

Programming or Flexibility?

Design of Programmable Applications with Biologists

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In Situ

- New interaction paradigms:
 - multi-scale (or zoomable) interfaces,
 - interactive information visualization,
 - bimanual interaction,
 - video and non-speech audio,
 - augmented or mixed reality.
- Participatory design
 - development of new participatory design methods,
 - make the role of context explicit in the design process.
- Engineering of interactive systems
 - component-based architectures (customizable and dynamic addition or substitution of interaction techniques).

Programming situations

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- variation: search for patterns in a sequence, *except repeated ones*
- finer control on the computation: control in what order multiple sequences are compared and aligned
- simple operations: search in a DNA sequence for the characters other than A, C, T and G

Parsing and scripting example

This example shows the report of a program searching for registered well-known patterns in a given protein sequence.

| <u>Access#</u> | <u>From->To</u> | <u>Name</u> |
|----------------|---|------------------|
| PS00005 | 39->41 | PKC_PHOSPHO_SITE |
| | Pattern [ST].[RK] matched | |
| | Site 39 TTR 41 | |
| PS00005 | 71->73 | PKC_PHOSPHO_SITE |
| | Pattern [ST].[RK] matched | |
| | Site 71 TSK 73 | |
| PS00008 | 20->25 | MYRISTYL |
| | Pattern G[^EDRKHPFYW]..[STAGCN][^P] mat | |
| | Site 20 GILAAI 25 | |

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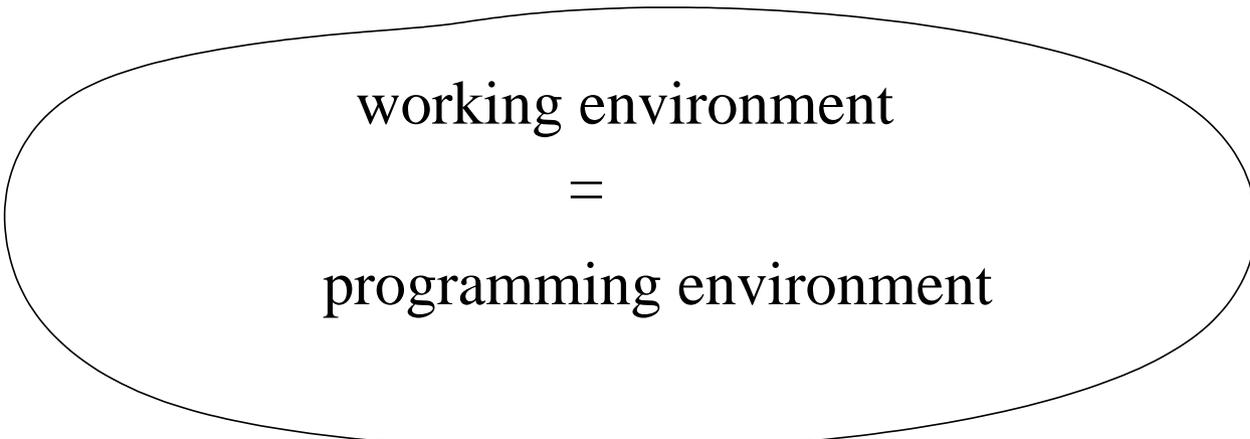
It's too difficult to program *a little*.

Approaches

- enable Programming In The User Interface
(*programmability*)

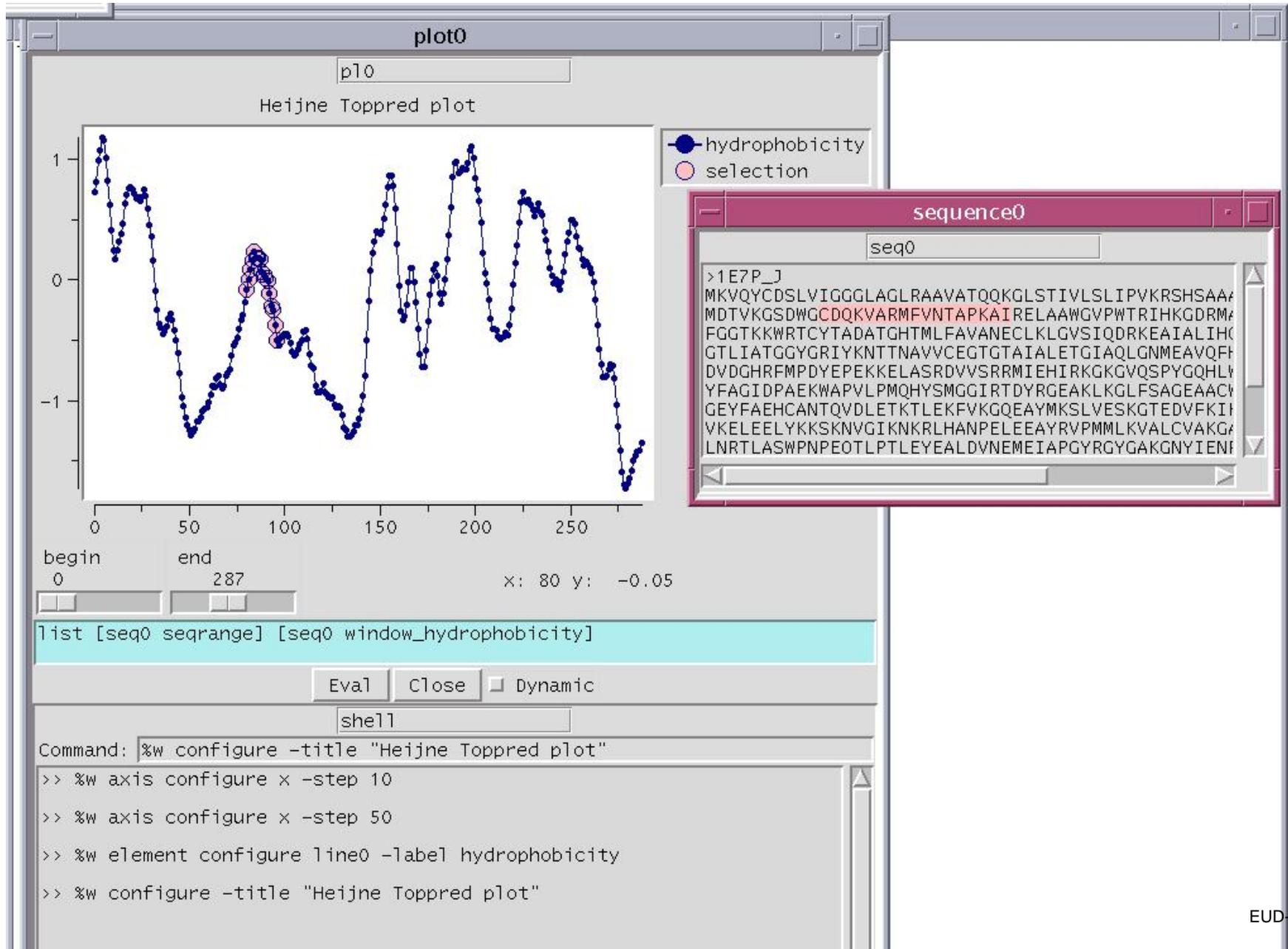
Programming In The User Interface

What we want:



working environment
=
programming environment

biok: graphical objects



biok: tags

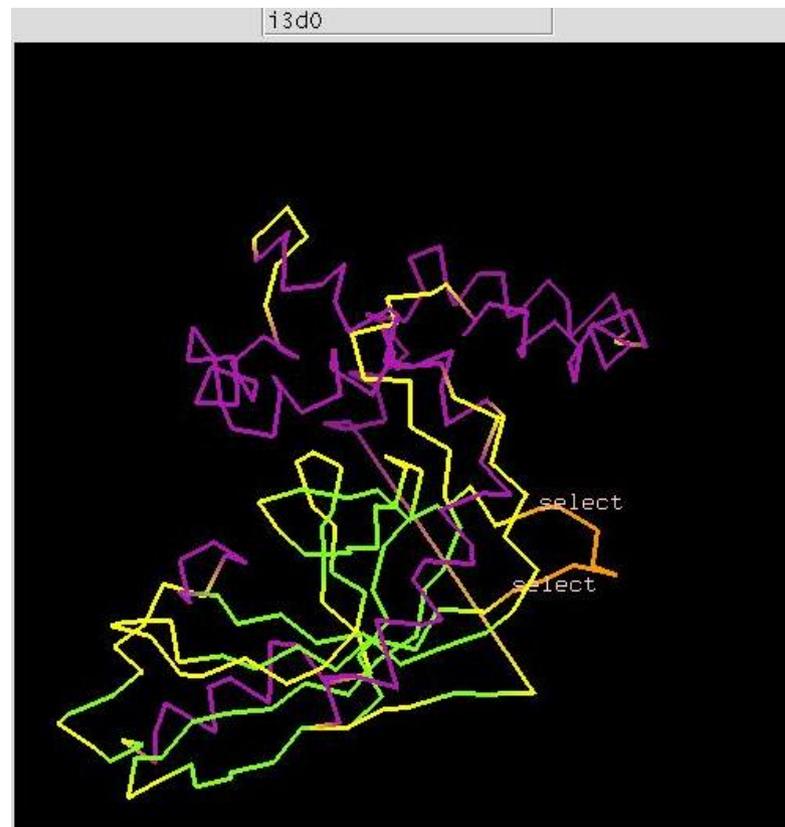
spreadsheetalig0

spread0

S

| | 8 | 9 | 10 | 11 | 12 | 13 |
|--|----------|--------|-------|--------|---------------|----------------------|
| 9012345678901234567890123456789012345678901234567890123456 | | | | | | |
| 1QS2 | SIITYKNV | EPTTIG | FNKSL | TEGNTI | NSDAMAQFKEQFL | DRDIKFDSYLDTHLTAQQVS |

Zoom In Zoom Out



biok: programming tags

The screenshot shows the TagEditor window for the `::PIDTag` class. The window title is "TagEditor". The "Class:" field contains `::PIDTag` and the "Super Class:" field contains `::ColTag`. There is a checkbox for "Parameter(s)?" which is currently unchecked. The "value" field is empty. The main text area contains the following Tcl code:

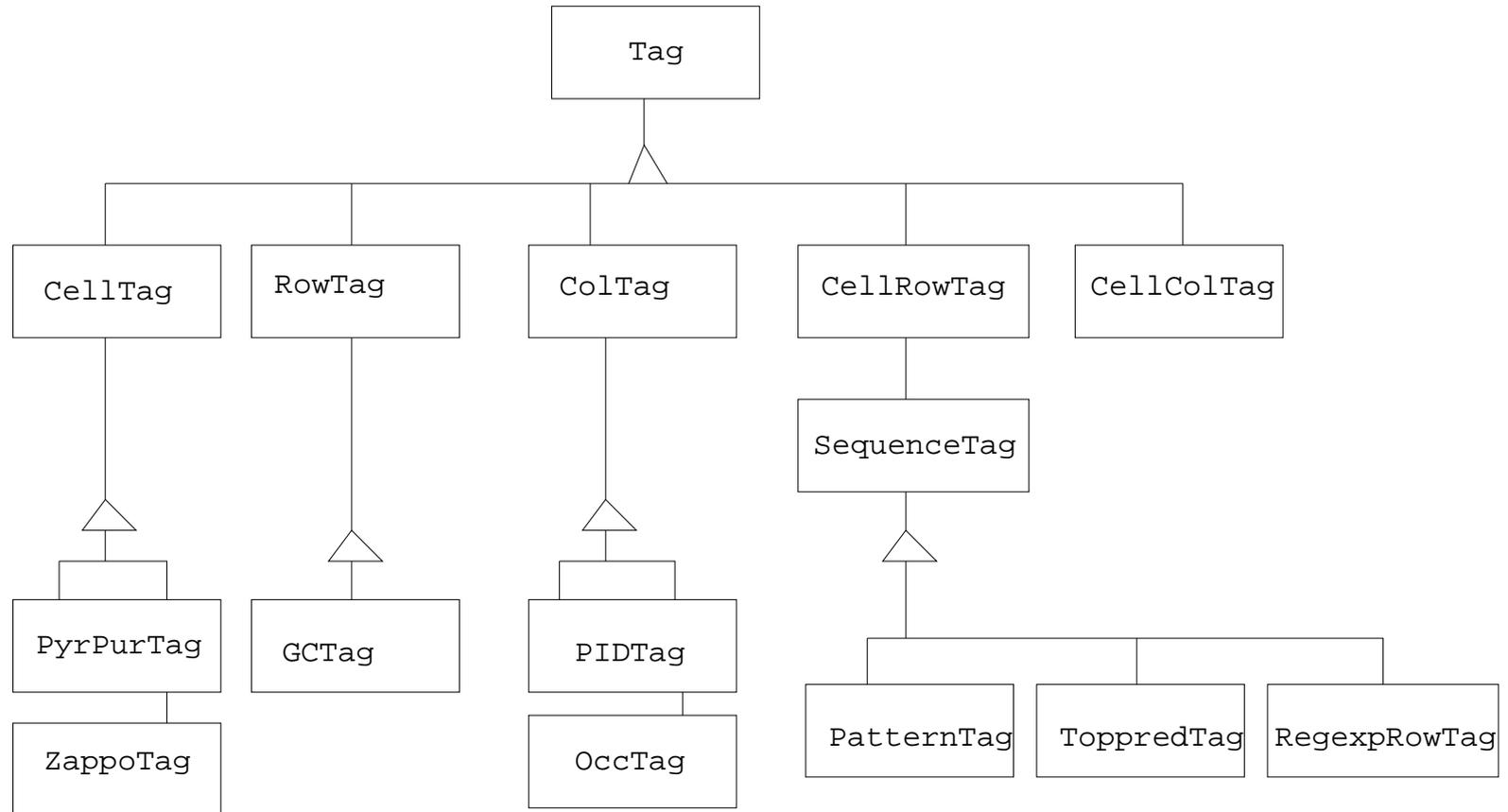
```
::PIDTag instproc value { col } {  
  [self] instvar objectalias  
  set pid [$objectalias colpid $col]  
  set result 0  
  foreach threshold [lsort -real [[self] getdefvalues]] {  
    if {$threshold >= $pid} {  
      set result $threshold  
      break  
    }  
  }  
  return $result  
}
```

Below the code area are buttons for "Define", "Save", "Print", "Search:", "Breakpoint", "Trace", and "Close". The "Try with param(s):" field is empty. The "Attributes:" section contains a table with 6 rows:

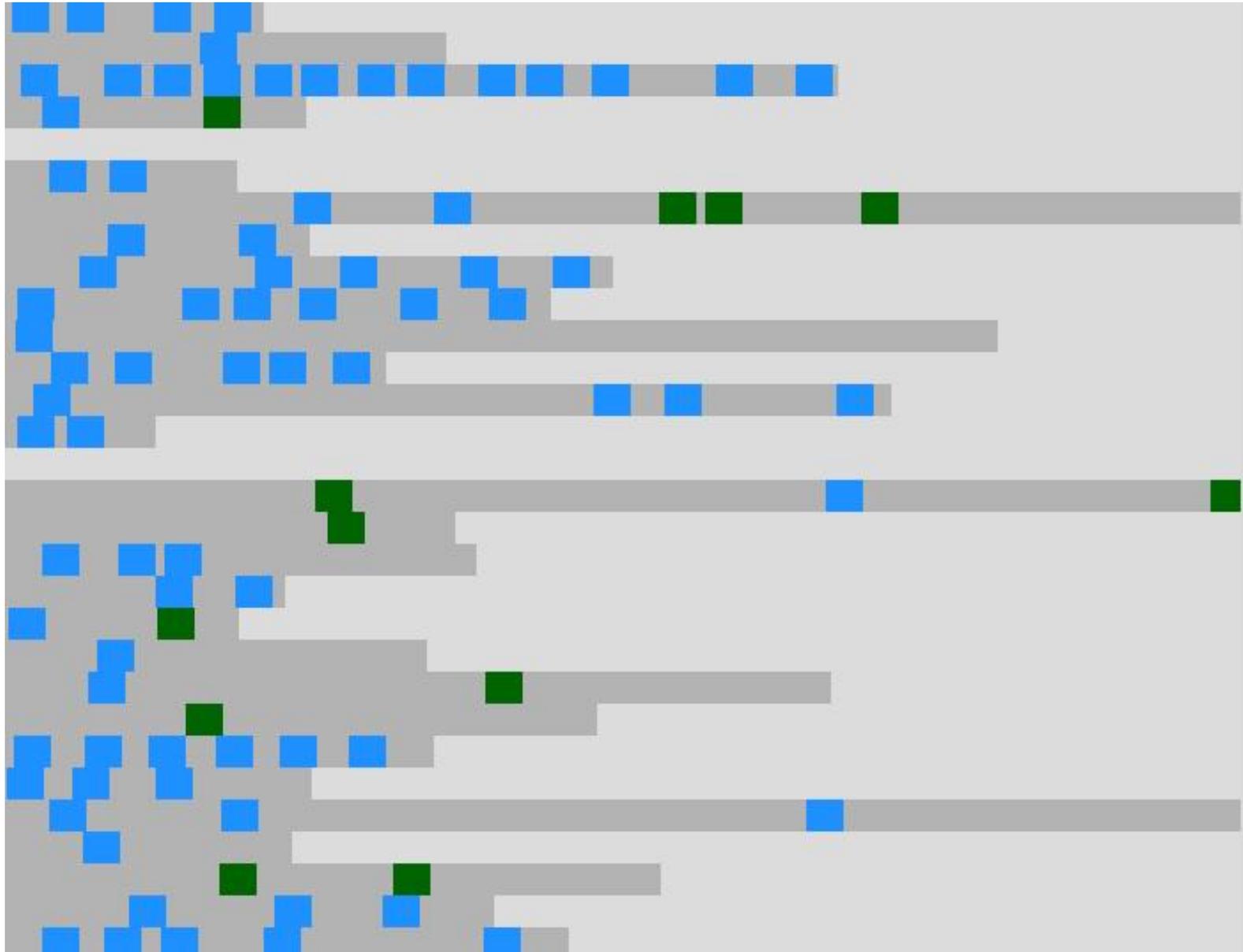
| Value | Attributes: | background: |
|-------|-------------|---------------|
| 0.1 | Attributes: | LightSkyBlue1 |
| 0.2 | Attributes: | LightSkyBlue3 |
| 0.3 | Attributes: | LightBlue1 |
| 0.4 | Attributes: | LightBlue3 |
| 0.5 | Attributes: | CadetBlue2 |
| 0.6 | Attributes: | CadetBlue4 |

Below the attributes table is a "Description:" field containing the text: "The PIDTag class displays percent identities in alignment sites." At the bottom of the window are buttons for "Done", "Show", "Define (session)", "Save (forever)", "Close", and "Remove".

biok: tags classes



biok: sub-classing tags



biok: sub-classing tags



biok: programming

The screenshot displays a software interface with two main windows. The top window, titled 'spreadsheetalig0', shows a sequence alignment of two proteins: BACTERIORH and CRUXRHODOP. The alignment is presented in a grid format with columns numbered 0 to 5. The sequences are: BACTERIORH MLELLPTAVEGVSSQAQITGRPEWIWLALGTALMGLGTLVFLVKGMGVSDPDAKKFYAI and CRUXRHODOP M--L-QS---GMSTYVP-G-GESIFLWVGTAGMFLGMLYFIARGWSVSDQRRQKFYIA. The alignment is color-coded: yellow for gaps, green for matches, and blue for mismatches. Below the alignment are 'Zoom In' and 'Zoom Out' buttons.

The bottom window, titled 'aligLength (::AligData)', is a script editor containing a Tcl procedure:

```
::AligData instproc aligLength { args } {  
  [self] instvar seqs  
  set max 0  
  if [info exists seqs] {  
    for {set i 0} {$i < [llength $seqs]} {incr i} {  
      set l [string length [lindex $seqs $i]]  
      debug bkp "i: $i l: $l"  
      if {$l > $max} {  
        set max $l  
      }  
    }  
  }  
  return $max  
}
```

 A 'debug' window is open over the script, showing the current state: 'i: 0 l: 58' and a yellow button that says 'Click here to continue'. At the bottom of the script editor are buttons for 'Define', 'Save', 'Print', 'Search:', 'Breakpoint', 'Trace', and 'Close'. Below these buttons is a field labeled 'Try with param(s):'.

biok programming: tracing

The screenshot displays a software interface with three main components:

- Methods stack:** A window titled "Methods stack" showing a list of method calls for object `t0`. The list includes:
 - [1] `::Field ::field1::field1 init`
 - [2] `::FieldData ::fielddata1 init`
 - [3] `==>`
 - [4] `::Field ::field1::field1 draw`
 - [5] `::FieldData ::fielddata1 update`
 - [6] `::Field ::field1::field1 redisplay`
 - [7] `==>`
 - [8] `==>`
 - [9] `==>`
 - [10] `==>`
 - [11] `::FieldData ::fielddata1 update`
 - [12] `::Field ::field1::field1 redisplay`
 - [13] `==>`
 - [14] `==>`
 - [15] `::FieldData ::fielddata0 update`
 - [16] `::Field ::field0::field0 redisplay`
 - [17] `==>`
 - [18] `==>`
- field1:** A window titled "field1" containing two input fields with values `c1` and `34`.
- field0:** A window titled "field0" containing an input field with value `c0`, a text area with `238` and `$c1 * 7`, and buttons for `Eval`, `Close`, and `Dynamic`.
- Spy:** A window titled "Spy" with two columns: "Called procs" and "Traced procs".
 - Called procs:** `::FieldData value`, `::GraphObject fillsc`, `::GraphObject hidede`, `::GraphObject histor`, `::GraphObject into`, `::GraphObject name`, `::GraphObject title`, `::History add`, `::History init`, `::History searchlabe`.
 - Traced procs:** `::Field draw`, `::Field init`, `::Field redisplay`, `::FieldData init`, `::FieldData update`.Buttons at the bottom include `Trace`, `UnTrace`, `Start`, `Refresh`, `Stop`, and `Close`. Item counts are shown as `item count: 26` and `item count: 5`.

Programming In The User Interface

working environment
=
programming environment

- learning by examples
- incremental programming
- easier switch between 2 modes (using/programming); programming as just a kind of advanced use (with several levels) (but programming should not be required for a standard use)

Approaches

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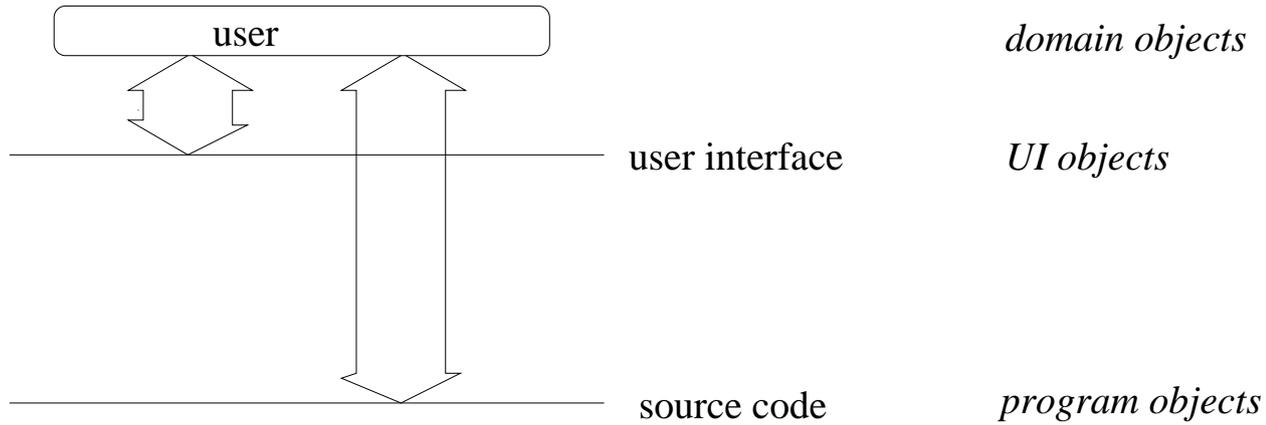
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 - MOP

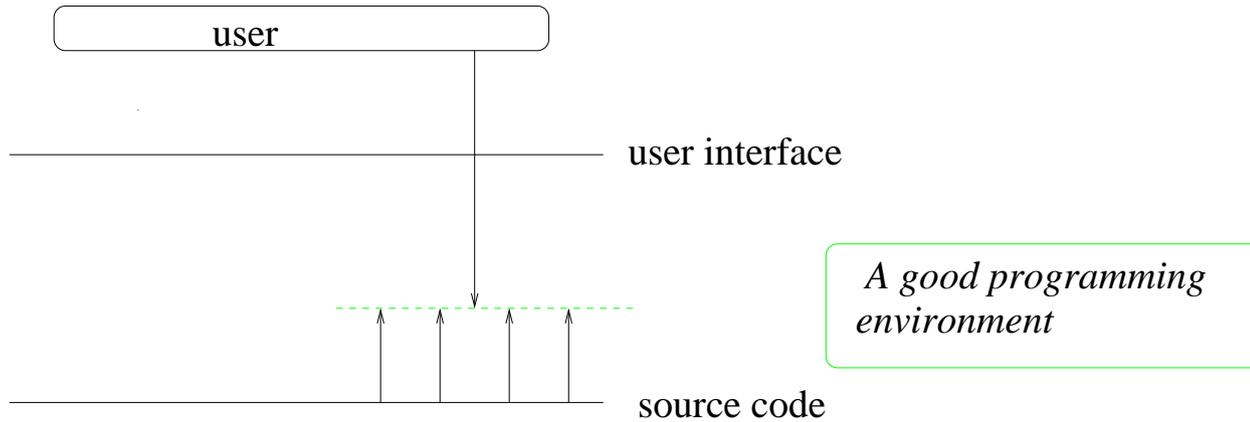
Modifiable systems

Cognitive distance issue:



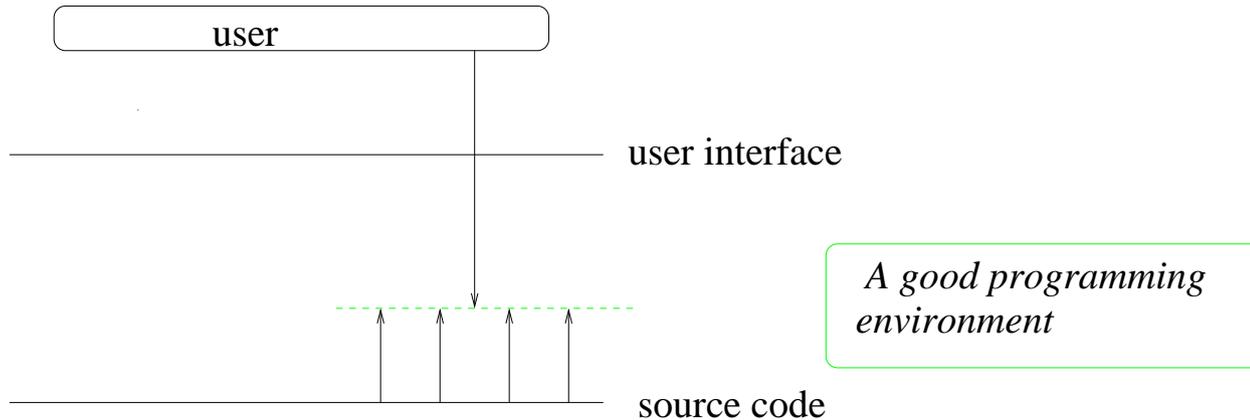
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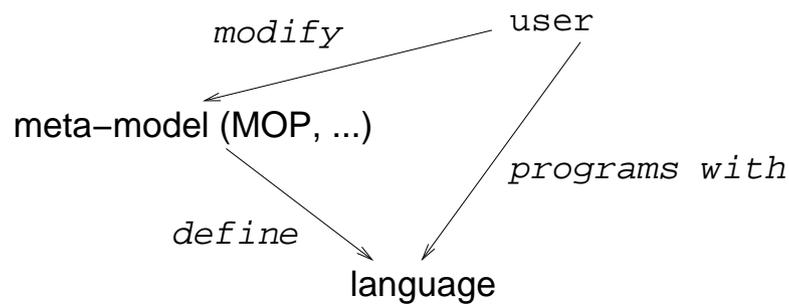


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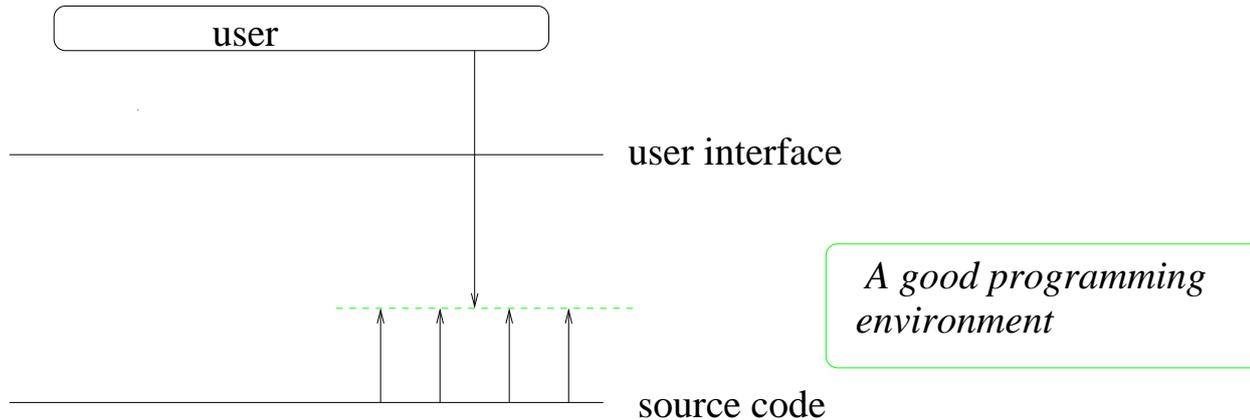


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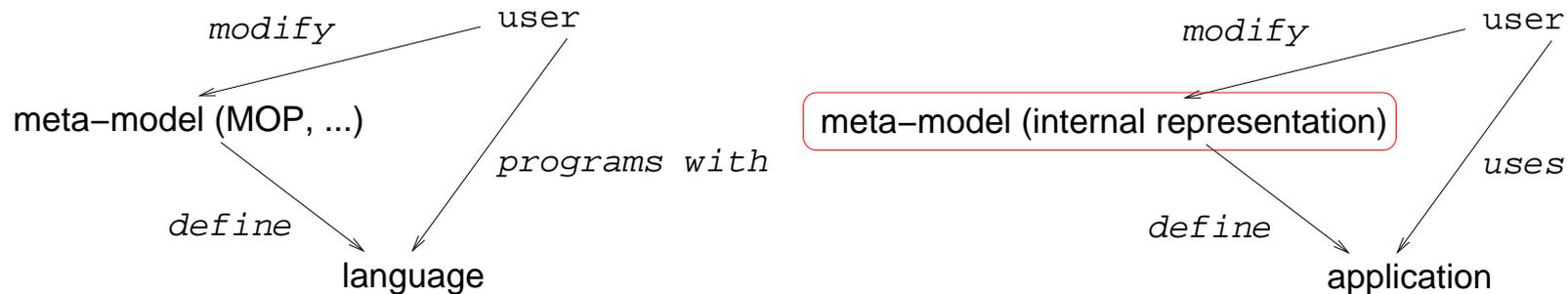


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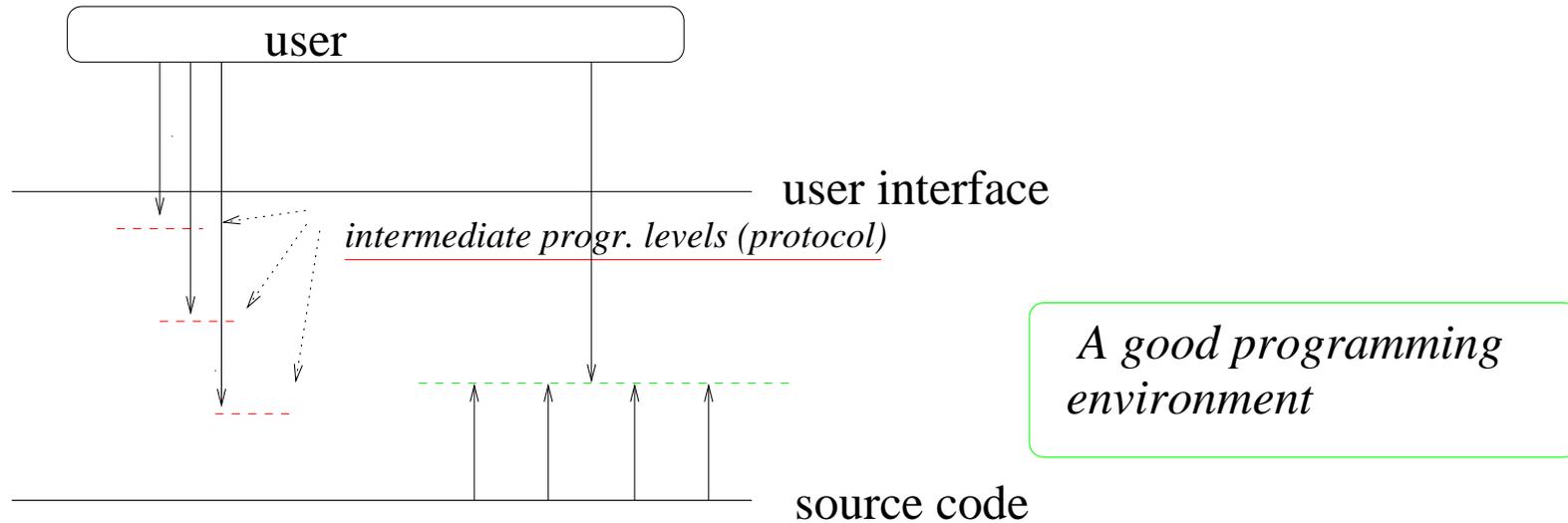


From MOP ... to MAP (Meta-Application Protocol):

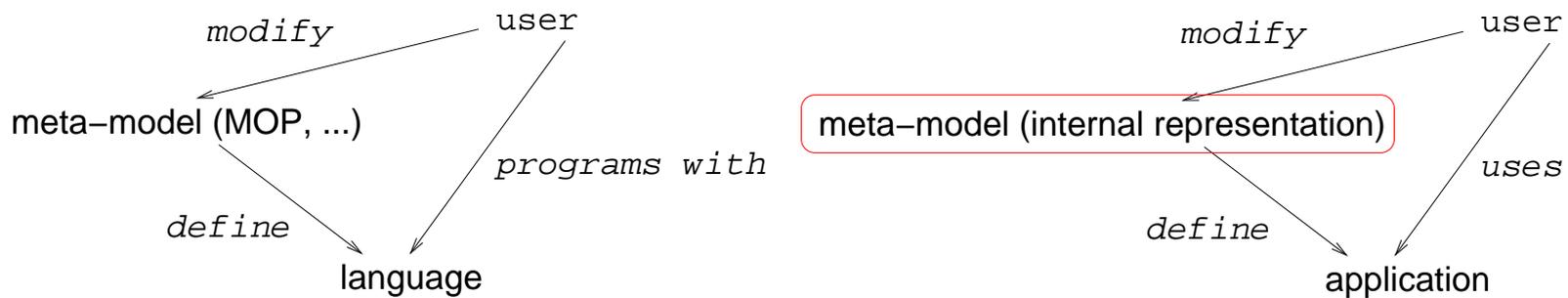


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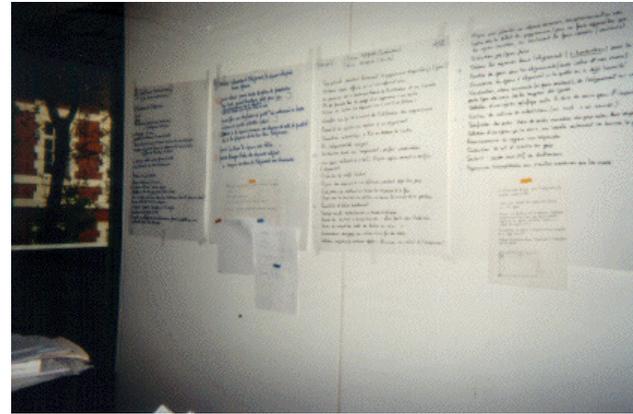
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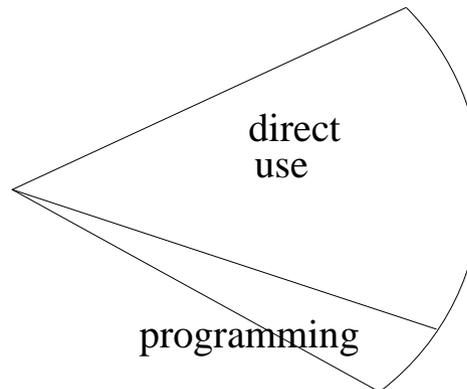
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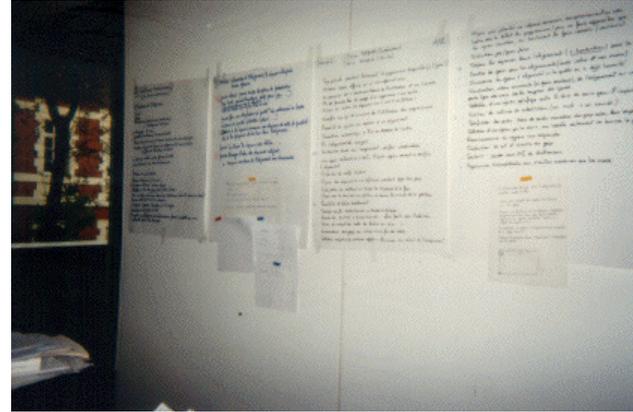
Participatory Design



- anticipate flexibility spots (EU-not-P versus EUP)



Participatory Design



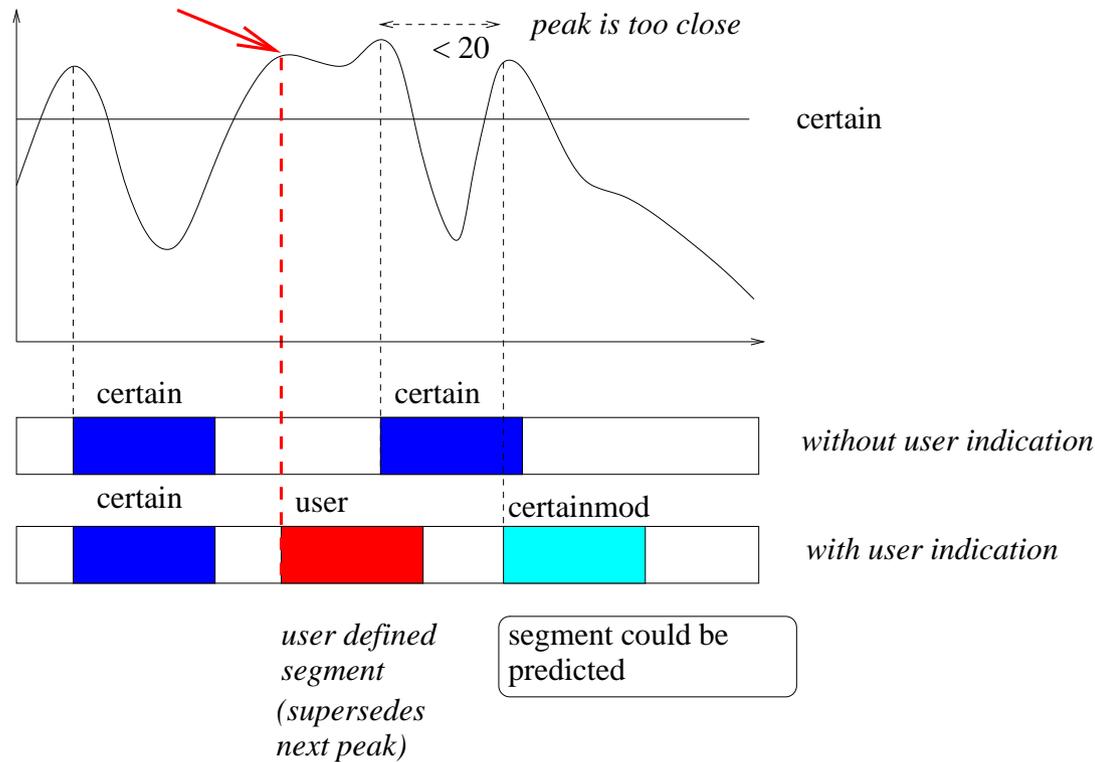
- rather *few* programming issues raised in design workshops

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 - participatory design,
- flexibility is provided in informal tools (spreadsheets, ...),
- flexibility is also more control on computation,
(*algorithmic flexibility*)

Algorithmic flexibility

A way to integrate user's knowledge in computation neither as parameter nor as programming (using interception techniques (AOP?)).



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