus [6] color painted all individuals of ant colonies (size 6-90 for each colony) and filmed the colonies for 30 minutes. Interactions between individuals were manually extracted by watching the videos. Using time-ordered (dynamic) networks they analyzed the temporal and spatial dynamics of information flow.

Recently, automated tracking of insects has become technically feasible [28, 10, 12]. Using automated high resolution tracking data, which includes all individuals of the complete comb over a long time period allows for more advanced anaysis focusing on temporal dynamics. Mersch et al. [18] automatically tracked all individuals of six ant colonies over a period of 41 days. Applying the Infomap community detection algorithm to the physical contact networks for each day, revealed three distinct and robust groups. Each group represents a functional behavioral unit, with individuals changing groups as they age.

The majority of social insect interaction networks studies, due to previously technical limitations, aggregate temporal tracking data into a single static network [17, Chapter 15]. Automatic tracking allows shifting more towards the temporal and dynamic investigation.

## 1.2 Research Goal

The aim of this thesis is to investigate whether the provided data set of tracked honey bees is useful for creating worker-worker interaction networks using spatial proximity as a proxy for interactions between bees. Thus, I need to implement a pipeline to infer networks out of the data set. Furthermore I want to find out if the resulting networks are suitable for social network analysis.

I want to achive my research goals by answering the following questions:

1. *Is it possible to infer networks with the provided honey bee tracking data?*
   What challenges and limitations does the data set imply? What pipeline parameters are necessary?
2. *What kind of worker-worker interaction networks emerge and how are they structured?*
   How are those networks characterized and are they different from a random network?
3. *Does the network display a meaningful community structure?*
   Are those communities robust in terms of pipeline parameters?
4. *How are communities characterized?*
   Do they reflect known colony behavior in terms of age and spatial distribution?
5. *How do the communities emerge over time?*
   Are they stable regarding their properties? How do members move between communities?

This work is meant to be the foundation for further more hypothesis-driven research using a network science approach to study the complex system of honey bee colonies and their collective behavior.

## 1.3 Methodology

explorativ Network Science Approach.

## 1.4 Outline

[TODO]

# Chapter 2

# Theretical Background

The following chapter gives a short introduction into social network analysis (SNA). It introduces animal interaction networks as a special type of network. It defines terms and concepts used throughout this work and explains networks metrics and algorithms of which we will make use of.

Social network analysis is a way of mapping and measuring specific relationships and flows between entities

mapping and measuring of relationships and flows between people, groups, organizations, computers, URLs, and other connected information/knowledge entities.
Social network analysis (SNA) is the process of investigating social structures through the use of network and graph theories.[1] It characterizes networked structures in terms of nodes (individual actors, people, or things within the network) and the ties, edges, or links (relationships or interactions) that connect them.

number of nodes/vertices $N$ (size of the network)
number of links/edges $L$
$D$ is density $D = \frac{2L}{N(N-1)}$ $k$ degree of a node $n$, $k_i$ of $n_i$
$\langle k \rangle$ average degree
definitions taken from Barabási [2]

$\langle C \rangle$ average clustering coefficient

* number of nodes $N$
* number of links $L$
* density $D$
* average degree $\langle k \rangle$
* average weighted degree, average strength $\langle s \rangle$
* max and min (weighted) degree
* global clustering coefficient $C_\Delta = \frac{3\times\texttt{number of triangles}}{\texttt{number of connected triples}}$ (transiticvity undirected) [29]

* Number of components (Connesctedness): components = subnetworks, A component is a subnet of nodes in a network, so that there is a path between any two nodesthat belong to teh component, but one cannot addany more nodes to it that would have the same property.

* Average shortest path (average path length) $\langle d \rangle$: The average of the shortest path between all pairs of nodes.

* Diameter $d_{\mathtt{max}}$:The longest shortest path , or the distance between the two furthest nodes.

## 2.1 Animal Interaction Networks

Networks where individuals are nodes and edges are defined as interaction events between individuals are called *interaction networks*, sometimes also contact networks. Those interactions used as an edge can be of different types [9]:

- spatial proximity [16, 23],
- physical contact (usually with antennae, "antennation") [18] [TODO anschauen: 10, 67, 80]
- a food exchange event (trophallaxis) [TODO anschauen: 15, 68, 69, 93]
- or specific communication signals [TODO anschauen: 38, 56]

directed and undirected
weighted and unweighted

define proximity/association

## 2.2 Network Metrics and Algorithms

Basic terms

Graph: a set of nodes and a set of relationships between the nodes, given by a matrix or visualized as a picture showing dots connected by lines

Node: a component of a network with known relationships to others in the graph model representing the network; in a social network, this can be an individual (person or animal) or group; also called a vertex or point

Path length: the shortest number of ties between two nodes

Sociomatrix: for a group with n members, an nn matrix with each group member along the vertical and horizontal axes and each entry in the grid as the weight of the social relationship, if any, between the two intersecting individuals

Tie: a relationship between two components of a network, where the two related components are nodes in the graph model representing the network; in a social network, these can be any sort of social relationship, such as social interactions or information transfer; also called an edge or link

Individual (local) measures

Betweenness centrality: centrality based on the number of shortest paths between every pair of other group members on which the focal individual lies

Centrality: a measure of an individual's structural importance in a group based on its network position

Closeness centrality: centrality based on the shortest path length between a focal individual and all other members of the social group

Degree centrality: centrality based on the number of direct ties an individual has

Indegree (reception): the number of ties directed towards an animal, e.g. the number of social interactions it receives

Node degree: the number of ties a focal animal has; the number of other animals with which the focal individual interacts

Outdegree (emission): the number of ties originating from an animal, e.g. the number of social interactions it initiates

Intermediate measures

Clustering coefficient: the density of the subnetwork of a focal individual's neighbours; the number of ties between neighbours is divided by the maximal possible number of ties between them

Cliquishness: how much the network is divided into cohesive subgroups; a clique is a set of nodes where each node is directly tied to each other

Group measures

Average path length: the average of all path lengths between all pairs of nodes in the network

Density: the number of realized ties divided by the number of possible ties in the network

Diameter: the longest path length in the network
Wey et al. [30]

Degree Distribution
Degree Centrality, Closeness Centrality, Betweenness Centrality
Clustering Coefficient
Modularity

Proximity (distance), strength, disparity, closeness, and betweennes are taken from Jeanson [16].

**Measures for weighted networks** strength $S_i$ measures the total weight of edges connected to a node $i$ and is definded as $S_i = \sum_{j=1}^{n} w_i j$ according to Barrat et al. [4]
closeness, computed using Dijkstra's algorithm with that edge attribute as the edge weight [22]
betweenness using dijkstra [7]

weighted clustering coefficient and weighted average clustering coefficient [26]

**Disparity** `https://github.com/aekpalakorn/python-backbone-network` Low values of disparity indicated that the weights of associations were of the same order and, consequently, that ants interacted homogeneously with all nestmates. In contrast, privileged associations between ants were evidenced by relatively large values of disparity showing the dominance of a few weights over the others. [5]

Disparity: For a given node i with connectivity ki and strength si different situations can arise. All weights wij can be of the same order si/ki . In contrast, the most heterogeneous situation is obtained when one weight dominates over all the others. A simple way to measure this "disparity" is given by the quantity Y2 introduced in other context [12] ; [13];

$$Y_2(i) = \sum_{j \in \Theta(i)} (\frac{w_i j}{s_i})^2$$

**Centrality measures** betweenness and closeness eigenvector centrality (eigencentrality)

**Network Reduction algorithms (backboning)** k-core decomposition
minimum spanning tree
Global weight treshold
Disparity Filter

## 2.3 Temporal Networks

TODO

## 2.4 Community Detection

To understand the large-scale structure of networks, one can look at the networks so called community structure. Communities are naturally occuring groups in a network. Seperate graph into groups of nodes that have few links between them. The number and size of communities is not fixes (as compared to graph partitioning!). [20, p. 371]

In network science we call a community a group of nodes that have a higher likelihood of connecting t each other than t nodes from other communities [2, p. X]. A networks's community structure is uniquely encoded in its wiring diagram [2, p. X]. A community is a locally dense connected subgraph in a network [2, p. X].

In other words, all members of a community must be reached through other members of the same community (connectedness). At the same time we expect that nodes that belong to a community have a higher probability to link to the other members of that community than to nodes that do not belong to the same community (density). While this hypothesis considerably narrows what would be considered a community, it does not uniquely define it. Indeed, as we discuss below, several community definitions are consistent with H2.
groups of vertices with a higher-than-average density of edges connecting them
meaning of communities in animal social networks

There are a lot of different approaches and algorithms who adress the detection of communities. Fortunato [13] gives an extensive overview about well known types of algorithms for further reading. The algorithms used in this work, for static and dynamic detection, are described in the following sections.

### 2.4.1 Leading Eigenvector

Newman [21] propose an algorihtms which uses the eigenvectors of matrices for finding community structures in networks.

stackoverflow
leading.eigenvector.community is a top-down hierarchical approach that optimizes the modularity function again. In each step, the graph is split into two parts in a way that the separation itself yields a significant increase in the modularity. The split is determined by evaluating the leading eigenvector of the so-called modularity matrix, and there is also a stopping condition which prevents tightly connected groups to be split further. Due to the eigenvector calculations involved, it might not work on degenerate graphs where the ARPACK eigenvector solver is unstable. On non-degenerate graphs, it is likely to yield a higher modularity score than the fast greedy method, although it is a bit slower.

Leading eigenvector. This algorithm was proposed by Newman39. The heart of this algorithm is the spectral optimisation of modularity by using the eigenvalues and eigenvectors of the modularity matrix. First, the leading eigenvector of the modularity matrix is calculated, and then the graph is split into two parts in a way that modu-larity improvement is maximised based on the leading eigenvector. After that, the modularity contribution is calculated at each step in the subdivision of a network. It stops once the value of the modularity contribution is not positive. Its computational complexity of each graph bipartition. [31]

### 2.4.2 Communities in Evolving Networks

According to Aynaud et al. [1] and Bródka et al. [8] there are three main approaches for community detection in temporal networks (also called community tracking): (1) using a static community detection algorithm on several snapshots and then solving a matchig problem, (2) using algorithms who are directly suited for temporal networks and (3) using incremental or online algorithms when processing data streams. For each of the three approaches, several mehods already exist.

As community tracking is not the main focus of this work, I chose to apply the most intuitive approach aout of approach (1): detecting static communities for each snapshot and then matching those communities using set theory. Two communities at successive timesteps are matched if they share enough nodes. The *match value* (between 1 and 0) between two communities $C$ and $D$ according to [15] is defined as:

$$\texttt{match}(C, D) = \texttt{min}\left(\frac{|C \cap D|}{|C|}, \frac{|C \cap D|}{|D|}\right) \tag{2.1}$$

A high match value accurse, when two communities share a lot of nodes and are of a similar size. Communities with the highest value are matched. A threshold should be applied to more precicley define what “share enough nodes” means.

# Chapter 3

# Related Work

Look at [25] for static network analysis stuff they measured (ants, only small amount with observed interaction using 20 Minute videos).

## 3.1 Networks in social Insects and Honey Bees

In *Social Insects: A Model System for Network Dynamics* [9] a good overview is given about Role and Types of Networks in Social Insects.

## 3.2 Spatial Proximity Networks

TODO short summary, also on network sience methods:
*Long-term dynamics in proximity networks in ants* [16]

*Contact networks and transmission of an intestinal pathogen in bumble bee (Bombus impatiens) colonies* [23]

## 3.3 Temporal Aspects in Networks

## 3.4 Network Analysis Tools

# Chapter 4

# Approach and Implementation

In this chapter the basic work flow is described in detail. The process is mainly driven by an exploratory approach, but follows primarily Farines and Whiteheads [11] primary steps and key considerations for social network analysis to non-human animal data. The adapted and resulting process is visualized in figure 4.1.

The dataset was first analysed regarding data quality and to form an understanding of the dataset and the behaviour of bees in general. Those findings were used to define nodes and infer associations to build the network, respectively derive the parameters for the network pipeline. The static and temporal networks are analysed using network science tools and methods. For testing hypothesis the networks are combined with spatial and age information. Each step is explained within the following sections.

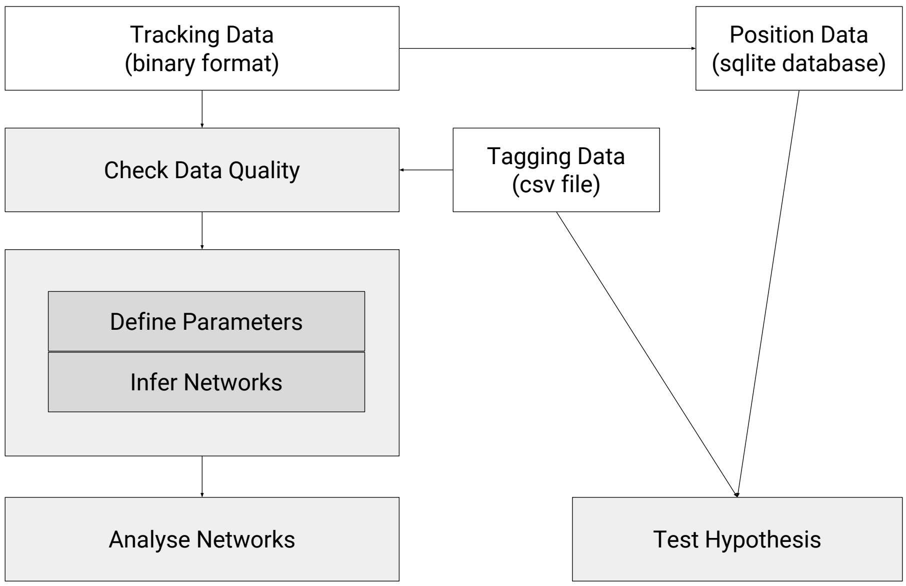



**Figure 4.1:** Steps of the Research Approach

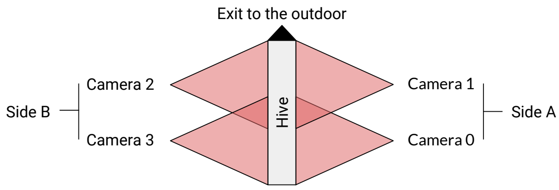



**Figure 4.2:** Camera Setup in 2016

## 4.1 The Dataset

The dataset derives from video files, that capture tagged honey bees of one colony in an observation hive. Each individual of the colony, including about 3000 bees, were tagged with circular 12-bit markers (figure 1.1, section 1). Four cameras were used to film the hive. The setup of the cameras is illustrated in figure 4.2.

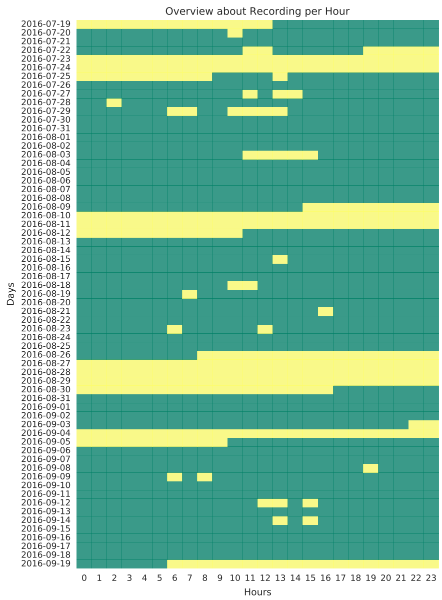



**Figure 4.3:** Recording Season with maintainance and failures: *Green* indicates recording went without any big interruption; *Yellow* indicates maintainance work or technical failures of one or all cameras. This is calculated using the expected number of files produced by each camera per hour.

The recording season lastet nine weeks (63 days), around the clock, from 19.07.2016 until 19.09.2016, with some interruptions due to maintainance and technical failures. I chose four consecutive days (30.07, 31.07, 1.8,2.8), marked in figure 4.3 for further analysis and the 26.07. for testing purpose.

The recording resolution of each camera is three frames per second, with 1024 frames per video file. For each frame, bees were detected by using an image analysis pipeline, which is explained in detail in [28]. The resulting detection data is stored in a binary file format. A python library called *bb-binary*[1] provides easy access to the binary

[1] `https://github.com/BioroboticsLab/bb_binary`; Last accesed: 2106-02-16, 04:28PM

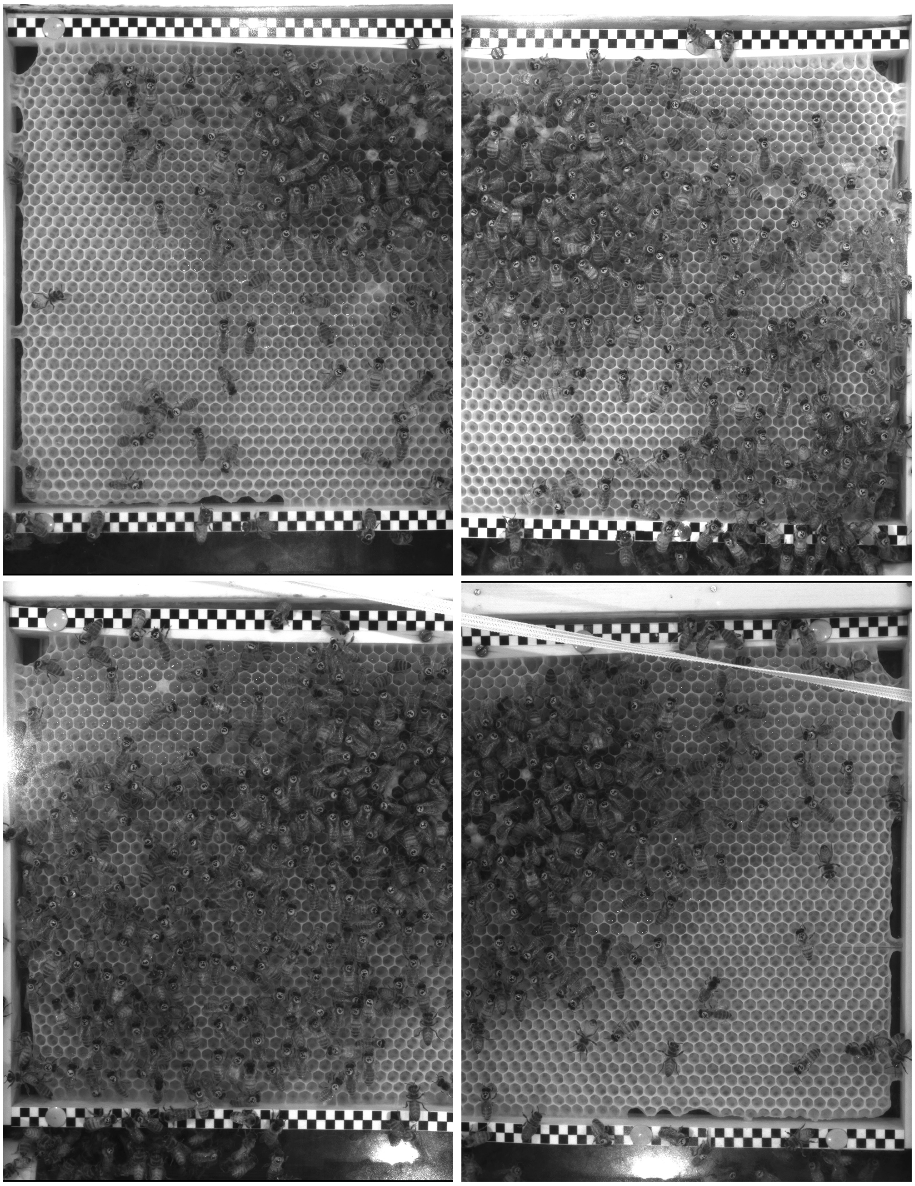


**Figure 4.4:** xxx

files. Each file in bb_binary file format corresponds to a video file of a single camera. The size of the complete dataset for 2016 is 470 GB, about 7.5 GB of binary data per day.

Exactly 3.191 bees were tagged. The tagging period was 67 days long. The tagging started on 28.06.2016 (22 days before the recording started) and lasted until 02.09.2016 (17 days before the recording ended). The young bees were tagged and then added to the hive, about noon each day. The overall tagging frequency is shown in figure 4.5. The hatching day for each bee was documented. Therefore the age of each bee at a certain point in time can be calculated.

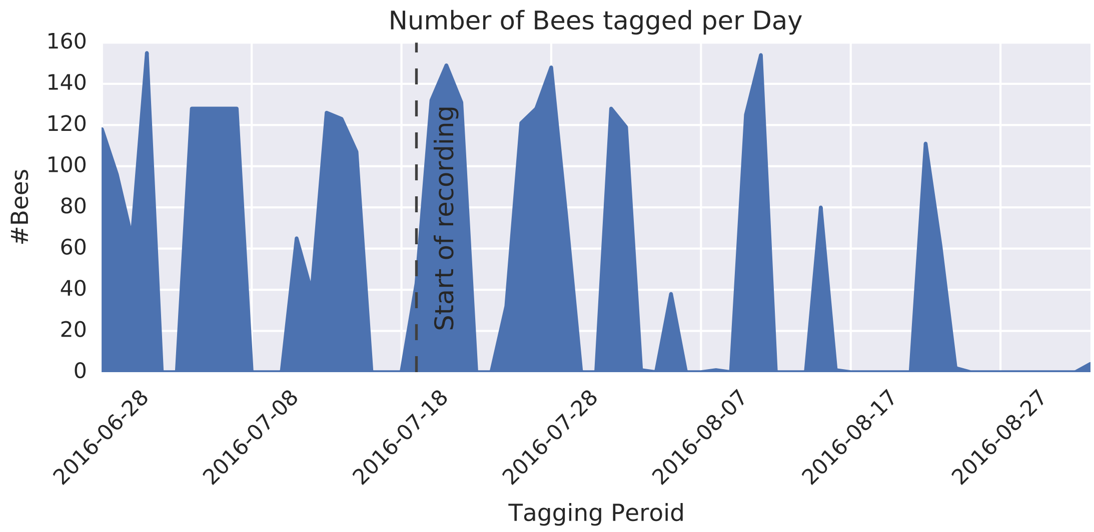



**Figure 4.5:** Tagging frequency of bees: The bees were primarily tagged during the week. On average 48 bees were tagged each day, considering only tagging days, the average is about 91 (±50) bees (median 118).

### 4.1.1 Structure of the Dataset

The data is organised in *frame container*, wich corresponds to a video file of a single camera. A frame container holds all *frames* for that specific video. Each frame has a list of all detected bees. A *detection* has the following attributes, which are relevant to this project:

- **xpos**: $x$ coordinate of bee with respect to the image in pixel
- **ypos**: $y$ coordinate of bee with respect to the image in pixel
- **radius**: of the circular 12-bit tag
- **decodedId**: decoded 12-bit id

Besides further information, the frame container specifies the camera, which took the video. A frame is also attributed with a timestamp. The data can be accessed iterating on the frame level, using two timestamps (start and end) for specifying the time interval. The complete data scheme can be found on github[2].

### 4.1.2 ID Probabilities and Confidence Level

With a 12-bit ID, 4096 bees can be tagged. Each bit of the decodedId is not a 1 or 0, but represents a probability between 0 and 255. It indicates the reliablility of the image analysis pipeline for that specific bit. A number closer to 255 represents a 1, a number closer to 0 a 0. A *confidence value* can be calculated for each ID. The

[2] `https://github.com/BioroboticsLab/bb_binary/blob/master/bb_binary/bb_binary_schema.capnp`; Last accessed: 2106-02-16, 04:46PM

confidence value of a single bit is its distance to 128, discretized to a value between 0 and 1. The confidence value of an ID is therefore the minimum of all bit confidences. [TODO: in leons Arbeit ist das gut erklärt]

The amount of data that remains for further processing and its quality depends heavily on the chosen *confidence level*. Figure **??** shows the relationship between confidence level, the amount of remainig data and the number of unique IDs.

### 4.1.3 Time Series of Bees

The original dataset (a number of frames containing bee detections), is transformed to binary *time series of bees*, depicted in figure 4.7 (left and middle). A time series of a bee is a sequence of zeros and ones indicating the absence and presence of a bee over a specified time interval. As expected the confidence level has an effect on the resulting time series of a bee. A high confidence leads to more gaps in the series and also to more shorter gaps (see figure 4.8).

### 4.1.4 Data Quality

The quality of the data could be indirectly checked using the age information of bees. On 26.07.2016, about half of the bee tags (2014 of 4096) were assigned to a bee. This day was chosen to determine the effects of the confidence level on data quality. At first, for each detection the age of that bee was calculated, a negative age was counted as a wrong detection. I assumed that the number of wrong detections indicated by negative age also occured in the positive half, but remained unseen, therefore I doubled the error. Secondly, the number of wrong unique IDs is also determinde using the age test. Figure 4.6 shows that even though the number of wrong detections decreases steadily with an increasing confidence level, but the number of wrong IDs only starts to decrease with a very high level.

Even with an confidence level of 100%, 30.2% of the unique IDs are wrong (have a negative age), corresponding to only 2.5% of detections. Therefore wrong IDs need to be filtered out anyway (independent of the confidence value), to obtain a more reliable dataset. A good indicator is the detection frequency of IDs. IDs with a negative age are on average less detected than IDs with a positive age.

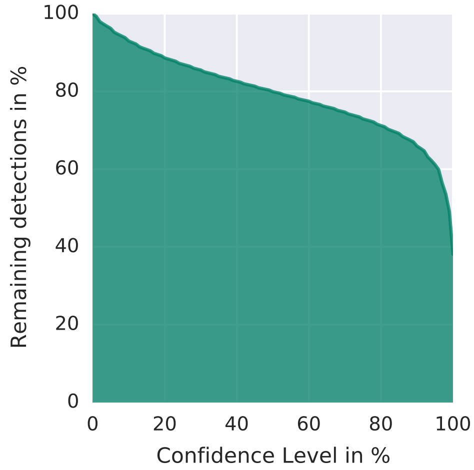
#### Frequency Filter

IDs who definately exists, but their age can to be determinded are excluded from the analysis completely. These are bees, who were tagged later ($n = 10$)[3] and IDs whos detection frequency is absurd high but there age is unknown ($n = 7$)[4]

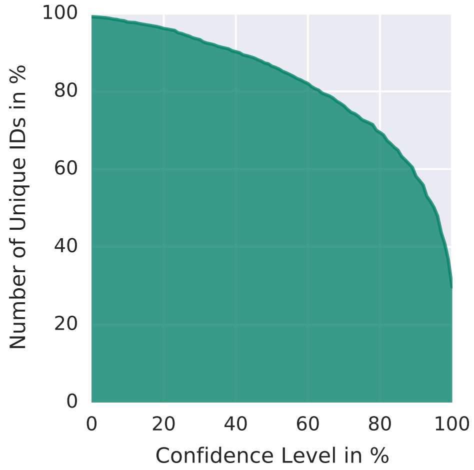
For each analysis day the number of detections per ID is obtained, excluding the mentioned IDs above. The frequency distribution tells that, IDs with a negative

[3]id= [2, 74, 2045, 3172, 3764, 3796, 3827, 3836, 3844, 3940]

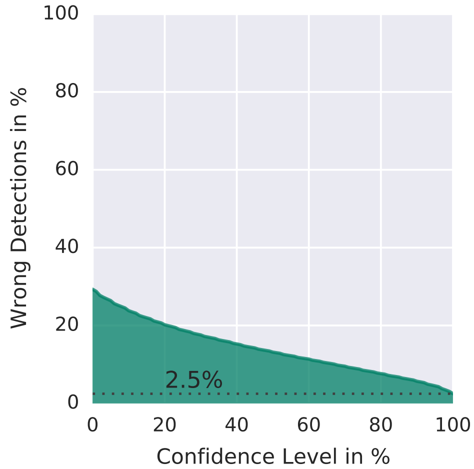
[4]id=[has changed! 17, 168, 801, 888, 2045, 2357, 2607]



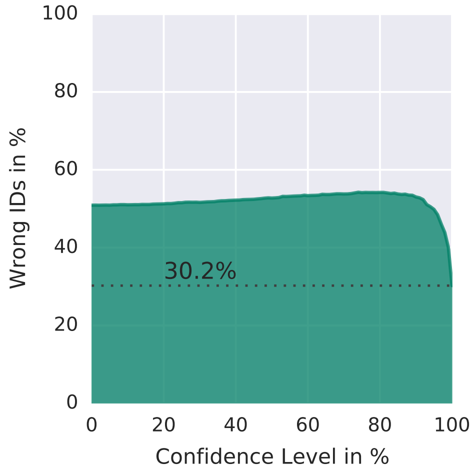

**(a)** Remaining Detections depending on the level of confidence.




**(b)** Number of unique IDs depending on the level of confidence.




**(c)** Wrong detections in relation to the level of confidence.




**(d)** Number of wrong IDs depending on the level of confidence.

**Figure 4.6:** The number of wrong detections decreases with an increasing level of confidence. In contrast, the number of false IDS becomes noticeably less only with a very high confidence level. The amount of remaining data decreases with an increasing confidence level. The number of unique IDs behave similar. (Dataset: 26.07.2016, 16:00-16:05) (Dataset: 26.07.2016, 16:00-16:05)

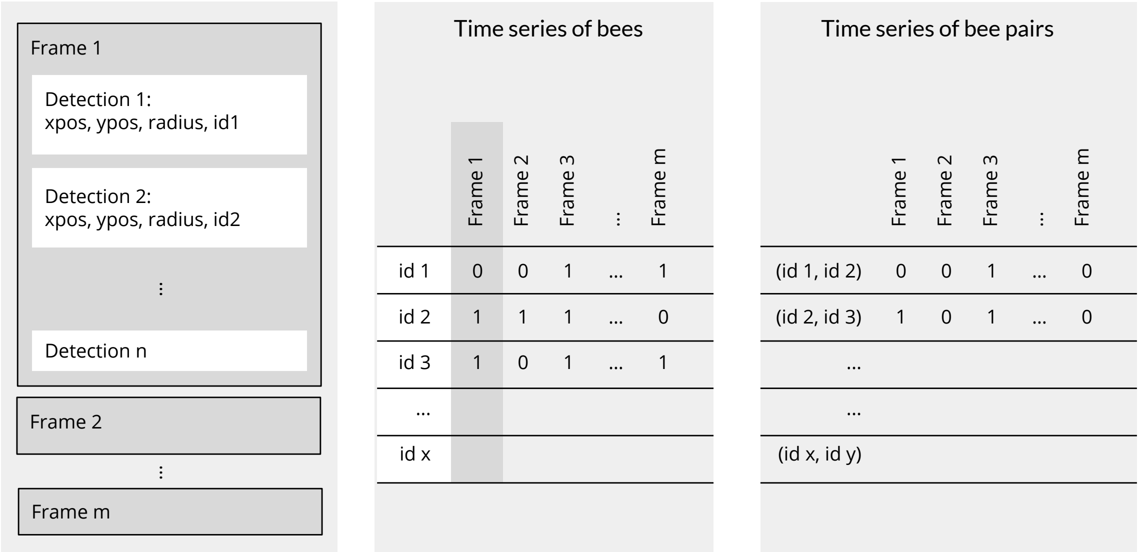



**Figure 4.7: Left:** original dataset - bb_binary data containing frames and detections; **Middle:** transformation to time series - zero indicating absence of the bee, one indicating presence of the bee; **Right:** transformation to bee pairs - zero indicating eighter one or both bees are not present at the same time or not close to each other, one indicating bees are present at the same time and nearby.

age are detected less often (704 frames $\pm 65$) than bees with a positive age (36.603 frames $\pm 2.345$). The cutoff is 99% of the negative IDs distribution. All IDs with a detection frequency below $4737 \pm 644$ frames are discarded. A list with possible (valid) IDs is kept for each day. Using this list, faulty detections can be filtered out beforehand.

### 4.1.5 Implications

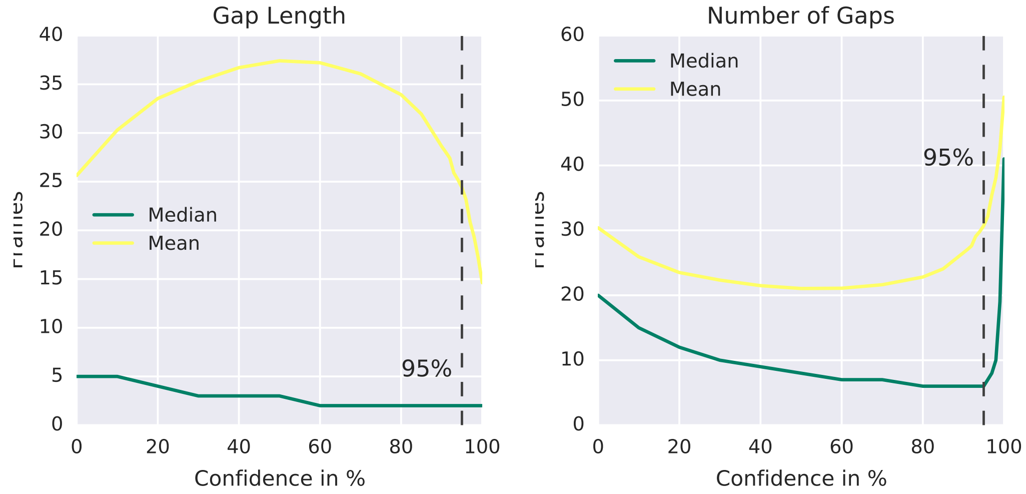
For further analysis I use the following days: 14.08.2016, 17.08.2016, 20.08.2016, 02.09.2016 with a confidence level of 95%. This period is chose because of XY.

Because bee time series contain a lot of short gaps (mean = 3, 95% confidence), the inferring of edges (bees who are close to each other at the same time), should be not that strict, or at least variable. This has to be taken into acoount, when looking at spatialy close bees.

## 4.2 Inferring Networks

The following part describes the pipeline for generating spatial proximity networks out of honey bee tracking data. A node in the network is a bee. They are distinguished by IDs. Only bees are in the network who interact at least once with another bee.

undirected and weighted, aggregated networks




**(a)** Length of Gaps depending on the level of confidence.

**(b)** Number of Gaps depending on the level of confidence.

**Figure 4.8:** Influence of the confidence level of the length of gaps and number of gaps: With an increasing level of confidence the average gap length decreases and the number of gaps per bee series increases. (Dataset: 26.07.2016, 16:00-16:05)

Two bees are associated (spatially close to each other), if their distance is minor to a *maximum distance*. As everything is very close in a bee hive this value is hard to choose. Only this criteria is very week, meaning having a resolution of three frames per seconds results in interactions which could only last for 0.33 seconds. So an additional parameter the *minimum contact duration* is introduced, it is the minimum time they have to spend at least nearby to be called associated.

Taking the fragmentation of tracks into account, it is obvious that two bees could be nearby but not at the very same time, but slightly shifted. So the minimum contact duration would be too errow prone. To overcome this issue one could correct the bee tracks, by filling gaps of varius sizes and interpolating the position of that bee accordingly. This is rather time consuming for this amount of tracking data (TODO: naja so doll auch nicht, scipy.ndimage.morphology.binary_dilation) and also considering, that the tracking data is going to be improved in the future, then manipulating the raw data seems senseless. I rather perform a gap filling (maybe similar to binary dilation) on the time series of pairs, but not on the bee tracks, because this is independent of the input data.

Edges are attributed with two parameters. The first one is the frequency of contacts, so how often they share a close position. The second parameter is the total duration of contact, how many time frames in total they spend close by.

### 4.2.1 Network Pipeline

The network pipeline takes as input a path to the bb-binary data and outputs a graph in graphML file format. The pipeline takes the following parameters:

- path to data
- confidence in percent
- gap size in frames - this is used to corret the time series of bee pairs
- maximum distance in px - define what close means (spatial proximity)
- minimum contact duration in frames - how many frames bees need to spend nearby
- cutoff in percent - IDs with a number of total detections below X percent of the mean frequency are discarded
- start timestamp - start of network slice
- window size in minutes - size of time window for aggregating the network
- number of used CPUs for parallelization
- year - calculate IDs and set camera setup for 2015 or 2016

The pipeline is parallelized on frame level, that means, each process gets a portion (frames for a timeinterval of five minutes) of the data and extracts interactions/edges. The main process adds everything up and creates a network. The steps are the following:

1. **Filter detections by confidence**
   For each of the four camera the detections are filtered by the confidence level.
2. **Simple stitching**
   Each side of the hive consists of two cameras. The $x$-coordinates of each detection (of the right cameras) is moved further to the right, also adding an offset of $2 \times$ `maximum distance`. So the left and the right detection of each side of the hive are move into one reference system.
3. **Syncronize Cameras**
   For each side of the hive the cameras need to be syncronized. In the normal case the difference between consecutive frames should be about 0.332 seconds, due to technical problem this value can be lower (0.003 ) and higher (2.932) at certain times. Cameras 3 and 2 and cameras 1 and 0 are matched, frames without a match are dropped (shorter number of frames, matchen, threshold 0.33/2, minimum).
4. **Discard Detections with certain IDs**
   All detections whos ID is in a list are keept, other detections are discarded. (see frequency filter)
5. **Extract close pairs**
   For each side of the hive, all close pairs according to the maximum distance

parameter are calculated and then joined together.

6. **Generate time series of bee pairs**
The data structure (frames and detection) is transformed to time series of bee pairs.
7. **Correct pair time series.**
The time series of bees are corrected by filling in the gaps of length `gap size`.
8. **Extract edges**
The edges and its attributes (frequency and duration) are extracted from the time series of bees using the minimum contact duration parameter. A sequence of at least X ones counts as one interaction. The frequency of those series adn the total duration (number of ones) are the attributes.

### 4.2.2 Pipeline Parameters

For performing the network analysis, I chose the pipeline parameters as follows:

**Confidence** As explained in section4.1.2, the confidence is set to 95%.

**Maximum Distance** I chose the length of a bee body, according to Baracchi and Cini [3], as the maximum distance between two bees (figure 4.9a). The average bee length of 212px (±16px) was determinded by manually measuring the length of all bees ($n = 337$) in four images (one for each camera, 21.07.2016, 03:00PM) using the tool ImageJ[5].

**Gap Size** The gap size is set to two frames. This value corresponds to the median gap length in the time series of pairs (`mode` = 1, `mean` = 27). [TODO: what dataset was used (95% confidence, XXX% cutOff, XXXpx maximal distance, date, camera)]

**Minimum Contact Duration** This is set to three frames (one second). This corresponds to Mersch et al. [18], they as well exclude interactions below one second. Looking at the frequency distribution of chains of ones (1, 11, 111, and so on) of the pair time series (after filling the gaps), then: `mode` = 1, `median` = 2 and `mean` = 4. Three frames corresponds to 57% of all chains, this seem to be reasonable. [TODO: what dataset was used (95% confidence, XXX% cutOff, XXXpx maximal distance, date, camera)]

The networks are not thresholded (according to [11]).

## 4.3 Static and Temporal Analysis

Despite the possibility of generating networks of different granularity (resolution is minutes), here for further analysis daily networks (10h, two hours after sunrise until zwo hours before sunset) are aggregated.

[5] `http://imagej.net/Welcome`; Last accessed: 22.02.2016

### 4.3.1 Static Network Analysis

The following network properties were analysed for a static day and hour network. TODO: list of properties. (similar to what others have done) nodes, edges, density, diameter

### 4.3.2 Temporal Analysis

three day networks (2 days gap)
one network 2 weeks later

### 4.3.3 Community Detection

I tested all community detection algorithms implemented in python, to find an algorithm, which works well for my case of animal social networks. The three most common python libraries for network analysis were reviewed: NetworkX[6], igraph[7], and graph-tool[8])

The algorithm needs to fulfill the following criteria:

- Support for large and very dense networks ($N > 1000$, $D > 50$ %)
- Support weighted edges
- Fast runtime
- Detection of more than one community

Table 4.1 gives an overview about the twelve algorithms reviewed. Five algorithms did not terminate after 15 minutes and were therefore excluded from further investigations. The Louvain algorithm is the same as multilevel, but takes longer producing almost the same communities and therefore was also excluded. Walktrap was tested for different step size parameters as suggested in [24], the communities remained almost the same (only a few nodes switched communities).

I had a closer look at fastgreedy, leading eigenvector, multilevel, and walktrap regarding number of detected communities and community size for all three networks. Table 4.2 shows the results.

Finally, I chose the leading eigenvector community detection algorithm because [11] explain that this algorithm is often used with animal social networks and works well. There are comparative analysis of community detection algorithms, e.g. [31, 14].

[6] `https://networkx.github.io/`; Last accessed: 16.03.2016, 6:36 p.m.
[7] `http://igraph.org/python/`; Last accessed: 16.03.2016, 6:38 p.m.
[8] `https://graph-tool.skewed.de/`; Last accessed: 16:03.2016, 6:39 p.m.

**Table 4.1: Comparing community detection algorithms** Comparison of algorithms implemented in python. Criterias are the support of weighted edges, runtime and number of communities. A runtime indicated by − mean no termination after 15 minutes.

| | fastgreedy[1] | leading eigenvector[1] | louvain[2] | multilevel[1] | walktrap[1] | infomap[1] | label propagation[1] | edge betweenness[1] | k-clique communities[2] | optimal modularity[1] | spinglass[1] | statistical inference[3] |
|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Edge weights | × | × | × | × | × | × | × | | × | × | × | |
| Runtime in sec | 3.56 | 6.27 | 11.70 | 0.72 | 19.40 | 13.20 | 0.19 | − | − | − | − | − |
| Communities | 3 | 3 | 3 | 3 | 3 | 1 | 1 | − | − | − | − | − |
| | 473<br>434<br>15 | 488<br>434 | 469<br>453 | 462<br>427<br>33 | 490<br>431<br>1 | 922 | 922 | | | | | |

[1] igraph, [2] NetworkX, [3] graph-tool

**Table 4.2: X** X

| | fastgreedy | leading eigenvector | multilevel | walktrap |
|---|---|---|---|---|
| Network 1 | 473<br>434<br>15 | 488<br>434 | 462<br>427<br>33 | 490<br>431<br>1 |
| Network 2 | 504<br>467<br>7 | 503<br>475 | 481<br>439<br>58 | 372<br>311<br>294<br>1 |
| Network 3 | 534<br>388 | 537<br>385 | 505<br>415<br>2 | 310<br>390<br>231 |

## 4.4 Attributed Data and Hypothesis Testing

Hypothesis
(1) Communities reflect groups of bees working in different areas of the hive and
(2) Communities reflect different age groups

The data which was used to test the hypothesis (1) is saved in a sqlite database for faster access, because using bb_binary (parsing the data over and over again) was to slow. For testing if lists of positions (spatial ditribution) are different the test XY was used [TODO: what to use here]

For hypothesis (2) the data is stored as a csv file of birth dates of each bee. For testing if age goups are different the Kolmogorov Smirnov Test was used.

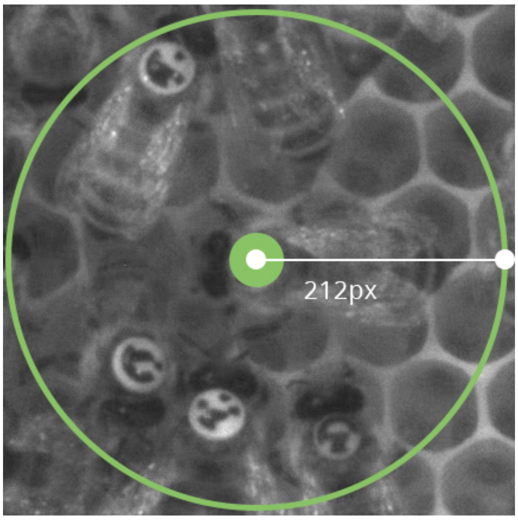
## 4.5 Implementation, Runtime and Complexity

For implementing the network pipeline python, with pandas and numpy, are used, because the bb_binary library, for accessing the tracking, data is only available in python. The networks, in graphML format, are created using the python library *NetworkX*[9] in version 1.11. iGraph for community detection
some bash scrips for generating multiple networks

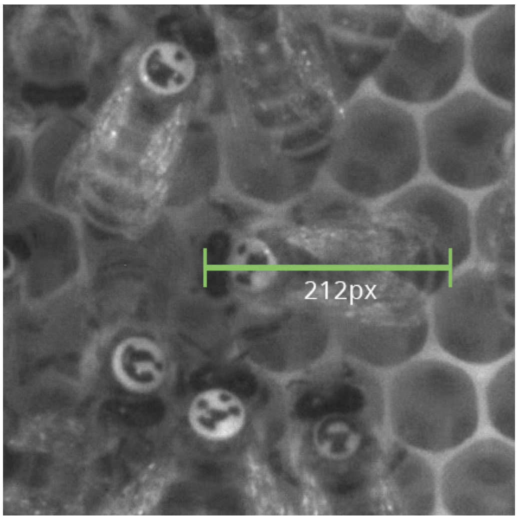
bottleneck is reading bb_binary data into pandas dataframes
using multithreading for distribution on frame level (a process gets X frames for processing)

maybe some table with how long nees what with how many cores (hom much RAM and so on)

[9] `https://networkx.github.io/` ; Last accessed: 2017-02-17, 08:07PM




**(a)** Contact Radius




**(b)** Bee Length

**Figure 4.9:** Distance Between Bees: A length of a bee is chosen as the maximal distance between bees.

# Chapter 5

# Results

I analysed three daily networks, these are refererred to below as #1, #2, and #3. Each network is aggregated for ten hours starting at 8 a.m. and lasting until 6 p.m. I chose the 20.08.2016, 22.08.2016, and 24.08.2016, because at this point in time the hive also contained tagged foragers (older bees). At the same time young bees were added to the colony (see table 5.1 for details). The age distribution for each network is shown in figure 5.1.

[TODO: PLOT How many nodes in the network stay the same over 3 timesteps? (will be going next step, same, new ones)]

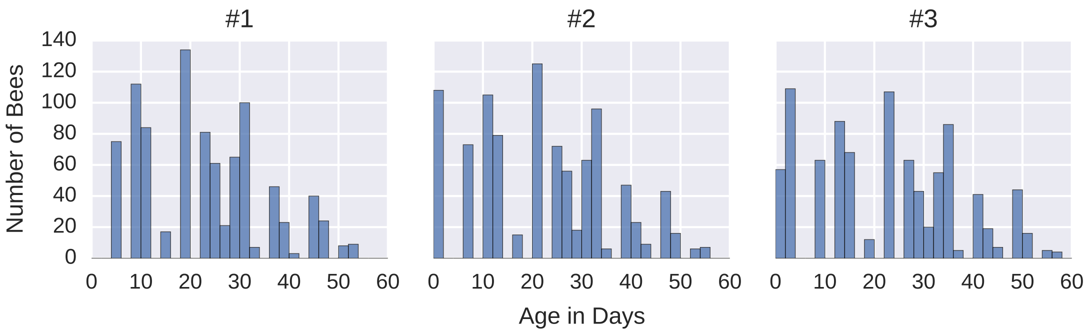



**Figure 5.1:** Age distribution per network: The width of a bar corresponds to two days.

| | 20.08.16 | 21.08.16 | 22.08.16 | 23.08.16 | 24.08.16 |
|---|---|---|---|---|---|
| Network ID | #1 | - | #2 | - | #3 |
| Number of added bees | 0 | 0 | 110 | 60 | 0 |
| Time added | - | - | 2 p.m. | 6 p.m. | - |

**Table 5.1:** Overview about networks and number of added bees.

| | $N$ | $L$ | $D$ | $\langle d_{\mathtt{max}} \rangle$ | $\langle d \rangle$ | $C_{\Delta}$ | $\langle k \rangle$ | $\langle s \rangle$ |
|---|---|---|---|---|---|---|---|---|
| #1 | 922 | 291179 | 0.69 | 3 | 1.32 | 0.79 | 631.62 | 5680.17 |
| #2 | 978 | 256066 | 0.54 | 3 | 1.46 | 0.72 | 523.65 | 3977.94 |
| #3 | 922 | 259421 | 0.61 | 3 | 1.39 | 0.75 | 562.74 | 4205.99 |

**Table 5.2:** Global network properties

## 5.1 Network type and properties

### 5.1.1 Global Structure - Network Level

Each network consists of one giant component. Table 5.2 summarizes basic network properties number of nodes, number of links, density, diameter, average shortest path length, global clustering coefficient, average degree, and average strength.

TODO: high density, small diameter, very short average path length, high clustering coefficient, high strength and degree, compared to what? random graph

TODO: calc network centralisation and add to table
TODO: PLOT degree and strength distribution
TODO: PLOT edge weight distribution

### 5.1.2 Local Structure - Node Level

[TODO: PLOT closeness, betweenness, local clustering coefficient, eigenvector centrality, weighted and unweighted]

### 5.1.3 Network type

[TODO: compare to random graph]
degree distribution random poisson or binominal, not random power law
giant component, connectedness
average path length and diameter very small, small world phenomenon
higher clustering coefficient than in random

## 5.2 Network Metrics in Relation to Age of Bees

[TODO: all plot in relation to age]

## 5.3 Community Detection

TODO: if time: show that communities are robust in terms of ilen.
TODO: age: müsste man eigentlich nochmal gegen ein randomisiertes Modell testen. Alter randomisieren
TODO: Communities centrality testen

Using the leading eigenvector (LE) algorithm in all three networks two communities with about the same number of nodes are detected. With walktrap in network 1 two communities and in network 2 and 3, three communities. The exact number of community members for algorithm is shown in table 5.1.

The first community (LE-C1, WT-C1) contains the queen and bees who are on average younger than the second community (LE-C2, WT-C3). For walktraps third community it is a middle-aged community (WT-C2). The age difference for network 1 is 8.4 days, for network 2 10.9 days, and for network 3 14.4 days on average for leading eigenvector communities.

The age distribution for each community and network is depicted in figure 5.2.

A two sample Kolmogorov–Smirnov test showed, that for leading eigenvector communities, the age distributions are significantly different ($p < 0.001$). For walktrap C1 with C2 and C3 are significantly different, but C2 and C3 are not that much significant. Exact $p$-values are shown in table 5.4

### 5.3.1 Spatial Distribution of Communities

The two communities detected by leading eigenvector are located in two different regions of the honeycomb. The older community (*orange* in figure 5.3)) is in all three networks closer to the hive exit and the younger community (*green* in figure 5.3)) is situated in the comb center. Walktrap revealed the same two communities like leading eigenvector for all three networks, with the same spatial distribution. For network 2 and 3, a third community (*gray* in figure 5.4)) is located between the young and old community.

### 5.3.2 Community members over time

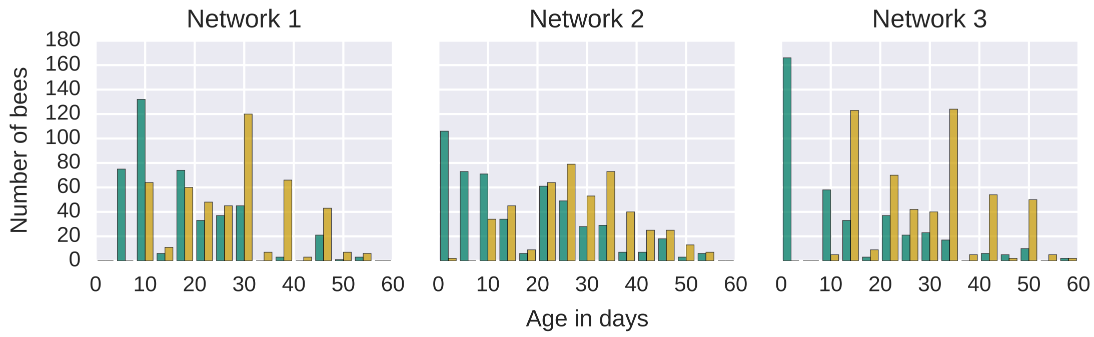
The match value between the two communities in successive time steps are calculated with formula (2.1) and presented in figure 5.5a for the resulting communities using the leading eigenvector algorithm and figure 5.5b for the communities detected with walktrap.

**Table 5.3: Overview about communities per network** Communities marked with * contain the queen. Age and standard deviation (SD) are measured in days.

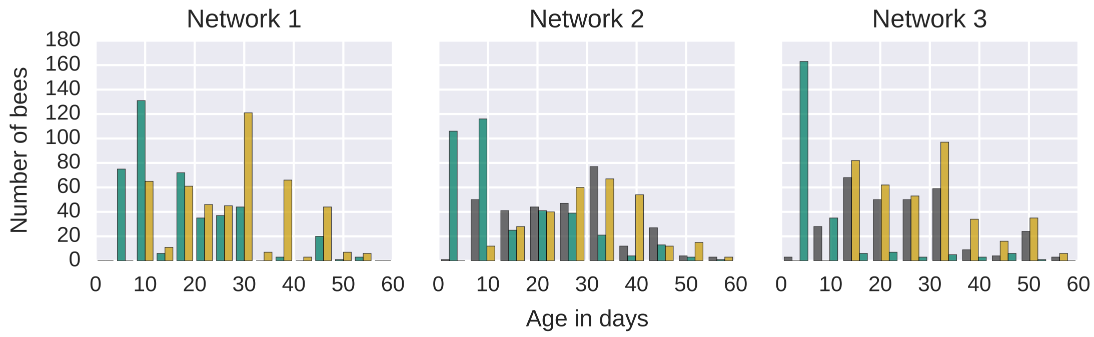
| | ID | Members | Proportion | Age | SD |
|---|---|---|---|---|---|
| Leading eigenvector | | | | | |
| Network 1 | C1 | ∗434 | 47.07% | 16.81 | ±17.91 |
| | C2 | 488 | 52.93% | 25.15 | ±19.49 |
| Network 2 | C1 | ∗503 | 51.43% | 15.44 | ±19.54 |
| | C2 | 475 | 48.57% | 26.37 | ±18.01 |
| Network 3 | C1 | ∗385 | 41.76% | 12.85 | ±20.24 |
| | C2 | 537 | 58.24% | 27.26 | ±17.84 |
| Walktrap | | | | | |
| Network 1 | C1 | ∗431 | 46.75% | 16.76 | ±17.92 |
| | C2 | 490 | 53.15% | 25.16 | ±19.48 |
| Network 2 | C1 | ∗372 | 38.04% | 12.98 | ±19.00 |
| | C2 | 311 | 31.80% | 23.11 | ±19.48 |
| | C3 | 294 | 30.06% | 28.15 | ±16.77 |
| Network 3 | C1 | ∗231 | 25.05% | 7.09 | ±19.60 |
| | C2 | 301 | 32.65% | 23.83 | ±17.22 |
| | C3 | 390 | 42.30% | 27.63 | ±18.48 |

**Table 5.4: Kolmogorov-Smirnov test** $p$-values for leading eigenvector (LE) and walktrap (WT) for each network and its communities.

| | | LE p-value | WT p-value |
|---|---|---|---|
| Network 1 | C1, C2 | 5.1e-32 | 3.3e-31 |
| Network 2 | C1, C2 | 7.6e-38 | 2.3e-32 |
| | C1, C3 | | 1.3e-44 |
| | C2, C3 | | 6.6e-05 |
| Network 3 | C1, C2 | 1.4e-64 | 1.8e-65 |
| | C1, C3 | | 3.9e-93 |
| | C2, C3 | | 2.6e-05 |




**(a)** Leading eigenvector

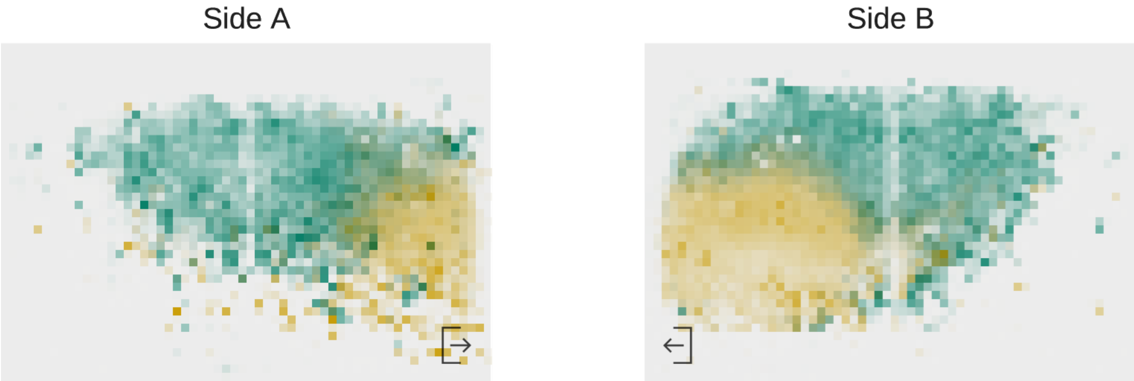



**(b)** Walktrap

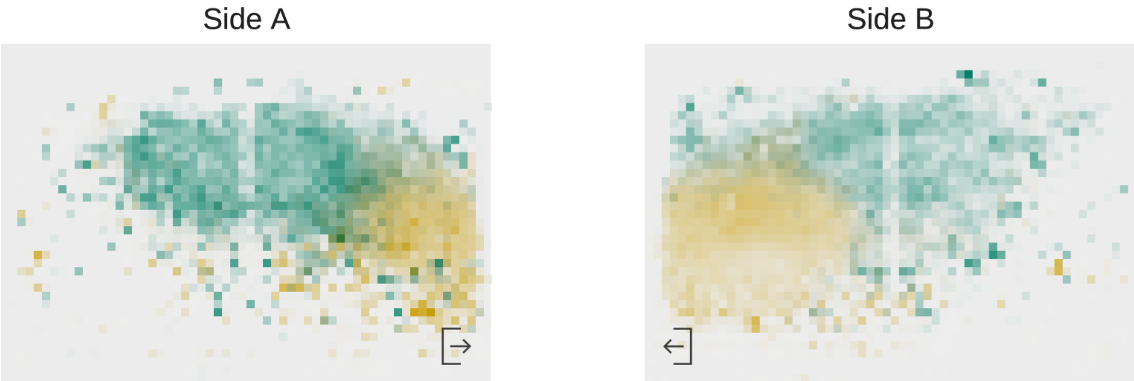
**Figure 5.2: Age distribution for each community and network** The *green* bar is the community containing the queen. The queens age is not included in the statistic. The *orange* bars coresspond to the second community, containing older bees. The *gray* bars is a third community only revealed by walktrap and contains middle-aged bees.

## 5.4 Summary

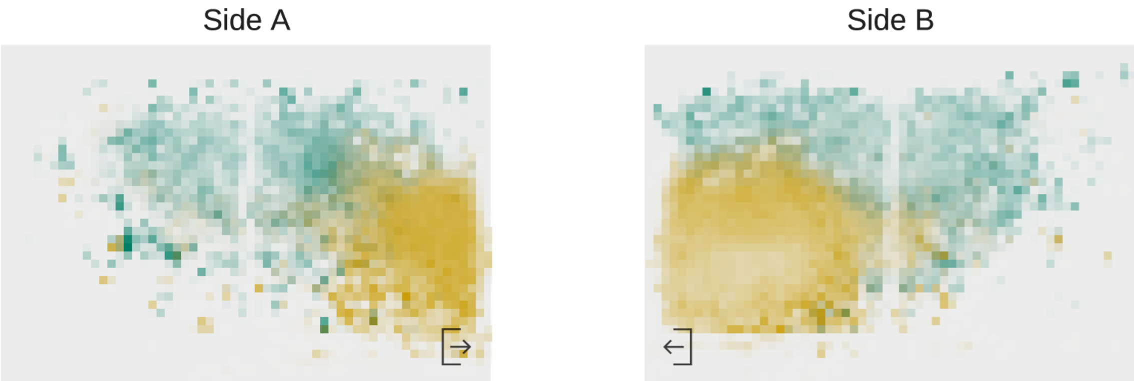
TODO




**(a)** Network 1

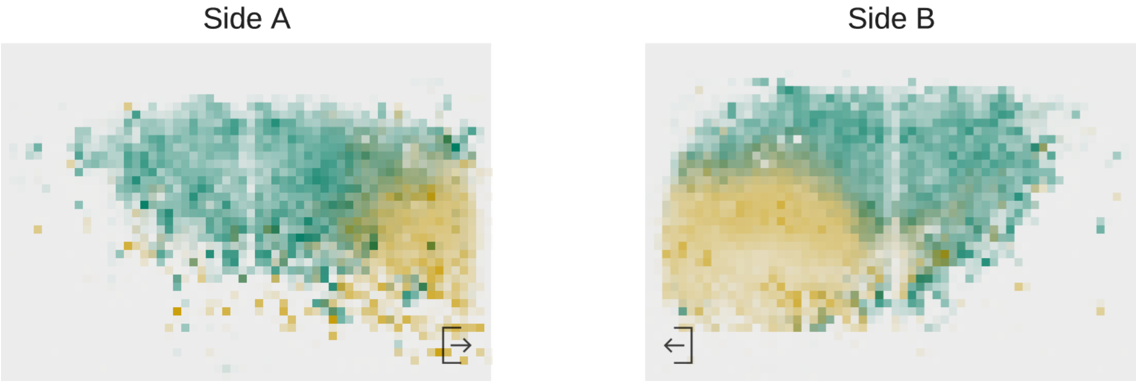



**(b)** Network 2

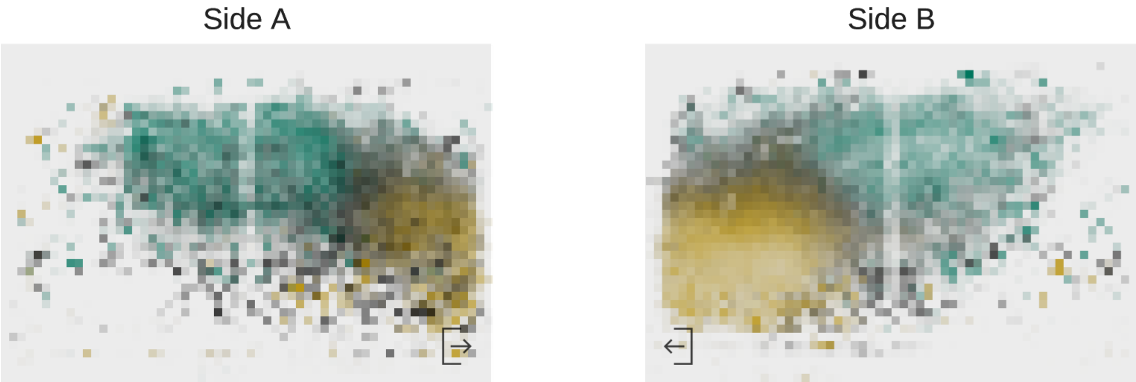



**(c)** Network 3

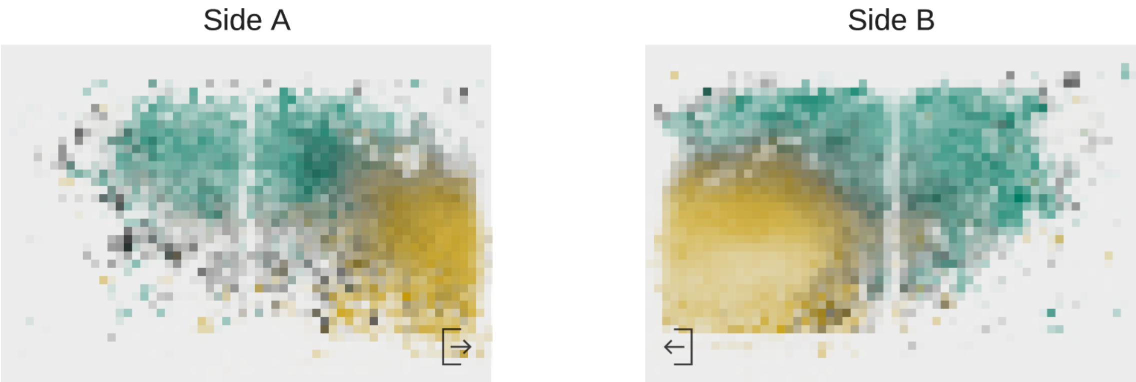
**Figure 5.3: Communities per network - leading eigenvector** The *green* colour represents the younger community, containing the queen. The *orange* color represents the older community. The hive exit on side A is on the bottom right and on side B on the bottom left. The data is aggredated for the complete timeframe of ten hours.




**(a)** Network 1

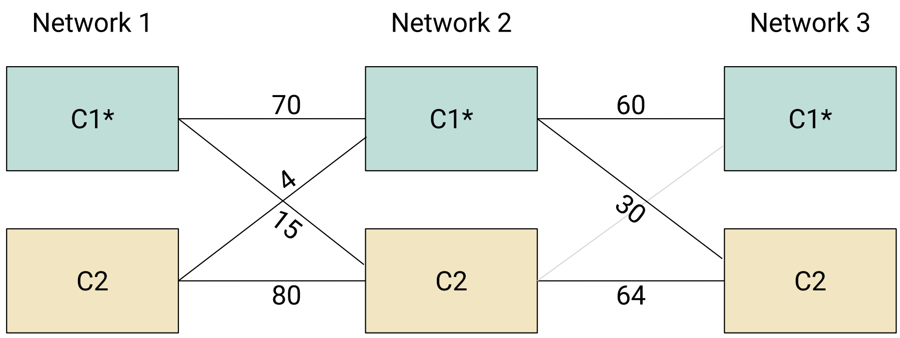



**(b)** Network 2

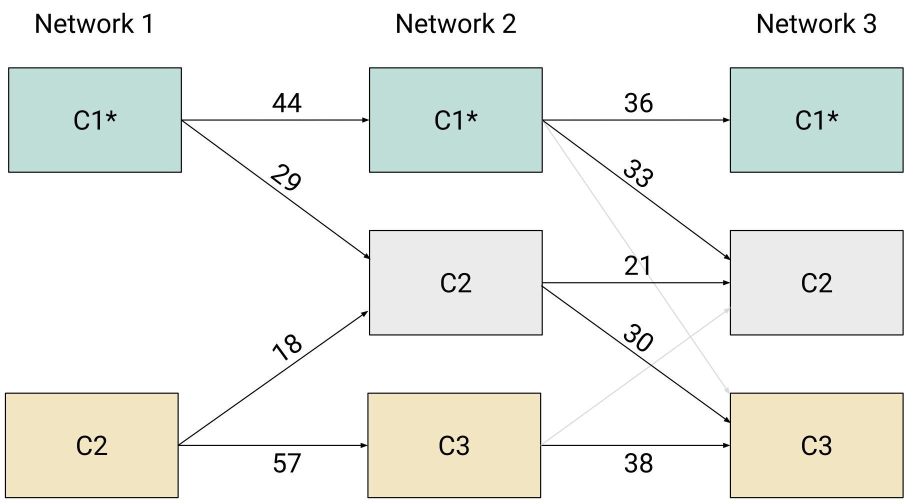



**(c)** Network 3

**Figure 5.4: Communities per network - walktrap** The *green* colour represents the younger community, containing the queen. The *orange* color represents the older community. The *gray* represents the middle-age community. The hive exit on side A is on the bottom right and on side B on the bottom left. The data is aggredated for the complete timeframe of ten hours.




**(a)** Leading eigenvector communities




**(b)** Walktrap communities

**Figure 5.5: Community matching** The numbers indicate the match values in percent. The community marked with * contains the queen. *Green* represents the younger community *orange* the older community, and gray the middle-aged community. The light gray arrow represents match values below three percent.

# Chapter 6

# Conclusion

## 6.1 Discussion

## 6.2 Limitation

contact duration and contact frequency
distances is are hard to measure, because hive is very small and dense (is spatial proximity a good proxy in this case)

nur weil man mehr daten hat, muss es nicht unbedingt besser werden
aber mehr daten (aufbereiteter guter datensatz), evtl. fragen stellen, an die man vorher noch nicht gedacht hat.

## 6.3 Summary

## 6.4 Future Work

Measuring the robustness of network community structure using assortativity [27]

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# List of Figures

# List of Tables

# Appendix A

# Appendix Stuff