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A BASIC Algorithm for Calculating the Postmortem Interval from Arthropod Successional Data

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ABSTRACT: A computer algorithm, implemented in the BASIC language, is presented for calculating the postmortem interval (PMI) from arthropod successional data. Entomology-assisted determination of the PMI promises to be a reliable technique in cases of homicide, suicide, accidental death, and unattended death due to natural causes. The program requires, as input, the identity of arthropod taxa recovered from human remains in a death scene investigation and machine-readable data on carrion-associated arthropod taxa and their known successional patterns of activity for the same geographical area. The program performs rapid comparisons of these lists and, on output, calculates an upper and lower estimate of the PMI, identifies the definitive taxa for these limits, and determines if the remaining corpse taxa have known successional patterns that are consistent for this estimate. An alternate output is provided if one or more corpse taxa do not overlap all the others at any single time in the succession. In that event, the user is prompted to recheck the identity of the non-overlapping taxon or taxa or reevaluate the environmental circumstances surrounding the case in question. Results of the analysis are saved to an ASCII file for output to a printer for making paper copies useful for the entomologist's Case Study Final Report. This program may make possible wider use of this technique in law enforcement and medical investigator offices that utilize both forensic entomologist expertise and IBM PCs (or compatible computers).

KEYWORDS: pathology and biology, BASIC algorithm, postmortem interval, forensic entomology, carrion arthropods, ecological succession, sarcosaprophagous insects, statistical protocols, postmortem decomposition

In the medicolegal investigation of death, one of the most critical questions is: "When did the death take place?" Accurate estimation of the postmortem interval (PMI), the period from death to discovery of a corpse, has special relevance in a homicide case because such knowledge can narrow the field of possible suspects in the crime [1]. In death scene investigations, estimating the PMI routinely falls upon the forensic pathologist, but if the remains are found in an advanced state of decomposition the case may be referred to a forensic anthropologist. However, a vexing problem faced in all current

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approaches is that as the PMI increases, the less accurate or wider ranging the PMI estimate becomes [1-3].

On the other hand, the use of entomological indicators in medicolegal death investigations promises to be a reliable technique for estimating the PMI in both early (for example, Ref 4) and advanced periods of cadaver decomposition [5,6]. Forensic (or medicocriminal) entomology applies the sequential arrival times (= succession), developmental timetables, and other biological characteristics of carrion-associated species to estimate the time of death in medicolegal investigations. Overlapping both pathological and anthropological indicators, the "usefulness window" for entomological indicators can range roughly from 1 day to 60+ days depending on the geographical setting and other abiotic and biotic factors. Case studies conducted in various temperate and tropical settings have shown that entomology-based PMI estimates, when compared with the actual intervals fixed by other means (that is, confessions, eyewitness testimony), have differed by only ± 48 h or less in human remains cases aged under 2.5 months [5-9].

Following work by M \acute{e} gnin [10], Johnston and Villeneuve [11], and Motter [12] on the entomology of human remains, forensic entomologists and ecologists have used non-human carrion to investigate postmortem decompositional processes and successional patterns of sarcosaprophagous arthropods (for example, Refs 13-23). The carrion-arthropod community generally develops as a continuum of gradual changes [24], but certain taxa (sarcosaprophagous flies and beetles) show recognizable and predictable patterns of successional activity (for example, Refs 15,16, and 18). Applications of these (and many other) entomological studies to medicolegal situations have helped medical examiners and law enforcement personnel pinpoint the time of death in cases of homicide, suicide, accidental death, and unattended death as a result of natural causes. Recent treatments of forensic entomology can be found in Leclercq [25], Keh [26], Smith [27], and Catts and Haskell [28].

In this paper, we present a computer algorithm for determining the postmortem interval from arthropod successional data. This algorithm, implemented in Sperry BASIC (BASIC 3.0, Version 1.0 © 1983, Microsoft Corp.), runs on IBM PCs (XT, AT, PS/2) and compatible microcomputers with 512 kb of memory and at least 32 kb of disk space for the program and the input and output files. A practical feature of this program is that the user is provided with an ASCII output file containing the results of the analysis, which can be printed out for use in the entomologist's Case Study Final Report [29]. The PMI estimation method is based on the algorithm of Goff and Odom [8] developed from business applications software (Apple Quickfile) for Apple IIE microcomputers. These programs complement Williams's [30] FORTRAN IV program for estimating the time of egg hatching of blow flies from larval weights at the time of corpse discovery and Reiter's graphical (isomegalen diagram) approach [31] to PMI estimation from blowfly length/age measurements for a wide range of temperatures. The authors hope that the present program will make possible wider use of this technique in law enforcement and medical investigator offices that use both forensic entomologist expertise and IBM PCs (and compatible computers).

Methods

Estimating the PMI

Entomology-assisted determination of the PMI is a two-step process. Arthropods sampled from human remains (hereafter called the "corpse fauna") in a death scene investigation are referred to (or collected by) an entomologist for identification, rearing, and analysis. Members of the corpse fauna are then compared with the same taxa whose successional patterns from the same geographical region are known from previously

verified death cases or from postmortem decomposition studies of nonhuman carcasses (hereafter called the "baseline fauna"). Comparison of these faunas yields an upper and lower estimate of the PMI, whose limits may converge on the same day or may be several days (or more) apart depending on the actual PMI and various biotic and abiotic factors. The taxa defining these limits also accompany the estimate (hereafter called the "definitive taxa").

To illustrate this procedure, consider the hypothetical occurrence matrix shown in Fig. 1. In this example, there are nine columns representing postmortem Days 1–9 in the succession and there are eight kinds (rows) of baseline taxa labeled A through H. Data in the body of the matrix are listed in binary form: if Taxon A occurs on Day 2 a "1" is inserted in Row A and Column 2; otherwise there is a "0" (here Taxon A occurred on Days 1–4, Fig. 1). The number of nonzero entries in a given column indicates the taxonomic richness of that time-specific sample, whereas the number of nonzero entries in a given row indicates the number of occurrences or the "residence time" of that taxon on carrion.

In this hypothetical case, representative samples of the corpse fauna are collected at the crime scene and brought to the entomologist's laboratory. Further suppose that upon analysis the corpse fauna was found to contain several taxa and that four were members of the baseline fauna: Taxa B, D, G, and H (note: all corpse taxa may not be members of the baseline fauna⁴). The PMI can now be estimated. The lower and upper limits for the PMI correspond to the first and last days the four taxa are found together in the succession, respectively. For these data, the lower and upper limits are Days 3 and 5, respectively (Fig. 1). Taxon H becomes the definitive taxon for the lower limit because its arrival coincided with the Day 3 lower limit and Taxon D becomes the definitive taxon for the upper limit because its last day in the succession coincided with the Day 5 upper limit. Known residence times for the remaining two corpse taxa are consistent, though not definitive, for this estimate: Taxon B, Days 2–7; and Taxon G, Days 1–8.

From the above example, estimation of the PMI, in theory at least, is a relatively straightforward procedure. In some crime scene investigations, however, before a PMI estimate is rendered, many corpse taxa may need to be compared with many more baseline taxa. In addition, various biotic (for example, vertebrate scavengers) and abiotic (for example, inclement weather) factors may confound the estimation procedure. Therefore, the advantages of using a computerized procedure becomes clear.

Data Files

The ability of the forensic entomologist to perform accurate estimates of the PMI critically depends on the quality of field data collected from baseline studies of nonhuman carcasses. Pig carcasses are purported to be the best human model for such studies as a result of similarities in integument, size of thoracic cavity, and various internal features [32,33]. Some forensic entomologists have also used species determinations from previously verified death cases to supplement and validate their baseline records (for example, Refs 5 and 9). A systematic plan of daily sampling, chosen in advance, can insure fixed-interval sampling and uniform sampling effort over time. Therefore, a sampling regimen conducted at the same time(s) each day must be sought and the frequency of sampling and sampling effort should remain unaltered from the first day of carcass exposure up to or including the skeletal remains period of carcass decomposition. Since accurate PMI estimation also depends on a firm foundation in arthropod systematics, all

⁴Catts, E. P., personal communication, 2 August 1991.

DAYS	Postmortem Interval								
	1	2	3	4	5	6	7	8	9
TAXON A	1	1	1	1	0	0	0	0	0
TAXON B	0	1	1	1	1	1	1	0	0
TAXON C	0	1	1	1	1	1	0	0	0
TAXON D	1	1	1	1	1	0	0	0	0
TAXON E	0	0	0	0	0	0	1	1	1
TAXON F	0	0	0	0	1	1	1	1	1
TAXON G	1	1	1	1	1	1	1	1	0
TAXON H	0	0	1	1	1	1	1	1	1

FIG. 1—A hypothetical occurrence matrix.

carion-associated taxa should be identified to species and to life-history stage (egg, larval instar, nymph, pupa, adult) and physiological age, whenever possible.

Once baseline field data have been collected, they are entered in machine-readable form and stored as two files: a species list (PRN file, see Appendix I) and an occurrence matrix (DEK file, see Appendix II). The order of taxa listed in DEK and PRN must be identical. Both are created in standard ASCII and can be prepared using a resident line editor or word processor. (An optional BASIC program that creates a set of DEK and PRN files from inputted data is available from author K. S. upon request; see **Program Availability** section.)

The PRN file gives the biological name of each species and its life-history stage along with an arbitrary identification number (Appendix I). The contents of this file are displayed by the program each time the user selects a corpse taxon from this list. Assigning each taxon a unique number renders each selection unambiguous. Also note that by incorporating each taxon's generation (P1,F1,F2) and life-history stage or physiological age in separate rows of the occurrence matrix (for example, see Taxa 12, 13, and 22–26 of Appendix I) use of these data for PMI estimation can be enhanced.

The first line of DEK contains the number of time-specific samples, followed by the number of baseline taxa, the total number of nonzero entries in the occurrence matrix, and the time units the samples are based on (Appendix II). The second line identifies the corresponding PRN file for these data. The next set of data contains the time labels for the samples (Lines 3 and 4). The last set of data (Lines 5 and 6) before the occurrence matrix lists the total number of samples in which each taxon was found that may correspond to a taxon's residence time in the succession. The occurrence matrix assigns each baseline taxon a seven-character label, followed by its presence ("1") or absence ("0") in each time-specific sample.

The entomologist's field intuition should primarily guide the selection of taxa to include in the occurrence matrix; however, another (complementary) method might include making plots of the number of taxa found on 1, 2, . . . , n carcasses placed at each site (as replicates) to distinguish the numerically (and forensically) important taxa from the less important taxa [34, cited in Ref 35].

As more baseline samples on this fauna are collected from more habitats, seasons and ever-wider geographical areas, the user can combine this information into a set of cumulative DEK and PRN files, or create different sets of habitat- and season-specific files, or both. For example, the DEK and PRN files shown in Appendices I and II are cumulative taxonomic and successional records from six cat carcasses and two sites on O'ahu (Manoa Valley and Diamond Head Crater) in the Hawaiian Islands [36,37]. Thus, this data set, shown for illustration purposes, represents a regionally distinct fauna applicable to exposed human remains on O'ahu aged 76 days or less. Additional sampling

at these two sites could reveal expanded residence times for some species and perhaps even additional carrion-arthropod species.

Decompositional rates and arthropod successional activities in human remains can vary widely, even within a single site [38 and references therein]. Such variation, fueled by both abiotic (for example, weather conditions, altitude) and biotic (for example, size of the local species pool, presence of vertebrate scavengers) factors, can confound the PMI estimation procedure, particularly the upper limit of the estimate. Therefore, as part of an ongoing program in forensic entomology, the user should also conduct comparative field studies that simulate succession and postmortem decomposition under different exposure modes such as partial/shallow burial, full/partial immersion, sun/shade exposure, clothed/unclothed exposure, full exposure/shelter concealment, and exposure to vertebrate/invertebrate-only scavengers at one or more sites. These additional postmortem studies could permit closer matching of field data with the environmental circumstances surrounding a given case.

Results and Discussion

Program Execution

In addition to the DEK and PRN files, PMI.BAS (Version 1.0 © 1991 The Rockefeller University) requires, on input, a case reference number for use in the entomologist's Case Study Final Report [29]. Following this initialization procedure, a sensitivity analysis is performed on the baseline data (Fig. 2). This analysis has two components. The first component calculates the mean time interval between consecutive samples and its standard deviation to determine if the samples were collected at a fixed time interval. In fixed-interval cases, the standard deviation will be zero. The second component of the sensitivity analysis determines if any of the baseline taxa reportedly leave and reappear in the succession. If such taxa are present, their identities are displayed. Irregular sampling intervals and discontinuities of baseline taxa, alone or in combination, can potentially distort estimates of the PMI. If irregular intervals and discontinuities occur among samples and taxa in the baseline data, the user may wish to adjust the estimated PMI upper or lower limits accordingly. Results of this two-part sensitivity analysis are saved to the output file PMI.OUT (see Appendices III and IV).

Using the input files described in the previous section, the program calls up the taxonomic list in PRN and prompts the user to input the ID number of each corpse taxon found on the remains whose successional timetable has been recorded in DEK. Next, the program computes the period(s) of overlap when all corpse taxa co-occur in the succession, then the first and last periods such overlap occurs (corresponding to the lower and upper limits for the PMI estimate), and finally the definitive taxa for those limits. It is reasonable to assume that either limit may have more than one definitive taxon. If this occurs, the program identifies and saves the names of all definitive taxa. A list of the corpse taxa whose known successional patterns are consistent with these limits also is recorded. All of the above results are saved to the output file PMI.OUT (see Appendix III).

The above procedures require that all corpse taxa overlap each other at least once in the succession. However, if one or more of the corpse taxa do not co-occur with all the others at any time in the succession, the analysis is redirected to another section of the program (Fig. 2). Non-overlapping corpse taxa may indicate misidentified taxa or unusual environmental circumstances of the case in question (for example, partially submerged corpses can harbor faunas of differing successional ages at the same time [39] or the

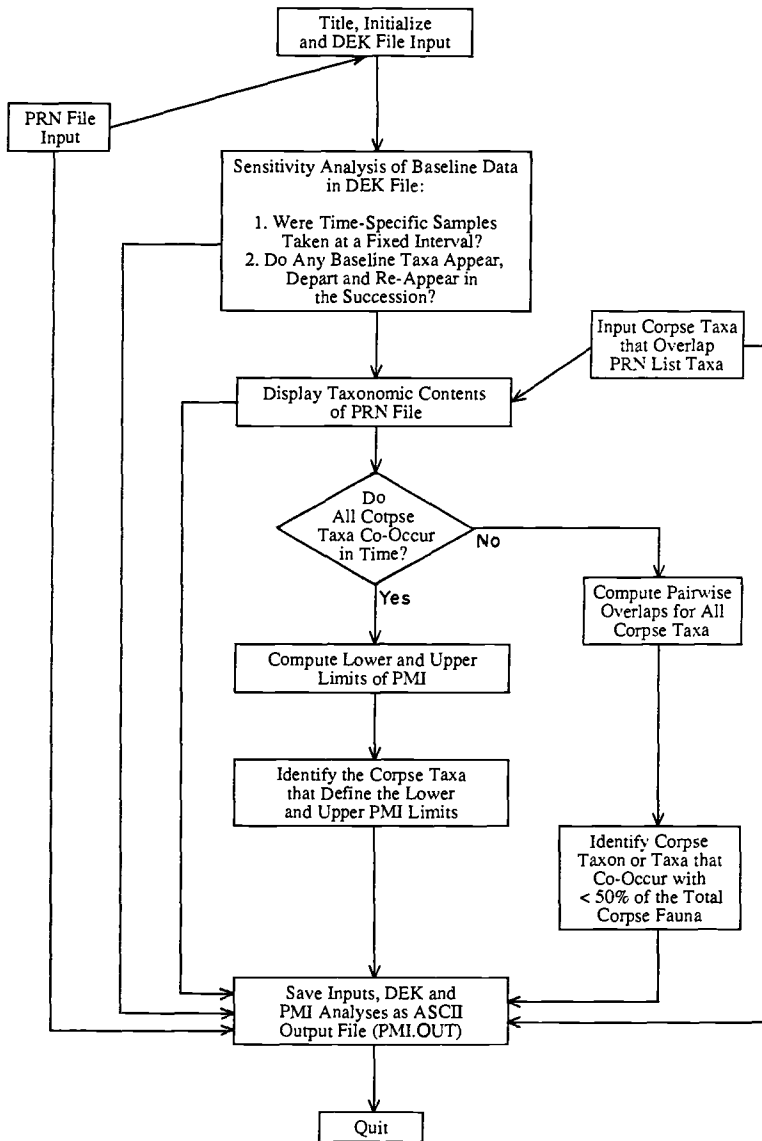


FIG. 2.—Flowchart to illustrate the major components of PMI.BAS.

location where death occurred and discovery was made may not be the same⁵). To identify the false or misleading taxa the program first computes the amount of overlap for all pairwise combinations of corpse taxa. These joint occurrences are stored in matrix form. The program then searches each row of the overlap matrix and identifies the taxon or taxa that co-occur with fewer than one-half the total corpse fauna. An alternate output to PMI.OUT includes a matrix of the joint occurrences and the identity of the false or

⁵Leclercq, M., personal communication, 22 July 1991.

misleading taxon or taxa (note: to avoid confusion self-overlaps along the diagonal are set to zero; see Appendix IV).

Simulated runs with hypothetical data reveal that the program may incorrectly identify false or misleading taxa if their numbers exceed 25% of the total corpse fauna. One should be mindful, however, of the extremely unlikely possibility that an experienced entomologist will incorrectly identify a quarter or more of the corpse taxa sampled from the death scene or at autopsy. Therefore, the presence of non-overlapping corpse taxa will more likely be due to the environmental circumstances surrounding the case in question such as one of the examples cited above. Re-running the program with either a partial and correct listing or a full and revised listing of the corpse fauna should give similar results.

Other Possible Uses of the Program

It is worth noting that this program can also be implemented using other kinds of forensically important entomological data. For example, larval weight or size records of important sarcosaprophagous fly and beetle species could be assembled in the same way as succession-based data files. Like the succession-based procedures used above, PMI estimates based on larval ages or sizes would require comparisons of corpse-associated larvae with larvae of known ages or sizes reared previously under constant or fluctuating temperatures in the entomologist's laboratory. Methods for using data on larvae weight/length versus temperature and development time can be found elsewhere⁶ (for example, Refs 31, 40, and 41). Consequently, in some medicolegal investigations, it might be possible to use successional data to get a rough estimate of the PMI and then use age or size data or both as a way of verifying or even narrowing the estimate, or vice versa.

In addition to performing sensitivity analyses of the baseline fauna, this program could also be used to perform sensitivity analyses of the corpse fauna. For example, one could investigate how the width of the PMI estimate (that is, the upper limit minus the lower limit) might be affected by (a) variation in arthropod sampling effort at the death scene or morgue, (b) recruitment of previously unused or underused taxa in the PMI estimation procedure such as members of the soil mesofauna [42], and (c) differences in taxonomic resolution of the data. Such analyses might suggest ways one might adjust the data-gathering procedures at the crime scene or morgue to add greater precision to entomology-assisted PMI estimation in future medicolegal cases. Although these questions merit further study, they are beyond the scope of this (methodological) paper; however, we plan to investigate them in the future.

A Cautionary Note

It is a foregone conclusion that any new tool or approach has the potential for misuse (or abuse!) as well as the potential for opening new avenues of research. Investigator-written programs (as opposed to commercially available ones) are widely used and shared among active researchers of a discipline. Through repeated scientific exchanges, these programs may be revised and improved, and may even find new application. However, a computer printout of results, like the one shown in Appendix III, has the potential for projecting unjustified precision of a PMI estimate in a death scene investigation.⁷ Consequently, if this program is to be used with entomological evidence in a medicolegal investigation, we strongly recommend the following:

⁶Marchenko, M. I., personal communication, 7 August 1991.

⁷Wells, J. D., personal communication, 15 July 1991.

- a printed copy of the computer analysis and the corresponding DEK and PRN files should be attached as adjoining addenda to the entomologist's Case Study Final Report (rather than as a set of stand-alone documents),
- the data source(s) used for constructing the DEK and PRN files should be documented in the text and cited in the References section of the Case Study Final Report,
- the program cited in the report should bear clear labeling as a tool used in aiding estimation of the PMI, and
- the computer results must support the entomological evidence on which the conclusion of the report is based.

Other features of the entomologist's Case Study Final Report should follow guidelines and format suggested by Catts [29].

Finally, we cannot overstate the need for entomologists to gather, refine, and validate their own life-history data on locally occurring carrion-arthropod species. If such efforts are to be successful, they must have the logistical and financial support of local medical investigator and law enforcement offices. An early priority for such collaboration must also include educating death scene personnel on proper methods of sampling and preserving entomological specimens from human remains at the crime scene and at autopsy⁸ [for details, see Refs 43–46]. Depending on the extent of geographical coverage desired by the user and other factors, several collecting seasons may be required before the accumulated data can be used by the entomologist in death scene investigations. Once these baseline data become established and verified, this program may complement, but must never substitute for, ongoing field and laboratory studies of locally occurring carrion-arthropod species.

Program Availability

Machine-readable copies of the interactive BASIC computer programs PMI.BAS and the DEK and PRN file generator, and the data input and output files listed in the Appendices, are available to forensic researchers on receipt of a formatted (IBM-PC or compatible) 5¼-in. double-sided, double-density (or high capacity) disk and disk mailer (self-addressed with proper postage affixed or provided). For details on format and conditions of use, contact: Dr. Kenneth Schoenly, The Rockefeller University, Box 20, 1230 York Ave., New York, NY 10021-6399.

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⁸Burger, J. F., personal communication, 19 July 1991.

APPENDIX I

PRN file containing the cumulative (1986) taxonomic list of the Hawaiian Islands carrion fauna for Manoa Valley and Diamond Head Crater (compiled from Refs 6, 36, and 37)

HAWAIIAN ISLANDS FAUNA"	
(BASELINE DATA OF GOFF AND EARLY 1986)"	
" 1. Acaridae	"
" 2. Gamasida	"
" 3. Necrobia rufipes adults	"
" 4. Necrobia rufipes larvae	"
" 5. Dermestes spp. adults	"
" 6. Dermestes spp. larvae	"
" 7. Histeridae adults	"
" 8. Histeridae larvae	"
" 9. Oligota spp. adults and larvae	"
"10. Creophilus maxillosus adults	"
"11. Oxytelinae adults and larvae	"
"12. Philonthus longicornis adults (P1)	"
"13. Philonthus longicornis adults (F1)	"
"14. Philonthus longicornis larvae	"
"15. Collembola	"
"16. Dermaptera adults and nymphs	"
"17. Diplopoda	"
"18. Chrysomya megacephala adults	"
"19. C. megacephala larvae (1st instar)	"
"20. C. megacephala larvae (2nd instar)	"
"21. C. megacephala larvae (3rd instar)	"
"22. Chrysomya rufifacies adults	"
"23. C. rufifacies larvae (1st instar)	"
"24. C. rufifacies larvae (2nd instar)	"
"25. C. rufifacies larvae (3rd instar)	"
"26. C. rufifacies pupae	"
"27. Phaenicia cuprina adults	"
"28. Milichiidae adults	"
"29. Atherigona orientalis adults	"
"30. Fannia pusio adults	"
"31. Fannia pusio larvae	"
"32. Musca domestica adults	"
"33. Musca domestica larvae	"
"34. Musca sorbens adults	"
"35. Ophyra spp. adults	"
"36. Otitidae adults	"
"37. Piophilidae adults	"
"38. Sarcophagidae adults	"
"39. Sarcophagidae larvae (1st instar)	"
"40. Sarcophagidae larvae (2nd instar)	"
"41. Sarcophagidae larvae (3rd instar)	"
"42. Sarcophagula occidua adults	"
"43. S. occidua larvae	"
"44. Scenopinidae larvae	"
"45. Hermetia illuscens larvae	"
"46. Xylocoris discalis adults & nymphs	"
"47. Pheidole megacephala adults	"
"48. Brachymeria fonscolombi adults	"
"49. Exoristobia philippiensis adults	"
"50. Tachinaephagus zealandicus adults	"
"51. Solenopsis geminata adults	"
"52. Spalangidae adults	"
"53. Isopoda	"
"54. Tineidae larvae	"
"55. Pycnoscelus surinamensis nymphs	"

APPENDIX III

Sample output. Data are from the case report of Goff and Flynn [6]

ESTIMATION OF THE PMI FROM ARTHROPOD SUCCESSIONAL DATA: COMPUTER RESULTS
(Baseline Datafile Used: hicumpmi.dek)

Case Number: 1

Date of Analysis: 06-21-1991

NOTE THE FOLLOWING:

1. In hicumpmi.dek, the Avg. Interval Between Samples is: 2.3 days (SD = 2.2)
[A Standard Deviation > 0 Means Consecutive Samples WERE NOT All Taken
at a Fixed Time Interval. If SD > 0, the Lower and/or Upper Limit(s)
May Need to be Adjusted Accordingly]
2. In hicumpmi.dek, 7 Species Leave(s) and Reappear(s) in the Succession:
 - Taxon 2. Gamasida
 - Taxon 15. Collembola
 - Taxon 17. Diplopoda
 - Taxon 27. Phaenicia cuprina adults
 - Taxon 29. Atherigona orientalis adults
 - Taxon 31. Fannia pusio larvae
 - Taxon 38. Sarcophagidae adults

[If any of the Above Taxa were Found on the Remains, the Lower and/or
Upper Limit(s) May Need to be Adjusted Accordingly]

TAXONOMIC CONTENTS OF DATAFILE: hicumpmi.dek

- | | |
|--|--|
| 1. Acaridae | 2. Gamasida |
| 3. Necrobia rufipes adults | 4. Necrobia rufipes larvae |
| 5. Dermestes spp. adults | 6. Dermestes spp. larvae |
| 7. Histeridae adults | 8. Histeridae larvae |
| 9. Oligota spp. adults and larvae | 10. Creophilus maxilloso adults |
| 11. Oxytelinae adults and larvae | 12. Philonthus longicornis adults (F1) |
| 13. Philonthus longicornis adults (F1) | 14. Philonthus longicornis larvae |
| 15. Collembola | 16. Dermaptera adults and nymphs |
| 17. Diplopoda | 18. Chrysomya megacephala adults |
| 19. C. megacephala larvae (1st instar) | 20. C. megacephala larvae (2nd instar) |
| 21. C. megacephala larvae (3rd instar) | 22. Chrysomya rufifacies adults |
| 23. C. rufifacies larvae (1st instar) | 24. C. rufifacies larvae (2nd instar) |
| 25. C. rufifacies larvae (3rd instar) | 26. C. rufifacies pupae |
| 27. Phaenicia cuprina adults | 28. Milichiidae adults |
| 29. Atherigona orientalis adults | 30. Fannia pusio adults |
| 31. Fannia pusio larvae | 32. Musca domestica adults |
| 33. Musca domestica larvae | 34. Musca sorbens adults |
| 35. Ophyra spp. adults | 36. Otitidae adults |
| 37. Piophilidae adults | 38. Sarcophagidae adults |
| 39. Sarcophagidae larvae (1st instar) | 40. Sarcophagidae larvae (2nd instar) |
| 41. Sarcophagidae larvae (3rd instar) | 42. Sarcophagula occidua adults |
| 43. S. occidua larvae | 44. Scenopinidae larvae |
| 45. Hermetia illuscens larvae | 46. Xylocoris discalis adults & nymphs |
| 47. Pheidole megacephala adults | 48. Brachymeria fonscolombi adults |
| 49. Exoristobia philippiensis adults | 50. Tachinaephagus zealandicus adults |
| 51. Solenopsis geminata adults | 52. Spalangidae adults |
| 53. Isopoda | 54. Tineidae larvae |
| 55. Pycnoscelus surinamensis nymphs | |

Examination of the Remains in This Case Yielded 9 Immature and Adult Taxa
That Overlap the Above List:

3. Necrobia rufipes adults

- 4. *Necrobia rufipes* larvae
- 5. *Dermestes* spp. adults
- 6. *Dermestes* spp. larvae
- 7. *Histeridae* adults
- 13. *Philonthus longicornis* adults (F1)
- 26. *C. rufifacies* pupae
- 43. *S. occidua* larvae
- 45. *Hermetia illuscens* larvae

The Lower Limit Estimated From These Data Is: 34 days

The Taxon or Taxa that Define(s) the Lower Limit is(are):

- 13. *Philonthus longicornis* adults (F1)

The Upper Limit Estimated From These Data Is: 37 days

The Taxon or Taxa that Define(s) the Upper Limit is(are):

- 43. *S. occidua* larvae

Other Taxa Listed Below are Consistent (Though NOT Definitive) With the Above Estimate:

3. <i>Necrobia rufipes</i> adults	(days 10 to 76)
4. <i>Necrobia rufipes</i> larvae	(days 15 to 66)
5. <i>Dermestes</i> spp. adults	(days 6 to 58)
6. <i>Dermestes</i> spp. larvae	(days 11 to 58)
7. <i>Histeridae</i> adults	(days 4 to 51)
26. <i>C. rufifacies</i> pupae	(days 19 to 76)
45. <i>Hermetia illuscens</i> larvae	(days 30 to 76)

For These Data, a Postmortem Interval of 34 to 37 days is Estimated.

APPENDIX IV

Alternate output (hypothetical). The output shows that one of the corpse taxa (*Chrysomya megacephala* adults) does not overlap all the others in the succession. In this example, the user is advised to recheck the identification of this taxon or re-examine the environmental circumstances surrounding the case in question

ESTIMATION OF THE PMI FROM ARTHROPOD SUCCESSIONAL DATA: COMPUTER RESULTS
(Baseline Datafile Used: hicumpmi.dek)

Case Number: 2

Date of Analysis: 06-21-1991

NOTE THE FOLLOWING:

1. In hicumpmi.dek, the Avg. Interval Between Samples is: 2.3 days (SD = 2.2)
[A Standard Deviation > 0 Means Consecutive Samples WERE NOT All Taken at a Fixed Time Interval. If SD > 0, the Lower and/or Upper Limit(s) May Need to be Adjusted Accordingly]
2. In hicumpmi.dek, 7 Species Leave(s) and Reappear(s) in the Succession:
 - Taxon 2. Gamasida
 - Taxon 15. Collembola
 - Taxon 17. Diplopoda
 - Taxon 27. Phaenicia cuprina adults
 - Taxon 29. Atherigona orientalis adults
 - Taxon 31. Fannia pusio larvae
 - Taxon 38. Sarcophagidae adults
 [If any of the Above Taxa were Found on the Remains, the Lower and/or Upper Limit(s) May Need to be Adjusted Accordingly]

TAXONOMIC CONTENTS OF DATAFILE: hicumpmi.dek

- | | |
|--|--|
| 1. Acaridae | 2. Gamasida |
| 3. Necrobia rufipes adults | 4. Necrobia rufipes larvae |
| 5. Dermestes spp. adults | 6. Dermestes spp. larvae |
| 7. Histeridae adults | 8. Histeridae larvae |
| 9. Oligota spp. adults and larvae | 10. Creophilus maxillosus adults |
| 11. Oxytelinae adults and larvae | 12. Philonthus longicornis adults (P1) |
| 13. Philonthus longicornis adults (F1) | 14. Philonthus longicornis larvae |
| 15. Collembola | 16. Dermaptera adults and nymphs |
| 17. Diplopoda | 18. Chrysomya megacephala adults |
| 19. C. megacephala larvae (1st instar) | 20. C. megacephala larvae (2nd instar) |
| 21. C. megacephala larvae (3rd instar) | 22. Chrysomya rufifacies adults |
| 23. C. rufifacies larvae (1st instar) | 24. C. rufifacies larvae (2nd instar) |
| 25. C. rufifacies larvae (3rd instar) | 26. C. rufifacies pupae |
| 27. Phaenicia cuprina adults | 28. Milichiidae adults |
| 29. Atherigona orientalis adults | 30. Fannia pusio adults |
| 31. Fannia pusio larvae | 32. Musca domestica adults |
| 33. Musca domestica larvae | 34. Musca sorbens adults |
| 35. Ophyra spp. adults | 36. Otitidae adults |
| 37. Piophilidae adults | 38. Sarcophagidae adults |
| 39. Sarcophagidae larvae (1st instar) | 40. Sarcophagidae larvae (2nd instar) |
| 41. Sarcophagidae larvae (3rd instar) | 42. Sarcophagula occidua adults |
| 43. S. occidua larvae | 44. Scenopinidae larvae |
| 45. Hermetia illuscens larvae | 46. Xylocoris discalis adults & nymphs |
| 47. Pheidole megacephala adults | 48. Brachymeria fonscolombi adults |
| 49. Exoristobia philippiensis adults | 50. Tachinaephagus zealandicus adults |
| 51. Solenopsis geminata adults | 52. Spalangidae adults |
| 53. Isopoda | 54. Tineidae larvae |
| 55. Pycnoscelus surinamensis nymphs | |

Examination of the Remains in This Case Yielded 10 Immature and Adult Taxa That Overlap the Above List:

3. *Necrobia rufipes* adults
4. *Necrobia rufipes* larvae
5. *Dermestes* spp. adults
6. *Dermestes* spp. larvae
7. Histeridae adults
13. *Philonthus longicornis* adults (F1)
18. *Chrysomya megacephala* adults
26. *C. rufifacies* pupae
43. *S. occidua* larvae
45. *Hermetia illuscens* larvae

ALERT: At Least One Corpse Taxon DOES NOT Overlap the Others in the Succession.
The PMI is Indeterminate from These Death Scene Data!!!

Overlap Matrix of Corpse Taxa
(Number of Joint Occurrences Among Pairs of Corpse Taxa)

Sp. 3	0	20	23	22	22	4	0	19	15	12
Sp. 4	20	0	19	19	18	4	0	18	14	11
Sp. 5	23	19	0	22	26	4	4	17	15	10
Sp. 6	22	19	22	0	21	4	0	17	15	10
Sp. 7	22	18	26	21	0	4	6	16	15	9
Sp. 13	4	4	4	4	4	0	0	4	2	4
Sp. 18	0	0	4	0	6	0	0	0	0	0
Sp. 26	19	18	17	17	16	4	0	0	12	12
Sp. 43	15	14	15	15	15	2	0	12	0	5
Sp. 45	12	11	10	10	9	4	0	12	5	0

Recheck ID of (or the Circumstances Surrounding):

18. *Chrysomya megacephala* adults

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