SIMILARITIES AMONG FARA-LED IAR4D INNOVATION PLATFORMS

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Abstract

Multi-stakeholder partnerships network which is typified by the FARA-led Integrated Agriculture Research for Development (IAR4D) of the SSA-Challenge Program is an innovation platform (IP) composed of stakeholders bound together by their individual interests in a shared commodity or outcome. The result from such innovation platforms is largely influenced by the strength of the network. In this paper, similarities within and across platforms are assessed using the simple matching procedure. Results indicate consistency in conduct of Innovation Platform activities. Minor differences in IPs across various regions are consistent with impact outcome observed in the operation of the IPs

Keywords: Clustering, cohesiveness, impact, Sub-Saharan Africa

1.0 Introduction

Although agricultural innovation is seen as an important factor for economic growth and development, several aspects of this remain poorly understood. Recent work emphasizes interdependence among actors, network effects, joint learning, and social interaction (FARA, 2008). The main output of the Sub-Saharan Africa Challenge Program (SSA CP) is implementation of Integrated Agricultural Research for Development (IAR4D) and assessing whether it works or not. The challenge of the SSA-CP is to conduct research to identify the effects of the IAR4D approach and its different components in designing and implementing research targeted at the interface of processes driving productivity gains, efficient use of resources, the care of the environment, policies and markets that would increase demonstrably the delivery of the benefits to end users and have an impact and do so in a scientific, statistically-based manner. IAR4D is an action research approach for investigating and facilitating the organization of groups of stakeholders (including researchers) to innovate more effectively in response to changing complex agricultural and natural resources management contexts, in order to achieve developmental outcomes. At the core of this organization is the establishment of innovation platforms (FARA, 2009).

An innovation platform is comprised of a set of stakeholders bound together by their individual interests in a shared issue, objective, challenge or opportunity, dealing with which will improve livelihoods, businesses and/or other interests. An innovation platform refers both to the emergent properties of groupings of players and their processes, practices, and habits, as well as the formal structures that might give operational focus to activities and interactions. Although conceptually innovation platforms do not have geographical boundaries, a geographical boundary of a “site” is taken within the SSA-CP. This does not however mean that all innovation platform members will be from this geographical boundary, though a platform can be geographically defined. Indeed, stakeholders or actors will sometimes be from outside of the geographical site. However, the organization of the actors can be within and outside this boundary.

The performance of an IP may be assessed by several criteria, including and not exclusively confined to attendance of meetings, contribution at meetings, leadership and facilitating skills among others. The commitment of all parties in equal manner in an IP should hypothetically lead to maximum benefit for all. Procedures are available for generating or analyzing social network. For example, in UCINET (Borgatti, Everett and Freeman, 1999) there are routines for computing various measures of node centrality, including degree of closeness and ‘betweenness’, as well as for detecting core/periphery structures and locating each actor’s position in the structure. In this paper, however, interest is on identifying possible patterns of associations that may exist among the various IPs using a similarity measure. The study complements attempts by others to develop a measure of IAR4Dness (Pamuk and van Rijn 2013) that will indicate the extent to which the IPs function according to the IAR4D concept and investigate whether this can explain heterogeneous results (van Rijn *et al.* 2013; Pamuk 2013).

2.0 Methodology:

2.1 Pilot Learning Sites (PLS) and IP codings

The formation of the IPs in each of the PLS has been well documented (Adekunle, *et al.*, (2013 a, b). As this study is a comparison of the IPs, it is important to re-emphasize the fact that various teams (mainly researchers) were trained together on the principles and practice for setting up IPs. At the various learning sites, further training was undertaken together with non-research partners. Ultimately, IP partners were expected to work together as a team and as joint owners of the IP enterprise. There were 3 PLS: KKM covering the northern part of Nigeria (Kano, Kaduna) and Niger (Maradi); LK – Lake Kivu area invoving Uganda, Rwanda and eastern part of DR Congo; and ZMM – in southern Africa involving Zimbabwe, Malawi and Mozambique. Each PLShad 12 IPs making a total of 36 IPs or data sets (also referred to as UNITS). However, substantial amount of information could not be obtained from 4 of the IPS (ZMM) and were therefore excluded from the analysis. The codings facilitate ease of reference and graphical presentation.

Table 1: Basic coding of Innovation Platforms

Table 1: Basic coding of Innovation Platforms

ID	PLS	TF	IP_Code**	IP Name Focus
1	KKM	INRAN (N)	KGN	Groundnut
2	KKM	INRAN (N)	KSN	SLF
3	KKM	INRAN (N)	KVN	Vegetables
4	KKM	INRAN (N)	KLN	Livestock
5	KKM	IFDC (F)	KVF	Vegetables
6	KKM	IFDC (F)	KLF	Livestock
7	KKM	IFDC (F)	KRF	Rice
8	KKM	IITA (I)	KBI	Bunkure Maize-Legume-livestock
9	KKM	IITA (I)	KShI	Sha00 Sorghum-legume-livestock
10	KKM	IITA (I)	KMF	Maize Legume
11	KKM	IITA (I)	KSeI	Sefana Sorghum-legume-livestock
12	KKM	IITA (I)	KMI	Musawe Maize-Legume-livestock
13	LK	CIAT	LBaC	Banana (Ba)
14	LK	CIAT	LPC	Irish potato (P)
15	LK	CIAT	LBeC	Beans (Be)
16	LK	CIAT	LCC	Cassava
17	LK	ISAR	LGI	Gataraga
18	LK	ISAR	LRwI	Rwerere (Rw)
19	LK	ISAR	LMI	Mudende
20	LK	Makerere/ICRISAT	LPM1	Potato and soil and water conservation
21	LK	Makerere/ICRISAT	LPM2	Potato and soil and water conservation
22	LK	Makerere/ICRISAT	LPM3	Pineapple
23	LK	Makerere/ICRISAT	LSM	Sorgum
24	LK	ISAR	LReI	Remera (Re)
25	ZMM	Biodiversity Intl.	ZZB	Zomba
26	ZMM	Biodiversity Intl.	ZTB	Tyolo
27	ZMM	CIAT	ZBC1	Balaka
28	ZMM	Biodiversity Intl.	ZBB	Barue
29	ZMM	Biodiversity Intl.	ZMB	Milange
30	ZMM	CIAT	ZBC2	Barue
31	ZMM	CIAT	ZMC	Murehwa
32	ZMM	CIAT	ZHC	Hwedza

**** Note on IPcodes**: *The first alphabet represents the PLS (e.g. KKM is K), the second is IPName Focus code (e.g.Vegetable is V or location Barue is B) and the last is code for the task force (e.g. CIAT = C)*

2.2 Data

A supplementary questionnaire was designed at the midline date collection level to elicit information on all the thirty-two IPs. The survey was designed to capture the five dimensions of IAR4D as defined during the set-up of the program (Hawkins 2008; FARA 2009): (1) existence of IPs that are representative, inclusive and with diverse partnerships, (2) existence of non-linear, collective and collaborative interaction among IP actors, (3) research addresses key constraints and opportunities agreed by the IP in the context of entire value chains, (4) research process is multidisciplinary and participatory and (5) institutional and human capacity building for IAR4D actors to effectively participate. This survey included questions related to the formation and functioning of the IP (actors involved, attendance to various activities), the problems addressed (actions implemented, actors involved) and the subjective evaluation by the coordinators of the IP according to the five IAR4D criteria (see Annex). The survey was conducted among the IP coordinators through email in mid-2012. Some of the responses were binary (yes and no responses) while others were qualitative and quantitative in nature. Thus the data presented were of varying types. The data also serve additional purpose for IAR4Dness activities.

2.3 Similarity Measure

Associations may be expressed as similarities or distances. Most data sets may be thought of as a matrix of n units (rows) by p variables (columns). In deriving the measures, we now consider relationships between the n units. The first stage was to create a matrix A of n rows by n columns in which the $(i,j)^{th}$ element a_{ij} describes the association between the i^{th} and j^{th} unit. We considered the usual case where associations are symmetric, so that $a_{ij} = a_{ji}$.

Similarities are usually constrained to lie in the range [0,1] with 'self-similarities' taking the value 1. Distances or dissimilarities are complementary to similarities - they are usually non-negative with self-distances zero. Similarities may be converted to distances and vice-versa, e.g. by $d = 1 - s$.

Since, data were of varying types a general form of the similarity coefficient had to be used. Let s_{ijk} denote the similarity between units i and j, based on k^{th} (of p) variable. We take the average of s over all the k variables and define this as the similarity between units i and j. When all the variables are binary or qualitative, we need only define $s = 1$ when the values of the i^{th} and j^{th} samples are equal, and $s = 0$ otherwise, to obtain the same results as the simple matching coefficient. When some of the variables are quantitative the corresponding inter-unit distances are converted to similarities before inclusion in the similarity coefficient. If the conversion is by $s = 1 - d$, the distances are first constrained to lie between 0 and 1 by, for example, dividing by the maximum distance.

2.4 Clustering

Classifying items into groups is a natural way of summarizing information in a large body of data. In this instance, our interest was in determining if some form of aggregation may be observed among IPs. The assumption was that IPs that performed or operated in identical manner would most likely be similar. We had adopted the agglomerative hierarchical clustering method and the complete linkage (furthest neighbor) procedure (where the similarity between two groups is defined by similarity between their furthest members)

With the hierarchical methods the groups themselves are arranged in a hierarchy. Agglomerative hierarchical methods have the advantage of being computationally simple. The procedure may be outlined briefly as follows:

Start with n groups, each containing just one unit;

1. Join the two most similar units into a single group, so that there are now (n-1) groups;
2. Derive the similarity between this new group and every other group;
3. Join the two most similar groups to form a new group;
4. Return to step 3 and proceed iteratively until all units belong to a single group

In complete linkage the similarity between two groups is defined by similarity between their furthest members. Hard clustering using the Euclidean Distance and

3.0 Results and Discussion:

3.1 Similarity measures

The basic results of the analysis of similarities using the similarity measure are presented partially for emphasis in Tables 2a, 2b and 2c. These have been extracted from the overall similarity matrix involving the 32 Innovation Platforms. The analyses were done with GENSTAT Discovery Edition Version 4. The similarities range from 1 to 0.50, indicating strong associations among several IPs. The dataset is on processes involved in the operations of the platforms, and high similarity measures indicate that IPs were evaluated in identical manner by the IP coordinators, while the opposite is the case with similarity close to 0. The similarities are presented by the various IPs and shows, for instance how an IP (say KGN in Table 2a) relates with other IPs (in this case, KSN, KVN etc - in the KKM PLS).

IPcode	KGN	KSN	KVN	KLN	KVF	KLF	KRF	KBI	KShI	KMF	KSeI
KGN	1.00										
KSN	0.87	1.00									
KVN	0.78	0.84	1.00								
KLN	0.64	0.67	0.68	1.00							
KVF	0.58	0.57	0.57	0.68	1.00						
KLF	0.72	0.75	0.77	0.78	0.65	1.00					
KRF	0.69	0.72	0.77	0.77	0.66	0.86	1.00				
KBI	0.65	0.70	0.66	0.66	0.51	0.70	0.74	1.00			
KShI	0.65	0.70	0.66	0.66	0.51	0.70	0.74	1.00	1.00		
KMF	0.75	0.80	0.82	0.74	0.64	0.81	0.86	0.68	0.68	1.00	
KSeI	0.66	0.72	0.69	0.67	0.50	0.71	0.77	0.95	0.95	0.71	1.00
KMI	0.67	0.72	0.70	0.67	0.50	0.71	0.76	0.95	0.95	0.72	0.99

(Averaged similarities, excluding self similarities = 0.723)

Table 2b: Similarities among Innovation Platforms in Lake Kivu

IPcode	LBaC	LPC	LBeC	LCC	LGI	LRwI	LMI	LPM1	LPM2	LPM3	LSM
LBaC	1.00										
LPC	0.95	1.00									
LBeC	0.95	0.97	1.00								
LCC	0.90	0.91	0.91	1.00							
LGI	0.81	0.81	0.81	0.81	1.00						
LRwI	0.84	0.83	0.82	0.83	0.72	1.00					
LMI	0.80	0.80	0.81	0.82	0.81	0.79	1.00				
LPM1	0.79	0.78	0.78	0.79	0.78	0.77	0.76	1.00			
LPM2	0.82	0.81	0.81	0.79	0.79	0.80	0.79	0.76	1.00		
LPM3	0.80	0.79	0.82	0.79	0.76	0.78	0.83	0.75	0.77	1.00	
LSM	0.74	0.77	0.74	0.75	0.68	0.76	0.68	0.72	0.74	0.72	1.00
LReI	0.77	0.75	0.77	0.81	0.81	0.74	0.78	0.76	0.80	0.79	0.70

(Averaged similarities, excluding self similarities = 0.794)

Table 2c: Similarities among Innovation Platforms in ZMM Pil

ipcode	ZZB	ZTB	ZBC1	ZBB	ZMB	ZBC2	ZMC
ZZB	1.00						
ZTB	0.94	1.00					
ZBC1	0.77	0.76	1.00				
ZBB	0.75	0.76	0.70	1.00			
ZMB	0.75	0.74	0.69	0.97	1.00		
ZBC2	0.83	0.83	0.81	0.74	0.75	1.00	
ZMC	0.85	0.83	0.80	0.74	0.72	0.97	1.00
ZHC	0.84	0.83	0.81	0.74	0.75	0.99	0.97

(Averaged similarities, excluding self similarities = 0.809)

Table 3 provides a summary of the similarity indices for the various PLS and the overall. For instance it may be observed that the average mean index for KKM is lower than the overall average, and is the least among the 3 PLS. It also has the highest standard error and the highest coefficient of variation. It may also be noted that the lowest measure of similarity involved KVF (KKM, Vegetable Task Force, IFDC)..

Table 3: Summarized Statistics of Similarity Indices

Summary statistics for KKM		Summary statistics for LP	
Number of observations =	66	Number of observations =	66
Mean =	0.723	Mean =	0.794
Median =	0.705	Median =	0.792
Minimum =	0.497	Minimum =	0.677
Maximum =	1	Maximum =	0.975
Lower quartile =	0.664	Lower quartile =	0.763
Upper quartile =	0.772	Upper quartile =	0.812
Standard error of mean =	0.0137	Standard error of mean =	0.00707
Coefficient of variation =	15.35	Coefficient of variation =	7.233

Summary statistics for ZMM		Summary statistics ALL PLS	
Number of observations =	28	Number of observations =	160
Mean =	0.809	Mean =	0.767
Median =	0.785	Median =	0.766
Minimum =	0.689	Minimum =	0.497
Maximum =	0.987	Maximum =	1
Lower quartile =	0.747	Lower quartile =	0.711
Upper quartile =	0.837	Upper quartile =	0.812
Standard error of mean =	0.0165	Standard error of mean =	0.00754
Coefficient of variation =	10.79	Coefficient of variation =	12.43

3.2 Hard Clustering

The overall similarity matrix (presented as Appendix 1) provided the basic data for the dendrogram (hierarchical clustering) and Minimum Spanning Tree diagrams shown in Figures 1 and 2 respectively. The dendrogram provides the order in which IPs may be clustered, while Table 4 provides a summary of further classification of the IPs into five optimal clusters (groups) using the 'within sum of squares' criterion.

Table 4: Hard classification of IPs with Between Group Sum of Squares Criterion

GROUPING	IP Codes Represented	Remarks
1 (Eleven)	KGN , KSN , KVN , KLN KVF, KMF LMI, LPM1, LPM2, LSM, LReI	Group is characterized by absence of ZMM IPs and influence of four task force drivers (INRAN and IFDC in KKM and ISAR/ICRISAT in LK PLS)
2 (Five)	KBI, KShI, KSeI, KMI LGI	Group 2 has strong presence of task forces driven by IITA in the KKM PLS; similarity with an IP within LK PLS has been established
3 (Five)	LRwI, ZMB ZBC2, ZMC, ZHC	Mainly characterized by ZZM and a lone IP from LK PLS
4 (Five)	KLF, KRF LPM3 ZZB, ZTB	This is a mixed group with all PLS represented
5 (Six)	LBaC, LPC, LBeC LCC ZBC1 ZBB	Characterized by the absence of an IP from KKM

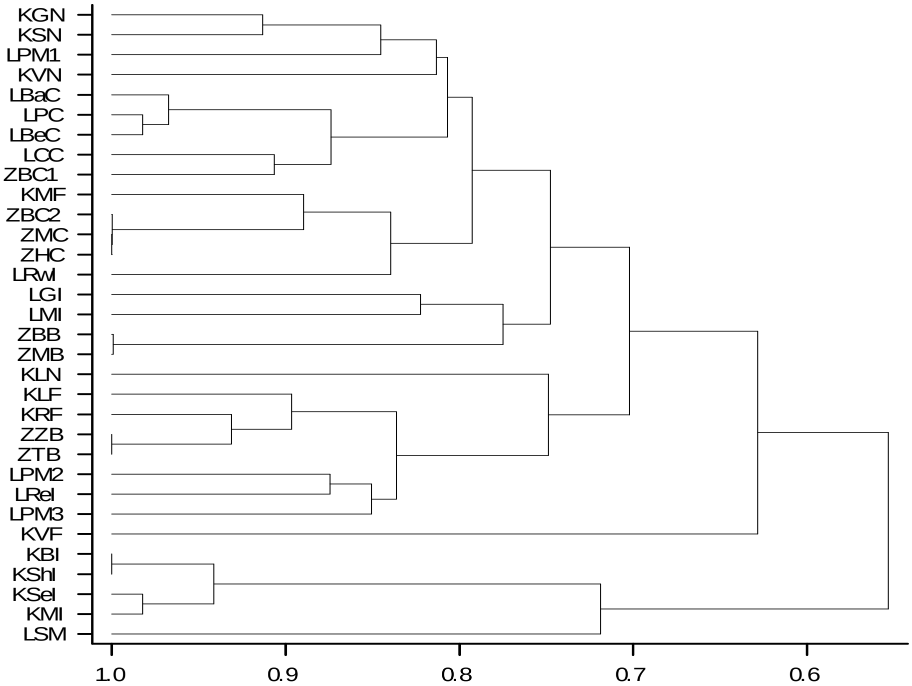

Figure 1: Hierarchical clustering of the 32 Innovation Platforms

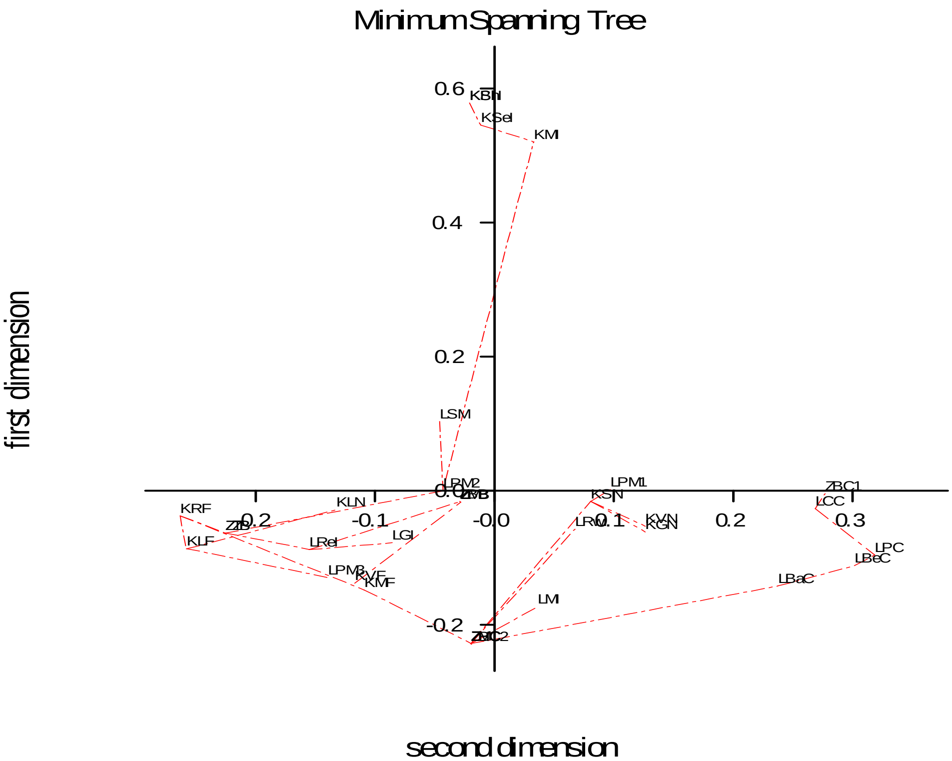

Figure 2: Corresponding minimum spanning tree diagram on 32 IPs

From **Figure 1**, one may observe the sequence at which hierarchical grouping of the IPs may be done. At the highest level of similarity, say 0.9 or better, groupings a={KMI, KSeI, KShI,KBI}, b={ZTB, ZZB, KRF, KLF}, c={ZBB, ZMB}, d={ZHC, ZMC}, e={ZBC1, LCC}, f={LBeC, LPC, LBaC} and g={KSN, KGN}. These groups clearly associate with PLS (first alphabet in code) and task force drivers (last alphabet in code). Further groups evolve as the similarity measure is relaxed. The dendrogram further shows that at similarity value of less than 0.6, two groups emerge. These are h= {LSM, KMI, KSeI, KShI,KBI} in one group and all the others i= {b, c, d, e, f, g} in the other group. **Figure 2** (Minimum Spanning Tree) shows clearly the location of group h and group i. The results reasonably suggest uniformity of the groups.

Considering that the nature of grouping may be determined by the choice of classification criterion and distance measure, non-hierarchical procedure was additionally adopted. The results in Table 5 for five-cluster classification do not contradict the earlier one suggested above, and further reinforces the influence of IP location and Task Force driver.

4.0 Conclusion

The key observations were that:

1. There were generally strong associations among the Innovation Platforms, IPs
2. Relatively lower similarities were observed among IPs within the KKM PLS, in addition to observed higher variation (when compared with other PLS) and lower consistencies.
3. There were generally uniformly strong associations among IPs in LKPLS and ZMM

In a report on the proof that the IAR4D concept works, Adekunle *et al.*, 2013(a, b) showed the considerable impact of the concept relative to traditional ARD practices. The observed results on the similarities and dissimilarities among the various IPs are consistent with the quantum of impact observed. It may also, indeed, be concluded that the closeness of similarities suggests consistency in the level of operations among the IPS, and points to the success of the training of IP operators at the onset of the project. There are however clear indications of location and task force specific influences on the evaluation of the Innovation Platforms. The outcome of this study therefore suggests the need to study further internal cohesiveness of IAR4Dness and how it possibly relates to the impact of the IPs.

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Appendix 1: Overall similarity indices within and across PLS

ipcode	KGN	KSN	KVN	KLN	KVF	KLF	KRF	KBI	KShI	KMF	KSeI	KMI	LBaC	LPC	LBeC	LCC
KGN	1															
KSN	0.87	1														
KVN	0.78	0.84	1													
KLN	0.64	0.67	0.68	1												
KVF	0.58	0.57	0.57	0.68	1											
KLF	0.72	0.75	0.77	0.78	0.65	1										
KRF	0.69	0.72	0.77	0.77	0.66	0.86	1									
KBI	0.65	0.7	0.66	0.66	0.51	0.7	0.74	1								
KShI	0.65	0.7	0.66	0.66	0.51	0.7	0.74	1	1							
KMF	0.75	0.8	0.82	0.74	0.64	0.81	0.86	0.68	0.68	1						
KSeI	0.66	0.72	0.69	0.67	0.5	0.71	0.77	0.95	0.95	0.71	1					
KMI	0.67	0.72	0.7	0.67	0.5	0.71	0.76	0.95	0.95	0.72	0.99	1				
LBaC	0.8	0.78	0.78	0.74	0.61	0.79	0.78	0.7	0.7	0.85	0.73	0.74	1			
LPC	0.82	0.8	0.78	0.7	0.6	0.79	0.76	0.68	0.68	0.84	0.69	0.7	0.95	1		
LBeC	0.82	0.8	0.77	0.7	0.6	0.79	0.76	0.66	0.66	0.85	0.69	0.7	0.95	0.97	1	
LCC	0.81	0.78	0.78	0.71	0.6	0.76	0.76	0.66	0.66	0.84	0.7	0.7	0.9	0.91	0.91	1
LGI	0.74	0.77	0.77	0.7	0.67	0.79	0.8	0.67	0.67	0.84	0.69	0.69	0.81	0.81	0.81	0.81
LRwI	0.76	0.78	0.84	0.69	0.57	0.71	0.72	0.71	0.71	0.81	0.74	0.74	0.84	0.83	0.82	0.83
LMI	0.8	0.79	0.81	0.69	0.64	0.8	0.78	0.65	0.65	0.83	0.65	0.66	0.8	0.8	0.81	0.82

LPM1	0.76	0.79	0.75	0.71	0.65	0.78	0.73	0.69	0.69	0.75	0.7	0.71	0.79	0.78	0.78	0.79
LPM2	0.76	0.84	0.81	0.73	0.56	0.82	0.8	0.79	0.79	0.83	0.82	0.82	0.82	0.81	0.81	0.79
LPM3	0.8	0.8	0.77	0.72	0.59	0.81	0.78	0.67	0.67	0.8	0.69	0.69	0.8	0.79	0.82	0.79
LSM	0.68	0.7	0.68	0.66	0.51	0.68	0.72	0.8	0.8	0.7	0.78	0.78	0.74	0.77	0.74	0.75
LReI	0.71	0.78	0.77	0.78	0.63	0.78	0.79	0.68	0.68	0.8	0.71	0.72	0.77	0.75	0.77	0.81
ZZB	0.73	0.81	0.81	0.75	0.64	0.84	0.83	0.71	0.71	0.83	0.73	0.73	0.81	0.82	0.82	0.79
ZTB	0.71	0.79	0.81	0.77	0.64	0.81	0.84	0.75	0.75	0.83	0.78	0.77	0.84	0.79	0.79	0.77
ipcode	KGN	KSN	KVN	KLN	KVF	KLF	KRF	KBI	KShI	KMF	KSeI	KMI	LBaC	LPC	LBeC	LCC
ZBB	0.65	0.71	0.72	0.77	0.69	0.8	0.79	0.7	0.7	0.79	0.73	0.74	0.75	0.73	0.73	0.74
ZMB	0.66	0.72	0.72	0.74	0.68	0.81	0.78	0.7	0.7	0.76	0.73	0.74	0.74	0.73	0.74	0.74
ZBC2	0.8	0.83	0.81	0.7	0.7	0.8	0.79	0.66	0.66	0.85	0.67	0.68	0.84	0.82	0.83	0.81
ZMC	0.79	0.82	0.8	0.71	0.7	0.79	0.79	0.64	0.64	0.86	0.65	0.66	0.83	0.82	0.82	0.81
ZHC	0.81	0.84	0.81	0.7	0.7	0.81	0.79	0.64	0.64	0.85	0.66	0.67	0.84	0.83	0.83	0.82

ipcode	LGI	LRwI	LMI	LPM1	LPM2	LPM3	LSM	LReI	ZZB	ZTB	ZBC1	ZBB	ZMB	ZBC2	ZMC	ZHC
LGI	1															
LRwI	0.72	1														
LMI	0.81	0.79	1													
LPM1	0.78	0.77	0.76	1												
LPM2	0.79	0.8	0.79	0.76	1											
LPM3	0.76	0.78	0.83	0.75	0.77	1										
LSM	0.68	0.76	0.68	0.72	0.74	0.72	1									
LReI	0.81	0.74	0.78	0.76	0.8	0.79	0.7	1								
ZZB	0.83	0.79	0.79	0.78	0.84	0.79	0.72	0.8	1							
ZTB	0.81	0.79	0.77	0.76	0.84	0.79	0.71	0.79	0.94	1						
ZBC1	0.78	0.85	0.81	0.79	0.8	0.78	0.74	0.8	0.77	0.76	1					
ZBB	0.75	0.68	0.73	0.76	0.75	0.69	0.68	0.77	0.75	0.76	0.7	1				
ZMB	0.73	0.65	0.74	0.76	0.75	0.71	0.66	0.76	0.75	0.74	0.69	0.97	1			
ZBC2	0.82	0.78	0.85	0.79	0.78	0.83	0.67	0.78	0.83	0.83	0.81	0.74	0.75	1		
ZMC	0.83	0.79	0.83	0.79	0.78	0.8	0.66	0.79	0.85	0.83	0.8	0.74	0.72	0.97	1	
ZHC	0.82	0.78	0.85	0.79	0.79	0.83	0.67	0.77	0.84	0.83	0.81	0.74	0.75	0.99	0.97	1