These projects focus on smart tools for bioinformatics research, to engage life scientists in more effective computational biology.

- Visualise & navigate previously uncharted relationships
- Chaining tools through workflow and mashups
- Providing simplified models for comparative studies
- Smart analysis tools for key applications

A general theme of the research is to investigate how industry standard Microsoft business tools and technologies can be extended to meet scientists' needs, while retaining their usability, convenience and familiar look and feel.

**SilverMap**
- A new approach to understanding comparative genomics using the familiar visual maps metaphor
- Central to these ideas is the concept of a distance measure, and allowing researchers to define one that best reflects the structure of their problem
- Shows relationships between genes organised according to BLAST similarity: navigation integrated with visualisation Silverlight BLAST explorer – sit on top of any data set
- Supports tagging, user annotations, live snapshots
- Extensions to regulatory networks, pan genomics (coming)

**SilverGene**
- A novel genomic visualiser hosted within most standard web browsers
- Implemented using Microsoft Silverlight
- Delivers highly interactive exploration at arbitrary scales
- Works with local or remotely accessed data
- Annotation, tagging, dynamic snapshots
- Full text query of user annotations & genomics features
- Supports custom tracks, GFF, visualise BioPatML motifs

**Bio2RDF**
- Allows users of one database to query numerous other web sources
- Find all PubMed abstracts related to their particular genome or set of genes
- Determine author expertise by finding the COGs of genes mentioned in their publications
- Identify other scientists working on similar organisms or sets of genes via Bio2RDF URI based tags
- Explore the interlinked Bio2RDF data graph using common URI’s to denote particular records on particular databases

**GPGlue**
- Builds on experience from GPFlow scientific workflow to bring dynamic, compose-as-you go, web-based scripting to the lab page
- Supports tagging, data persistence & forward linking
- Operations are automatically recorded, providing provenance and data dependency mapping
- Underpins the SilverMap BLAST explorer, SilverGene visualisation workflows

**BioMashups**
- Combine data and services from multiple sources
- Supports rapid, curiosity-driven exploration
- Real Bioinformatics: Protein analyses, RT-PCR design
- Eliminates installations & complex workflow software
- Supports reuse and sharing

**BioPatML**
- Biological systems described in well-defined, yet flexible and extensible formats
- Web 2.0 style sharing, tagging and publication
- Enhance exchange and re-use