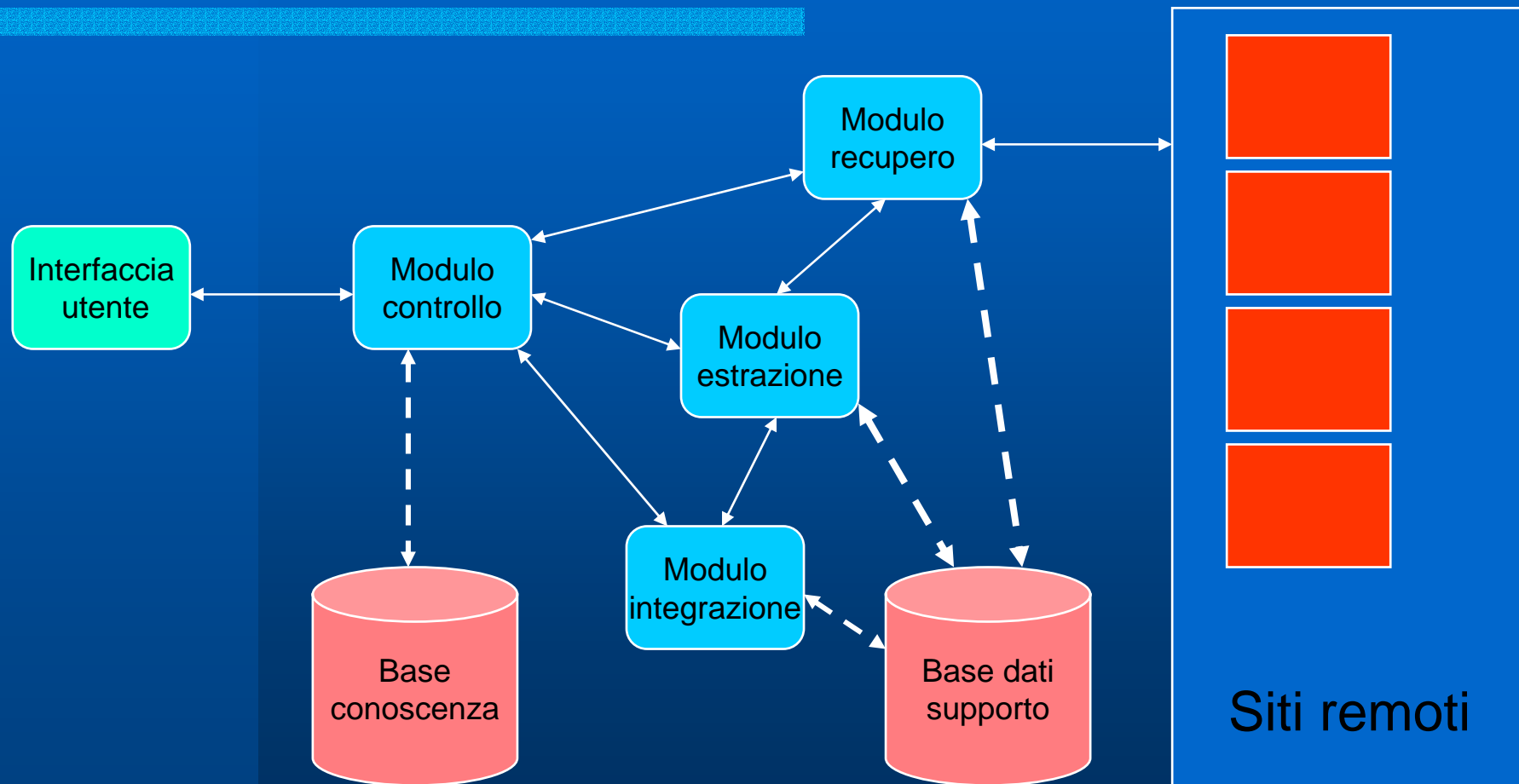


O2I OncoAgent

Università di Camerino

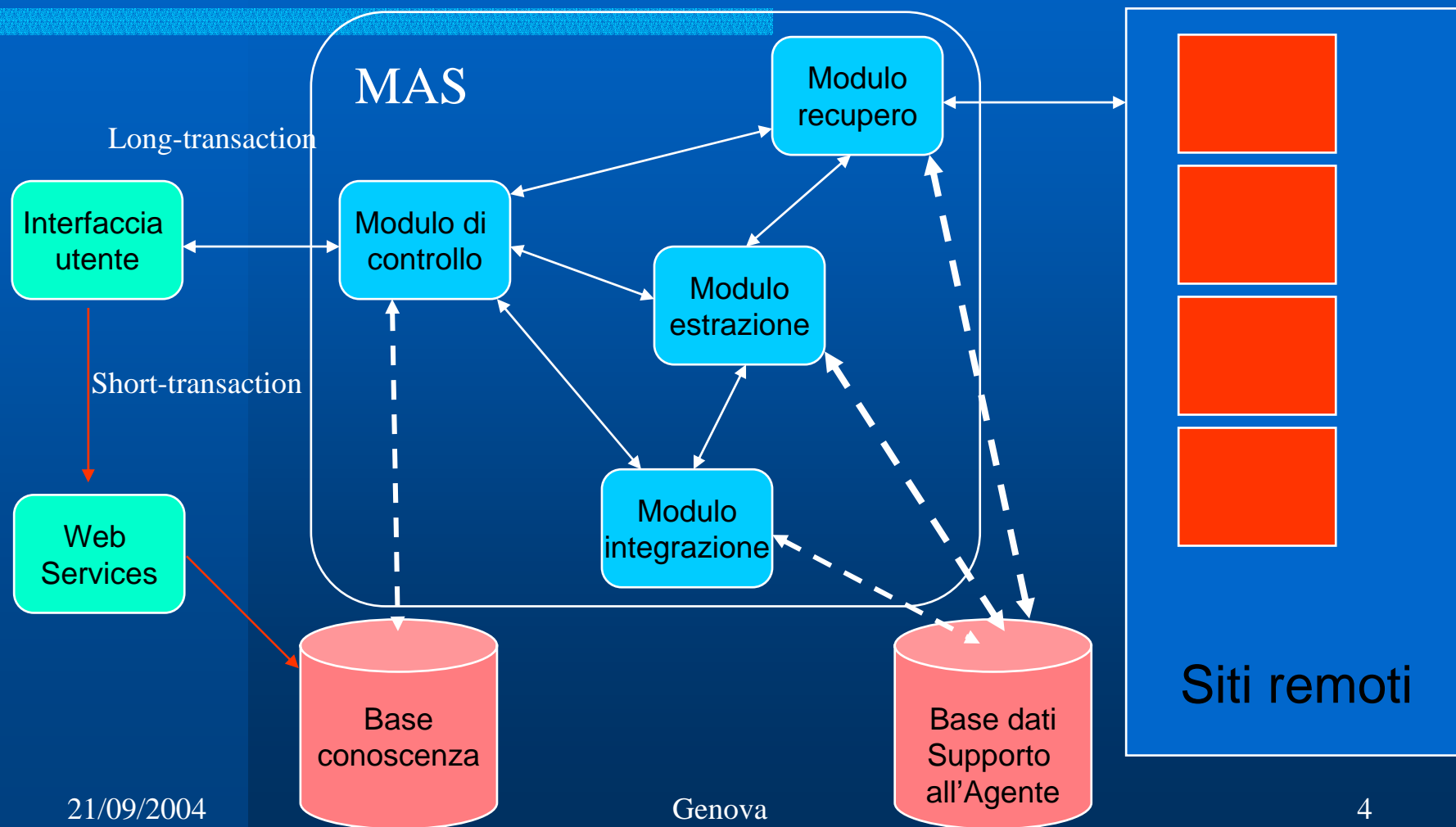
Schema funzionale – generale



Motore di ricerca – OncoAgent

- **Ipotesi per l'uso di MAS**
 - Long Transaction: necessità di tempi lunghi per fornire una risposta ad interrogazione
 - Grandi quantità di dati da analizzare
 - Possibilità di codificare la conoscenza dell'utente sull'agente
 - Possibilità di definire l'interrogazione come un workflow di attività correlate
 - ...
- **MAS – Multi-Agent System**
 - Modulo di controllo configura gli agenti utilizzando le informazioni memorizzate nella base di conoscenza
 - Moduli di recupero e di estrazione dell'informazione mettono a disposizione degli agenti gli strumenti necessari ad interrogare e wrappare una risorsa remota
 - Modulo di integrazione permette la condivisione della conoscenza di un agente con altri agenti, creando una base di supporto

Schema funzionale – MAS e OncoAgent

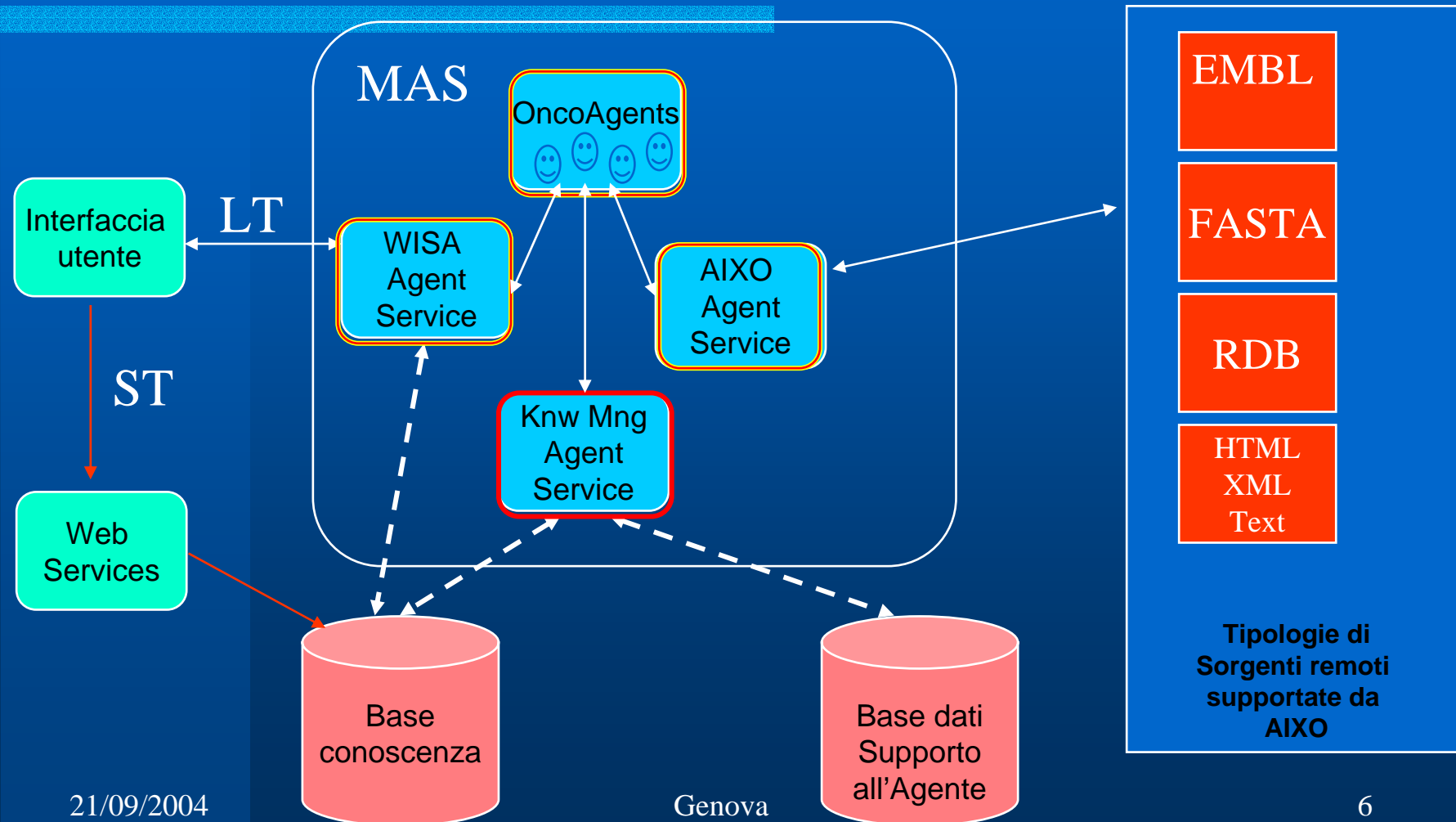


Motore di ricerca – MAS

- **MAS – Multi-Agent System**

- WISA + Pool OncoAgents ↔ Modulo di controllo configura gli agenti utilizzando le informazioni memorizzate nella base di conoscenza
- AIXO ↔ Moduli di recupero e di estrazione dell'informazione mettono a disposizione degli agenti gli strumenti necessari ad interrogare e “wrappare” una risorsa remota
- KW-MNG ↔ Modulo di integrazione permette la condivisione della conoscenza di un agente con altri agenti, creando una base di supporto

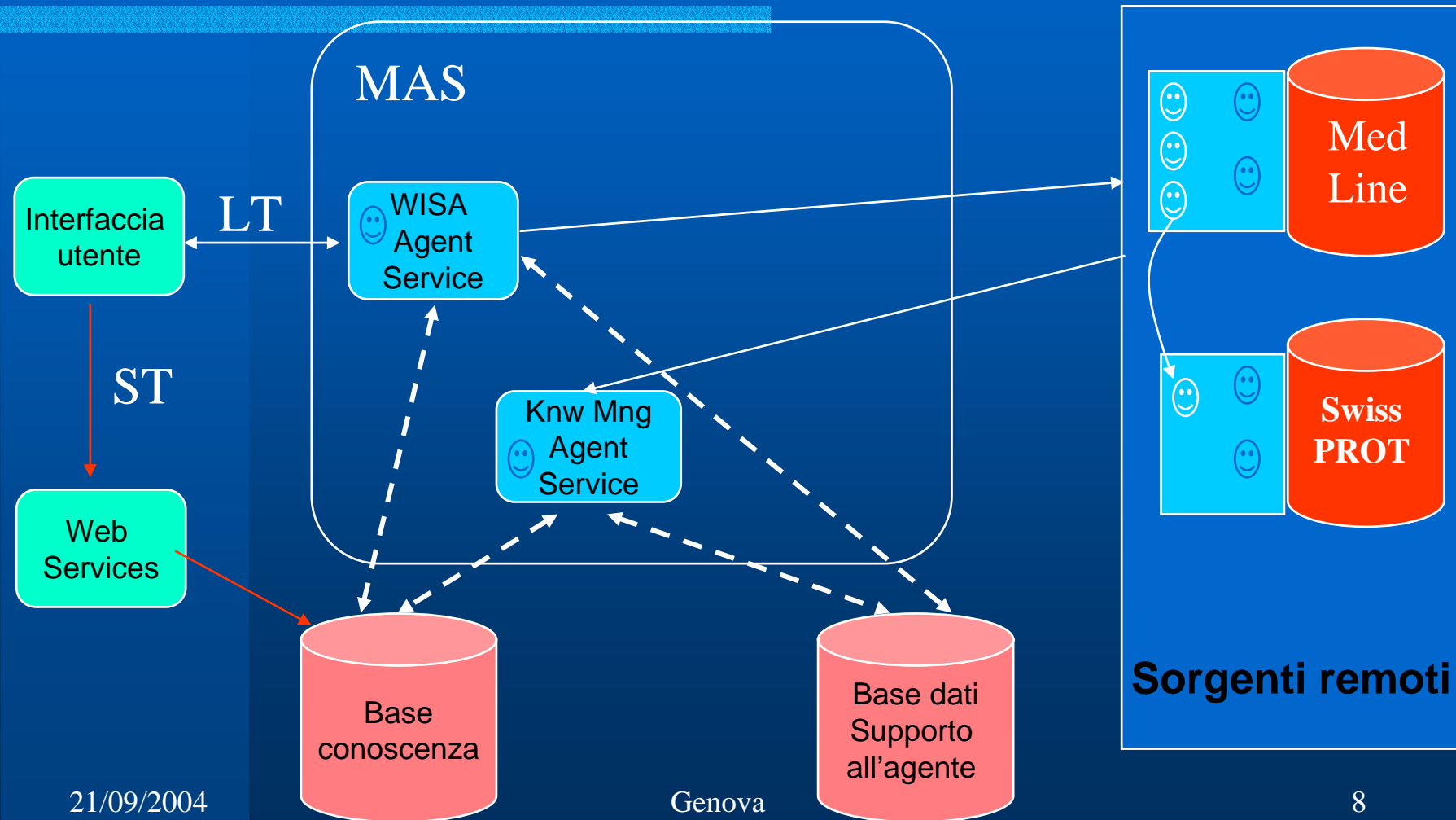
Schema ad agenti - MAS



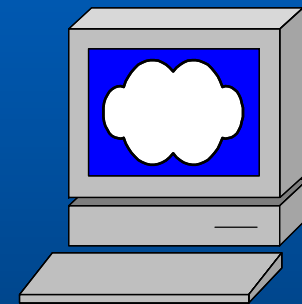
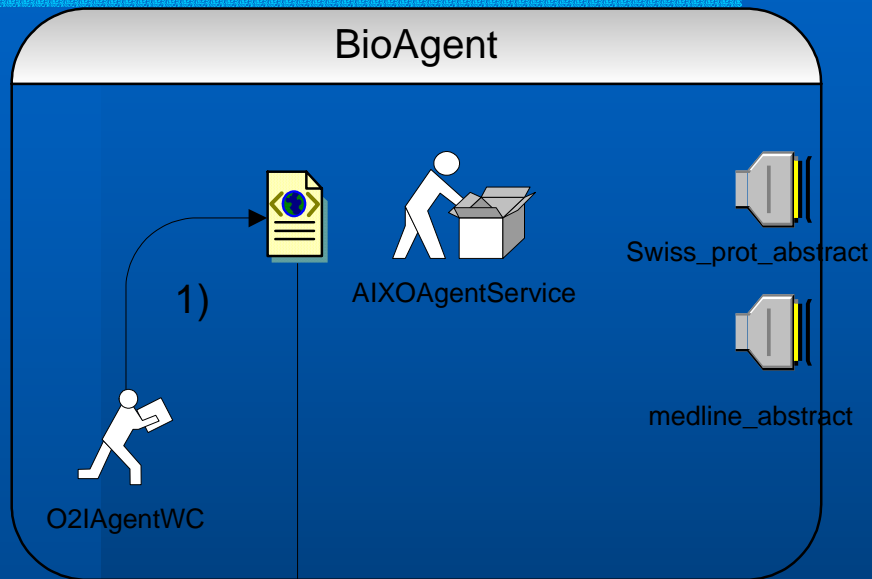
Motore di ricerca – MAS e codice mobile

- **Testare la mobilità nell'ipotesi di**
 - Grandi quantità di dati da analizzare
 - Possibilità di codificare la conoscenza “algoritmo/servizio” dell'utente sull'agente
 - Possibilità di definire l'interrogazione come un workflow di attività correlate
 - Elevato numero di interazioni tra user agent e remote service agent
 - Necessità di “personalized remote computing”
 - ...
- **MAS – Multi-Agent System**
 - **WISA + Pool OncoAgents ↔ Modulo di controllo:**
 - configura gli agenti utilizzando le informazioni memorizzate nella base di conoscenza
 - **AIXO ↔ Moduli di recupero e di estrazione dell'informazione**
 - mette a disposizione degli agenti gli strumenti necessari ad interrogare e “wrappare” una risorsa remota
 - **KW-MNG ↔ Modulo di integrazione**
 - permette la condivisione della conoscenza di un agente con altri agenti, creando una base di supporto

Schema ad agenti – agenti mobili



Esempio - step1

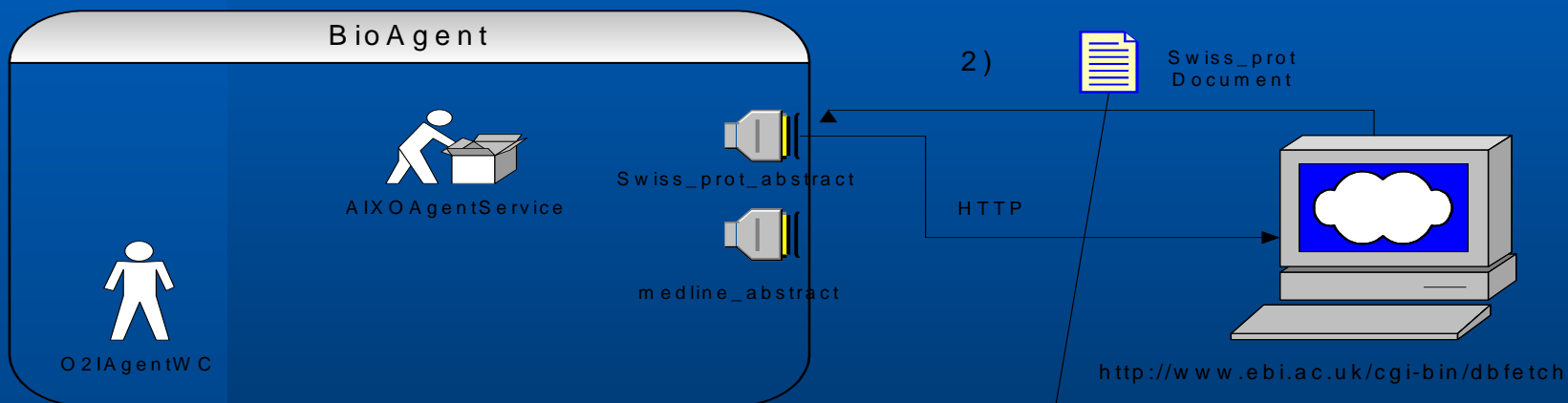


<http://www.ebi.ac.uk/cgi-bin/dbfetch>

```
<aixo_message>
  <wrapper xml_result="JDOM" id="swiss_prot_abstract" XQLstring="" >
    <parameter_access name="id" value="XXXXXXXXX"/>
  </wrapper>
</aixo_message>
```

Esempio - step 2

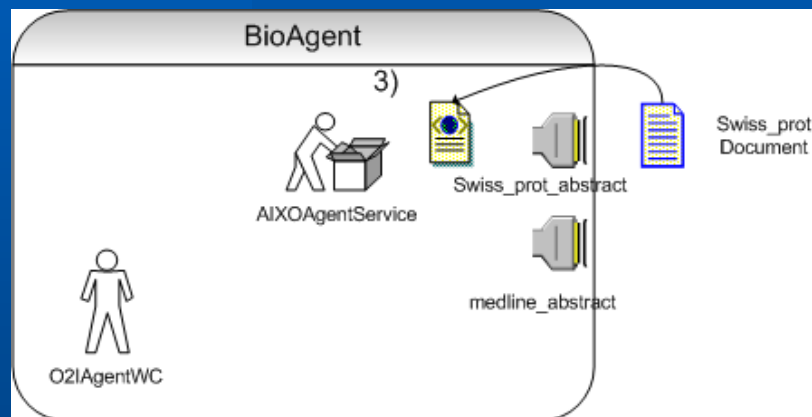
Proteina	Computer	KBytes	Rete	http access time(sec.)
P53_HUMAN	MyNotebook	49.6	Rete Ateneo	4.89
FOS_HUMAN	MyNotebook	4.72	Rete Ateneo	3.62
1433_ORYSA	MyNotebook	2.51	ADSL 640 Kbits/s	1.76
P53_HUMAN	Giasone	49.6	Rete Ateneo	2.37
FOS_HUMAN	Giasone	4.72	Rete Ateneo	1.63
1433_ORYSA	Giasone	2.51	Rete Ateneo	2.36



```

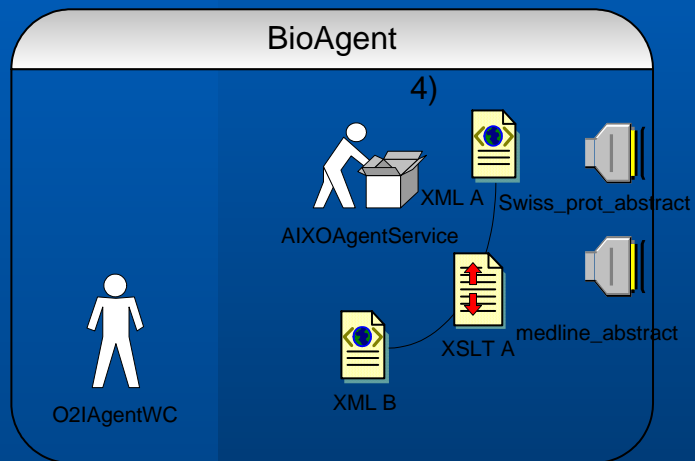
ID XXXXXXXXXXX STANDARD; PRT; 260 AA. AC Q06967;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-JUN-1994 (Rel. 29, Last annotation update)
DE 14-3-3-like protein S94.
OS Oryza sativa (Rice).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
... ..
    
```

Esempio - step 3



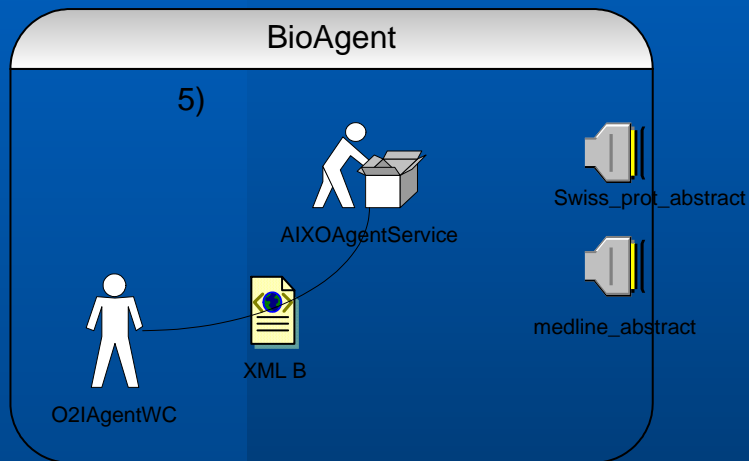
Proteina	Computer	KBytes	XML Translation time (sec.)
P53_HUMAN	MyNotebook	49.6	1.21
FOS_HUMAN	MyNotebook	4.72	0.11
1433_ORYSA	MyNotebook	2.51	0.06
P53_HUMAN	Giasone	49.6	1.11
FOS_HUMAN	Giasone	4.72	0.04
1433_ORYSA	Giasone	2.51	0.36

Esempio - step 4



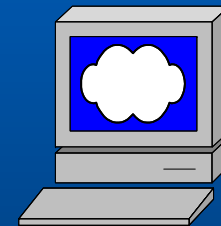
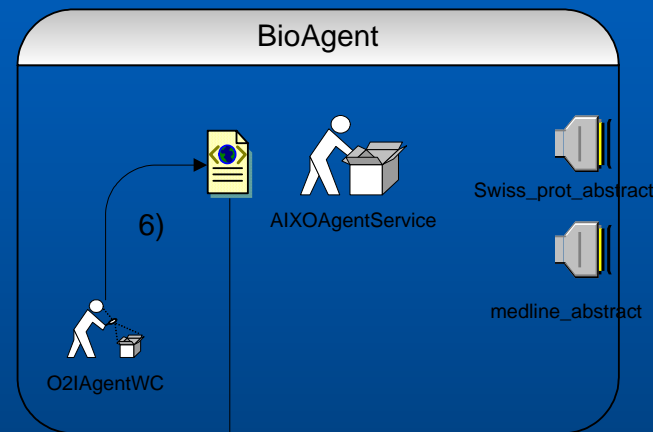
Proteina	Computer	XSLT time (sec.)
P53_HUMAN	MyNotebook	1.42
FOS_HUMAN	MyNotebook	1.1
1433_ORYSA	MyNotebook	0.6
P53_HUMAN	Giasone	0.7
FOS_HUMAN	Giasone	0.48
1433_ORYSA	Giasone	0.428

Esempio - step 5



Proteina	Computer	Message go and go back time (sec.)
P53_HUMAN	MyNotebook	1.87
FOS_HUMAN	MyNotebook	3.29
1433_ORYSA	MyNotebook	1.09
P53_HUMAN	Giasone	0.8
FOS_HUMAN	Giasone	0.9
1433_ORYSA	Giasone	0.68

Esempio - step 6



<http://www.ebi.ac.uk/cgi-bin/dbfetch>

```
<aixo_message>
  <wrapper xml_result="JDOM" id="medline_abstract" XQLstring="" >
    <parameter_access name="id" value="XXXXXXXXX"/>
  </wrapper>
</aixo_message>
```

<http://ensembl.unicam.it:8080/bioagent/>

Esempio – risultato intermedio

```
• <?xml version="1.0" standalone="no" ?>
• <SwissProt_entries>
• <SwissProt_Entry>
• <ID entry_name="P53_HUMAN" data_class="STANDARD" molecule_type="PRT" sequence_lenght="393" />
• <AC number="P04637" />
• <AC number="Q16848" />
• <AC number="Q9UBI2" />
• <DT date="13-AUG-1987" release="05" type="Created" />
• <DT date="01-MAR-1989" release="10" type="Last sequence update" />
• <DT date="28-FEB-2003" release="41" type="Last annotation update" />
• <DE>Cellular tumor antigen p53 (Tumor suppressor p53) (Phosphoprotein p53) (Antigen NY-CO-13).</DE>
• <GN>TP53 OR P53.</GN>
• <OS>Homo sapiens (Human).</OS>
• <OC>Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.</OC>
• <OX>NCBI_TaxID=9606;</OX>
• <RN num="1">
• <RP>SEQUENCE FROM N.A.</RP>
• <RX Bibliographic_db="MEDLINE" id="85230577" />
• <RX Bibliographic_db="PUBMED" id="4006916" />
• <RA>Zakut-Houri R., Bienz-Tadmor B., Givol D., Oren M.;</RA>
• <RT>"Human p53 cellular tumor antigen: cDNA sequence and expression in COS cells."</RT>
• <RL>EMBO J. 4:1251-1255(1985).</RL>
• </RN>
• <RN num="2">
• <RP>SEQUENCE FROM N.A.</RP>
• <RX Bibliographic_db="MEDLINE" id="87064416" />
• <RX Bibliographic_db="PUBMED" id="2946935" />
• <RA>Lamb P., Crawford L.;</RA>
• <RT>"Characterization of the human p53 gene."</RT>
• <RL>Mol. Cell. Biol. 6:1379-1385(1986).</RL>
• </RN>
• ...
```

Esempio – risultato finale

- `<?xml version="1.0" encoding="UTF-8" ?>`
- `<Abstracts>`
- `<MedlineCitation>`
- `<MedlineID>85230577</MedlineID>`
- `<AbstractText>A 2.5-kb cDNA clone for human p53 tumor antigen has been isolated. This clone contains the entire coding region including 135 bp upstream of the first ATG. Comparison of the nucleotide sequence of human p53 and mouse p53 demonstrates that the first ATG in human p53 corresponds to the second ATG (codon No. 4) in mouse p53. The human p53 comprises 393 residues and is longer than the mouse p53 due to six additional codons present at the region corresponding to exon 4 of the mouse p53 gene. The DNA sequence homology between the coding regions of mouse and human p53 is 81% and the conservation of homology is not equally distributed along the molecule. When inserted into SV40-based expression vectors the human p53 cDNA successfully directs the production of a polypeptide with an apparent mol. wt. of 55 kd which can be precipitated by monoclonal antibodies to p53.</AbstractText>`
- `</MedlineCitation>`
- `<MedlineCitation>`
- `<MedlineID>87064416</MedlineID>`
- `<AbstractText>Cosmid and lambda clones containing the human p53 gene were isolated and characterized in detail. The gene is 20 kilobases (kb) long and has 11 exons, the first and second exons being separated by an intron of 10 kb. Restriction fragments upstream of sequences known to be within the first identified exon were tested for promoter activity by cloning them in front of the chloramphenicol acetyltransferase gene and transfecting the resulting constructs into HeLa cells. A 0.35-kb DNA fragment was identified that had promoter activity. Results of primer extension experiments indicated that the mRNA cap site falls within this fragment, as expected. Analysis of the sequence upstream of the presumptive cap site indicated that the human p53 promoter may be of an unusual type.</AbstractText>`
- `</MedlineCitation>`
- `<MedlineCitation>`
- `<MedlineID>85267676</MedlineID>`
- `<AbstractText>Three clones for the human tumor antigen p53 were isolated from a cDNA library prepared from A431 cells. One of these clones, pR4-2, contains the entire coding region for human p53. This clone directs the synthesis of a polypeptide with the correct molecular weight and immunological epitopes of an authentic p53 molecule in an in vitro transcription-translation reaction. Although the pR4-2 clone contains the coding region for p53, it is not a full-length copy of the human p53 mRNA. Northern analysis showed that the p53 mRNA is approximately 2,500 nucleotides long, whereas the pR4-2 insert is only 1,760 base pairs in length. Analysis of the DNA sequence of this clone suggests that the human p53 polypeptide has 393 amino acids. We compared the predicted amino acid sequence of the pR4-2 clone with similar clones for the mouse p53 and found long regions of amino acid homology between these two molecules.</AbstractText>`
- `</MedlineCitation>`
- ...