analysed a large number of parasite species with variable distributions within the hosts sampled. Considering that only simple mathematical operators were used and that different configurations were not explored, one can expect there to be a huge potential for the application of this approach to solving assignment problems using parasites as tags, and it could be particularly useful in discrimination at finer geographical scales.

Future perspectives

GP might not be suitable for all types of problem, although it has an advantage when there is no ideal solution or when the variables are constantly changing [3]. A range of mathematical operators can be used in GP (arithmetic, trigonometric, Boolean and fuzzy logic). Fuzzy systems are particularly interesting for biological applications because they can be used to create rules using data that are incomplete, approximate or subjective [14,15]. Although GP can find good solutions to difficult problems, the evolved models might be capable of further optimization by local-search algorithms [16]. If this were done and the optimized models are retained and reincorporated into the population, one would have the computer equivalent of Lamarckianism (reverse encoding of learned improvements back into the genome). This approach can increase efficiency considerably [17]. Recently, GP applied to ecological modelling has also shown promise in predicting time-series changes [9,18] in which the focus is on replicating a pattern and, therefore, has potential for the detection and prediction of cyclic variations of parasite occurrence in studies of host–parasite dynamics.

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Letters

What are malaria parasites?

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The study of haemosporidian parasites (apicomplexan protozoans that infect the blood of different vertebrates) was boosted recently by the advent of PCR-based methods for the amplification of parasite DNA from blood samples [1–3]. Suddenly, it was possible to detect and identify these parasites quickly and accurately. For non-specialists, this method also enabled detailed analyses of parasite phylogeny and host–parasite co-evolution patterns. Birds and reptiles have rapidly become model groups for these studies, and terms such as 'avian malaria' and 'lizard malaria' have emerged as commonly used jargon in the literature when referring to diseases caused by haemosporidian parasites in vertebrates other than mammals [1–3].

Simultaneous studies of *Plasmodium* and other related genera have opened a debate about exactly what should be

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considered to be malaria parasites. Beyond the World Health Organization (http://www.who.int/en/) definition (that malaria is a human disease caused by four *Plasmodium* species that are transmitted by *Anopheles* mosquitoes), the traditional view accepts only *Plasmodium* species as being the true malaria parasites [4]. This view is justified by the fact that *Plasmodium* undergoes asexual reproduction in blood – a life-history trait that, apparently, has been lost during the evolution of other haemosporidian lineages [1]. However, based on the phylogeny of the group, some authors include other genera, particularly *Haemoproteus*, among the malaria parasites [1]. Purists might criticize this notion of malaria parasites, but it has been published in leading journals such as *Trends in Parasitology*, *Systematic Biology* and *Evolution* [1–3,5]. Because it might be pointless to seek one definition that best fits all circumstances, we should at least try to reconcile traditional concepts with new data.

The controversy stems from the incomplete knowledge of the phylogenetic relationships and pathogenicity of non-human malaria parasites. Recent phylogenetic analyses (based on both mitochondrial and nuclear DNA) have shown that morphological and life-history traits do not necessarily indicate relatedness within haemosporidian parasites [1,3]. Remarkably, the genus *Plasmodium* is paraphyletic with respect to *Haemoproteus* (Figure 1): avian and reptilian *Plasmodium* species are more closely related to *Haemoproteus* species than to mammalian *Plasmodium* parasites. In addition, *Hepatocystis* clusters within *Plasmodium* lineages of mammals [1]. Therefore, these results do not support the existence of a genus *Plasmodium*, the agent of malaria in the traditional sense, thus calling for further research to disentangle the evolutionary relationships of malaria parasites [6], in which *Haemoproteus*, *Hepatocystis* and other related genera should have a central role.

The typological conception of malaria parasites might be clinically useful, as long as it is restricted to parasite species for which malaria symptoms are directly identified. Some malaria symptoms such as deposition of haemozoin and anaemia are shared by *Plasmodium* and *Haemoproteus* parasites [7,8], whereas clinical differences

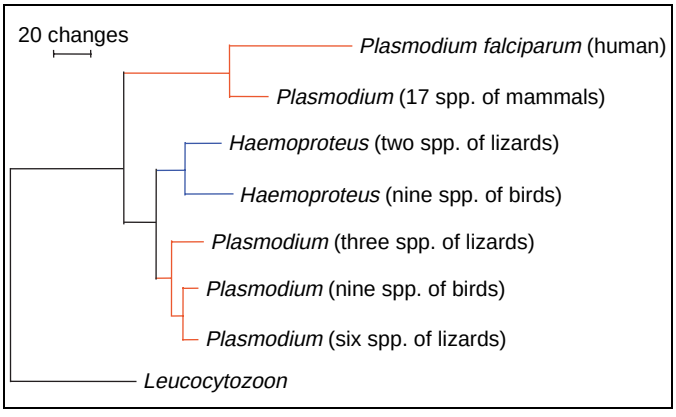

Figure 1. A phylogeny of malaria parasites based on cytochrome *b* sequences. The branch with 17 *Plasmodium* spp. of mammals includes the human parasites *Plasmodium vivax, Plasmodium ovale* and *Plasmodium malariae.* Colours represent the genera *Plasmodium* (red) and *Haemoproteus* (blue), as defined based on morphology and life-history traits. The sister genus *Leucocytozoon* has been included as an outgroup. Modified, with permission, from Ref. [1].

are sometimes more marked between particular species than between genera, such as recurring production of blood stages or cerebral lesions in some species of *Plasmodium*, or the formation of cyst-like bodies in muscle tissue in some species of *Haemoproteus* [4,9]. Although it is common wisdom that blood schizogony makes *Plasmodium* parasites more pathogenic than *Haemoproteus* parasites [4], the fact is that both genera include species that cause substantial levels of morbidity and mortality in natural populations, in addition to species that show hardly any pathogenicity, even at levels of parasitaemia observed in nature [9–11]. Such a diverse pathogenicity is also apparent through the phylogeny of malaria parasites, with loss of the malaria disease in some lineages over evolutionary time and gain of pathogenicity by originally harmless species as a result of host switching.

In summary, the typological definition of malaria parasites (i.e. only *Plasmodium* species) is useful as a working concept but it might be evolutionarily misleading, and further research is needed to support its use from a clinical perspective when extended to parasites of birds and reptiles. However, an evolutionary definition of malaria parasites (the monophyletic group formed by *Plasmodium*, *Haemoproteus* and, probably, other haemoproteids of mammals) is supported by recent molecular data, although it is incongruent with the conventional definition of malaria based on life-history traits that are exclusive to *Plasmodium* parasites. In our opinion, the evolutionary and the clinical or typological definitions can be useful, provided that it is made clear what is being talked about. It is evident that including the word 'malaria' in the title of an article, particularly in multidisciplinary literature, catches the attention of the general readership but this is not a primary issue of this letter. Instead, to increase knowledge of the causes of malaria diseases, we need to resolve the phylogenetic relationships in the diverse group of parasites responsible for these symptoms in mammals, birds and lizards, in addition to the fitness consequences and patterns of co-evolution among parasites, hosts and vectors. In this important research, it would be useful to call the organisms that are potentially responsible for causing malaria (at present or in evolutionary time), simply, malaria parasites.

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Trypanosomiasis Vector Research and Control Foundation

In support of the large-scale research and control initiatives against African and American trypanosomiasis, a new non-profit foundation has been approved by the Internal Revenue Service of the US Treasury Department. The Trypanosomiasis Vector Research and Control (TVRC) Foundation, based in Washington DC, will channel funds into research and control activities directed against Triatominae, the vectors of Chagas disease (American trypanosomiasis), and against Glossinidae, the vectors of African trypanosomiasis (sleeping sickness and nagana).

Control of Chagas disease relies heavily on elimination of the main domestic vectors, especially *Triatoma infestans* in the Southern Cone countries, and *Rhodnius prolixus* and *Triatoma dimidiata* in Central America and the Andean Pact countries. Large-scale international campaigns against these and other vectors, coordinated by the Pan-American Health Organization, have achieved considerable success but much is still to be done.

The TVRC Foundation works closely with the African Union through the Pan-African Tsetse and Trypanosomiasis Eradication Campaign (PATTEC) initiative and with the ECLAT network, which was set up to support the Chagas disease control activities.

For further information, contact Professor Waldemar Klassen, the TVRC Secretary, at the University of Florida (WKlassen@mail.ifas.ufl.edu).