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compounds found in drainage waters in East Anglia, and this indicates that the method assesses the risk of leaching in a realistic way.

CONCLUSIONS

Although simulation models are able to predict results of specific events, the input data they require and the time required to learn their operation often takes from several hours to many days. The operation of the present system is fast and can be learnt in a few seconds whilst a run takes about 20 minutes for each compound. A database, assembled from the literature and containing most of the properties of over 400 compounds can speed the preparation of input data. Additional information, such as soil texture diagrams, can be stored in the context-sensitive Windows Help system.

Expert systems of this type make it possible to transfer the results of research from the bench to the PC of the user within 24 hours and to present such results in an attractive and digestible form. For example, the new compounds announced at this conference have already been included in the database. The system may be of particular use during the initial "sifting" of applications by PSD. Future versions will include extended databases and context-sensitive help systems, together with additional sections on uptake through cuticles of plants and the influence of different European climates.

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Title A NEW METHOD OF DETECTING AND MEASURING SPATIAL NON-RANDOMNESS

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Perry & Hewitt (1991) introduced a new class of indices of aggregation for counts from a rectangular grid of samples. These differ from previous indices, being based directly on individual movement and spatial location and able to utilise all the spatial information in the sample. The indices are more powerful than traditional measures at detecting aggregation.

Perry (1994a) reported how a simple algorithm could be employed to construct such an index for general count data, not restricted to occur a grid, from any locations where the two-dimensional coordinates are known. This index is based on calculation of the minimum distance required for the individuals in the sample to move to an arrangement which is completely regular (i.e. in which all sample units have equal numbers of individuals). Examples of these analyses will be given for the moth *Xestia c.-nigrum* with data from the Rothamsted Insect Survey.

However, much data is in the form of maps, rather than counts, where the precise two-dimensional spatial coordinates of each individual is known. Indeed, this form of data occurs frequently in problems which span many disciplines other than entomology. Perry (1994b) outlined how the above approach may be extended to provide tests of randomness and indices of aggregation for such general two-dimensional data and empirically-based estimates of the foci of clusters in the data. These techniques may be used to provide an estimate of the point of invasion of a recently-introduced pest such as *Macrosiphum albifrons*. Examples of these analyses will be given with field data.

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Title AMINO ACID COMPOSITION OF INSECTS AND TROPHIC CHAIN RELATIONSHIPS

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Amino acid composition of 4 species of Orthoptera, 14 species of Carabidae beetles, 4 species of Staphylinidae beetles, 1 species of Cerambycidae beetles, 1 species of Chrysomelidae beetles, 4 species of Scarabaeidae beetles, 3 species of Elateridae beetles, 7 species of Silphidae beetles, 1 species of Tortricidae caterpillars, 2 species of Diptera larvae and 1 species of ants was studied in Central-Chernozem Reserve (Kursk region, Russian Federation). All herbivorous and saprovorous insects have 1-2 order higher concentration of essential amino acids than their potential food sources (live or dead plant tissues). Carnivorous insects have the similar amino acid composition that herbivorous and saprovorous insects. Low methionine and lysin content in plant food is assumed that microorganisms (gut or soil) are the source of essential amino acids for herbivores and saprovores. Hence, herbivorous and saprovorous insects are microbivorous in relation of amino acid and protein feeding. Microbial link in food chain is the obligate link between substrate (live and dead plant tissues) and herbivorous or saprovorous insects.