THE RELAIS PROJECT: AN EPI-INFORMATICS CONSTELLATION

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Introduction
Global disease control presents an information management problem. Routine epidemiological work generates vast amounts of data in various forms: outbreak reports, clinical samples, the results of laboratory analyses, genetic sequences, phylogenetic trees. Much of this data must in turn be distributed in a timely and secure fashion to scientists, field personnel and decision makers. Unfortunately and unremarkably, disease data currently tends to be dispersed over a variety of information systems, using incompatible formats. Where data sharing takes, it is on an ad hoc basis.

Material & methods
To this end, we have developed ReLaIS: the Reference Laboratory Information System. This loosely coupled constellation of software systems and databases allows allied laboratories to gather, query, visualise and share epidemiological data in semi-automated manner. Rather than force workers to adopt their style and data to a common format, and workflow the ReLaIS system instead makes it easy for data to be imported and communicated between systems. Analyses are controlled and visualised via web browser (TTW: through the web), so that remote workers may manipulate data just as easily as those in the lab, in a standardised environment.

ReLaIS is based upon a stack of free open source software, including the programming language Python, bioinformatics library BioPython, the MySQL database, the content management system Plone for web presentation and geospatial visualisation via OpenLayers. The choice is not ideological, but practical: By adopting widely used FOSS tools, we ensure that development time is lowered, individual components have been rigorously tested, any software developed can be redistributed without problems and there exists a large pre-existing body of expertise for development and deployment. Finally, low cost is an obvious attraction, especially where systems may need to deployed in impoverished areas.

ReLaIS also includes Amergin, a web-based platform for storing, editing and analysing molecular epidemiological data. By working through-the-web, operators gain a consistent analysis environment where expensive computations are carried out on a remote server and data is stored consistently and safely in a single location. Amergin engages with the ReLaIS workflow so that updated data flows to and from the system.

ReLaIS has been designed to be flexible and extensible for easy adoption and customisation for different laboratories and pathogens (currently the FMDV world reference laboratory, and Bluetongue reference laboratory at IAH-Pirbright by the end of 2007). Further, it has been constructed from widely used, open source software for which there exists a wide pool of expertise for support and modification and limited developmental and set-up costs.

Discussions & conclusions
Future developments include expansion of data and analyses (e.g. molecular structural functions), and the introduction of a tracking facility for field workers and clients to follow the analysis of their samples in real time.

References

