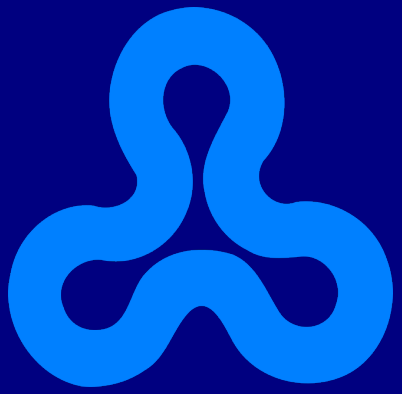
Language Oriented Programming with Cedalion



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Agenda

- **Overview:**
  - Language Oriented Programming (LOP)
  - LOP Languages
  - Cedalion, as an LOP Language
- **Case Study:**
  - DNA Microarray Design

Language Oriented Programming (LOP): Rethinking Software Development

- **Traditional Thinking**
  - Designing our ***software*** for a *programming language*.
- **New Thinking**
  - Design *programming languages* for our ***software***.
- **The Role of DSLs in LOP**
  - Implement them if you need to.
  - Keep them focused and interoperable.

LOP: Middle Out

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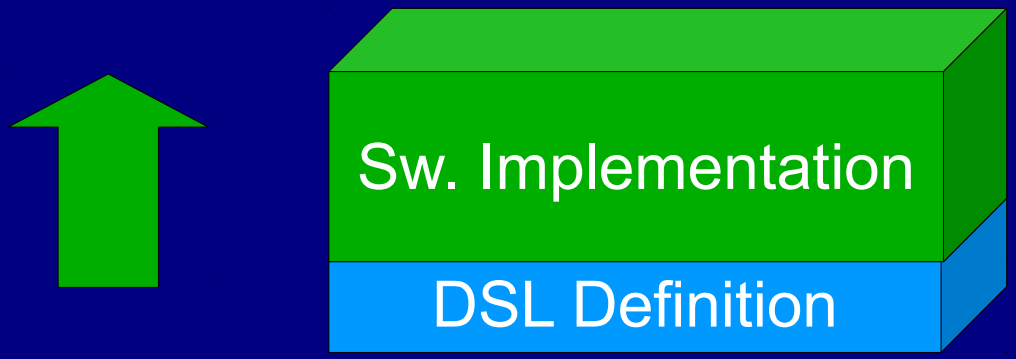
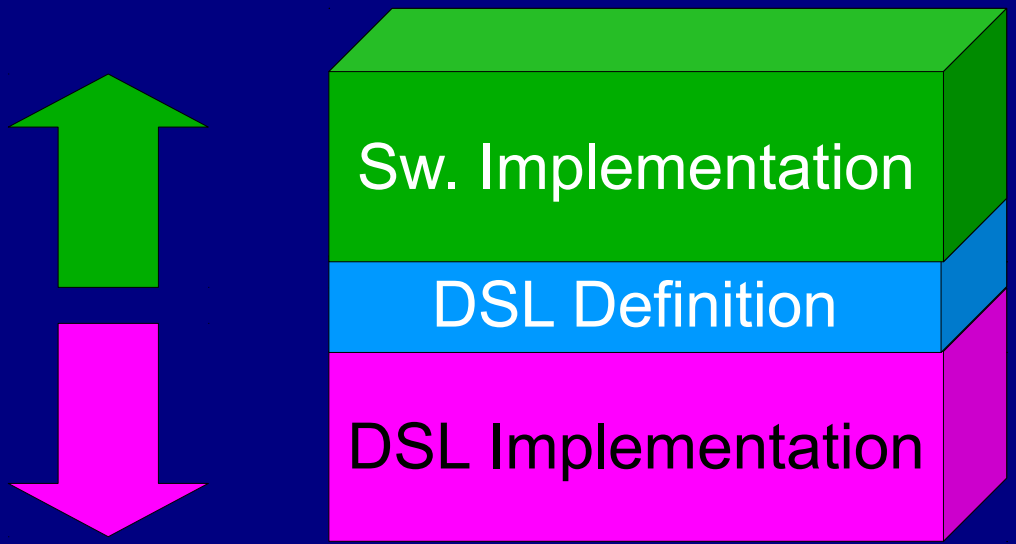


LOP: Middle Out



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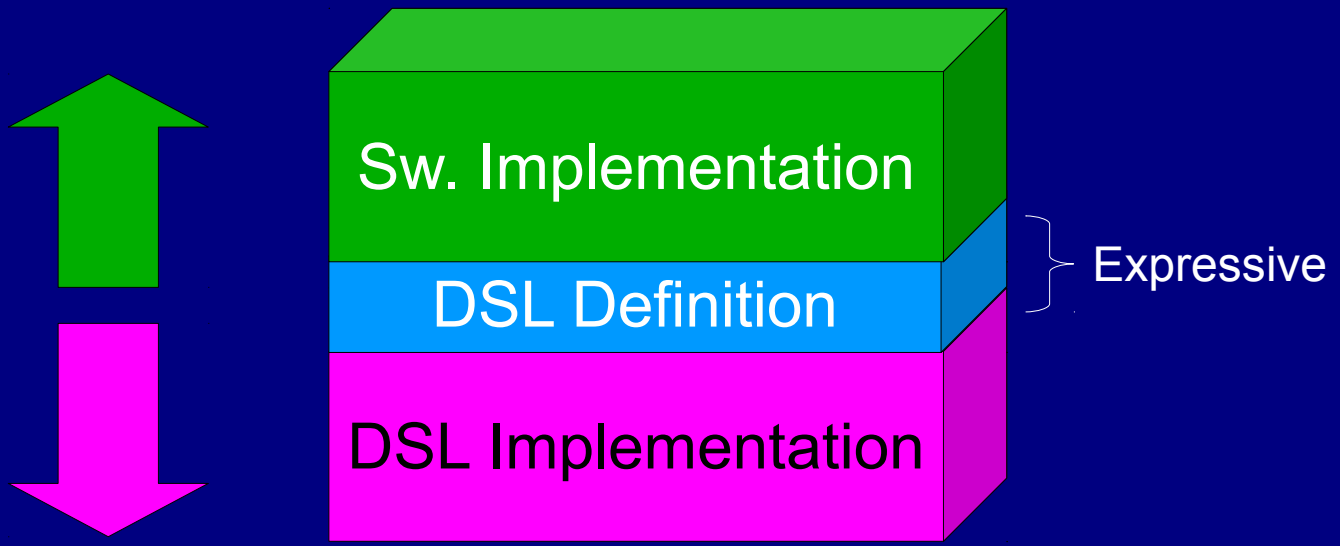

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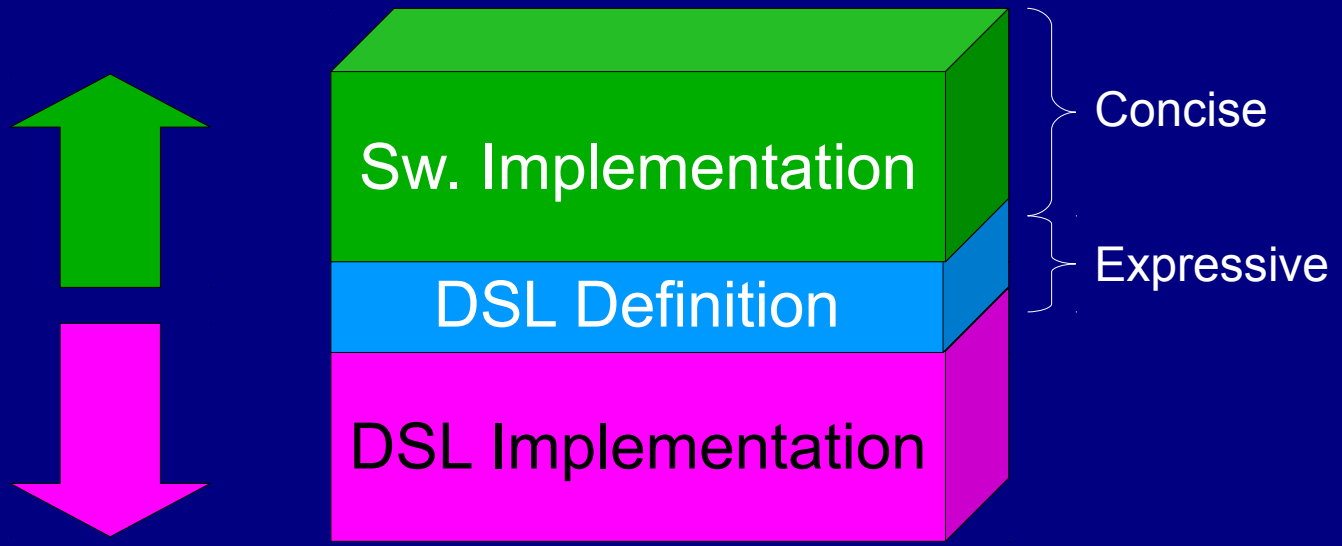

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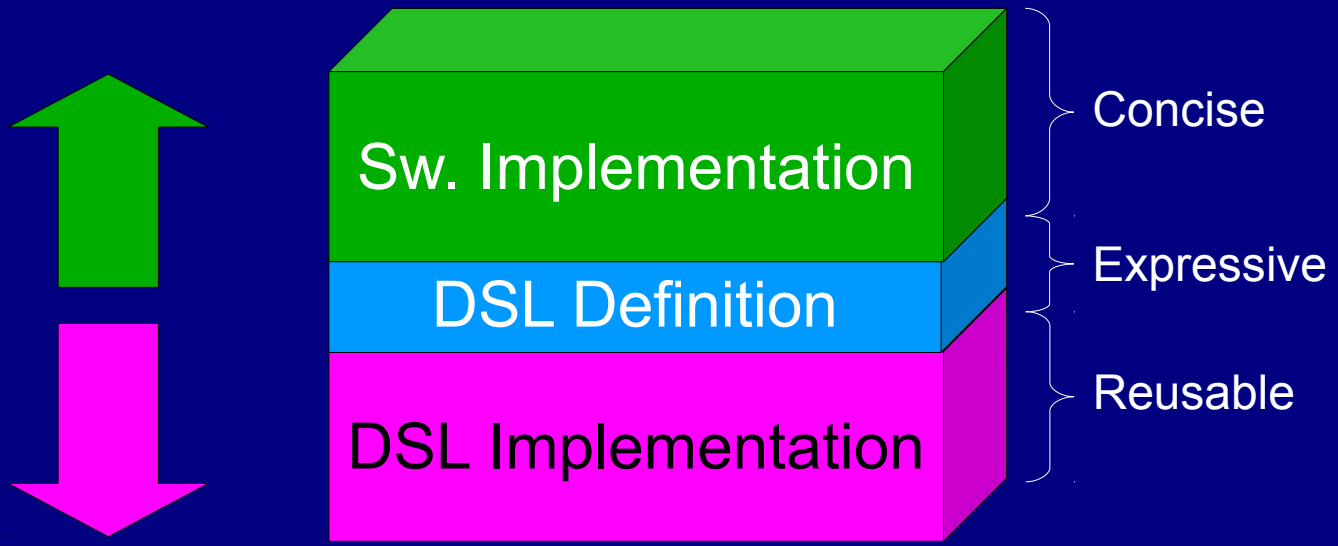

State of the Art

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Language Workbenches

- IDEs for developing DSLs.
- Use External DSLs.
- Use Projectional-Editing [Fowler05].
- DSLs: Easy to use; hard to implement.
- Examples: MPS, Intentional.

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- First used in Lisp in the 1960s.
- DSLs: Easy to implement; limited by the host language.

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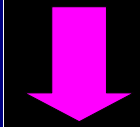

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LOP Languages: Rethinking LOP

- **LOP Languages**
  - Programming languages supporting LOP.
  - Just like OOP languages support OOP.
- **Definition**
  - An *LOP Language* is a programming language that can host *internal DSLs*, allows the definition and enforcement of *DSL schema*, and features extensible *projectional-editing*.

LOP Language Design Space

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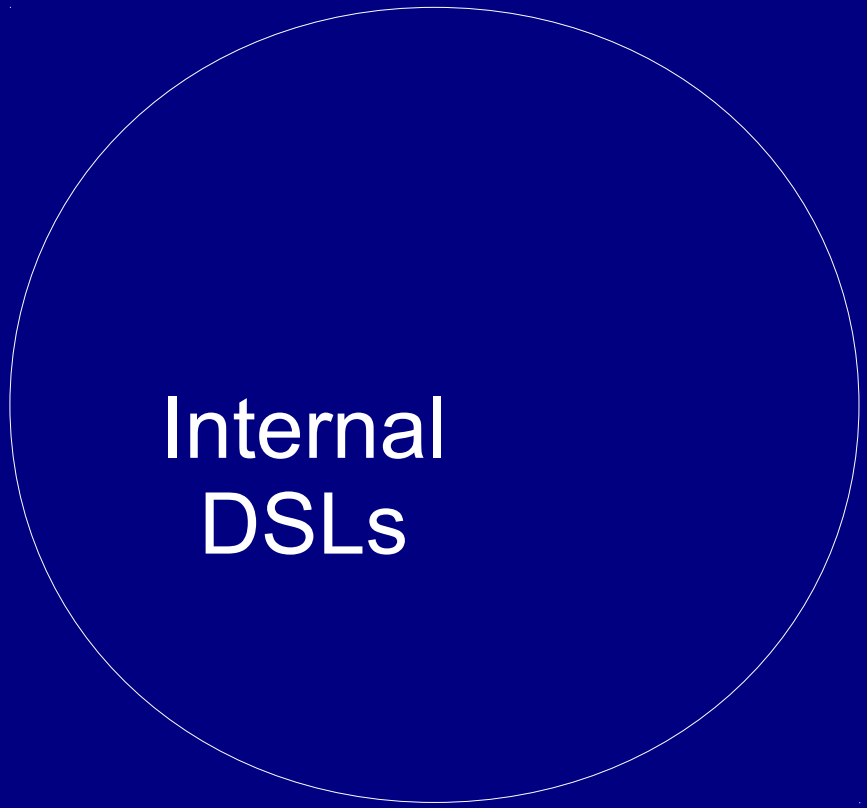

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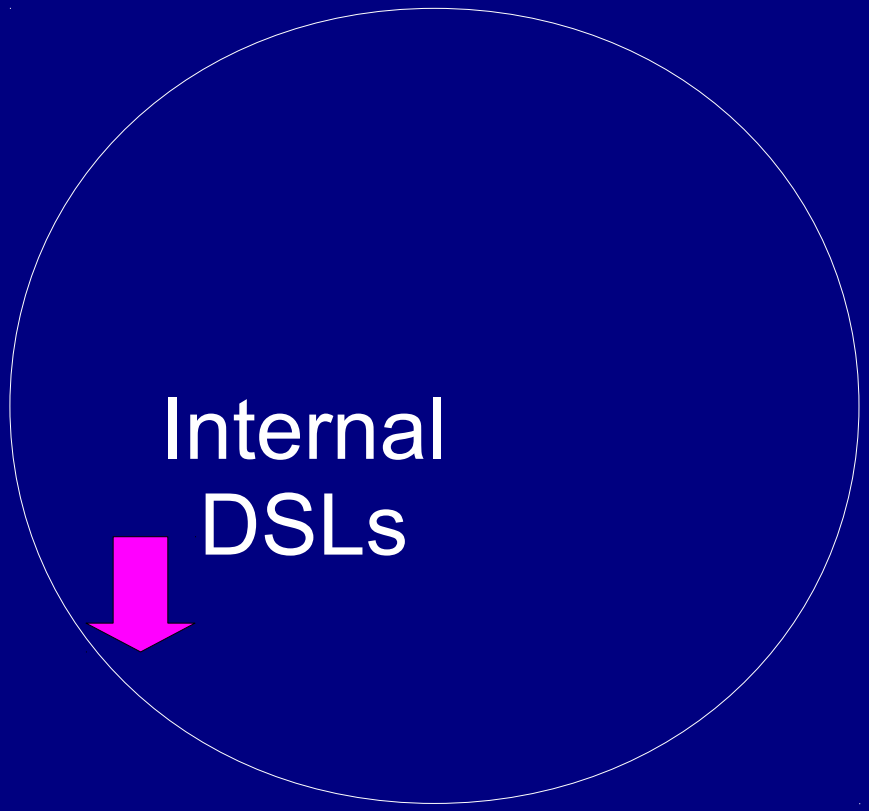

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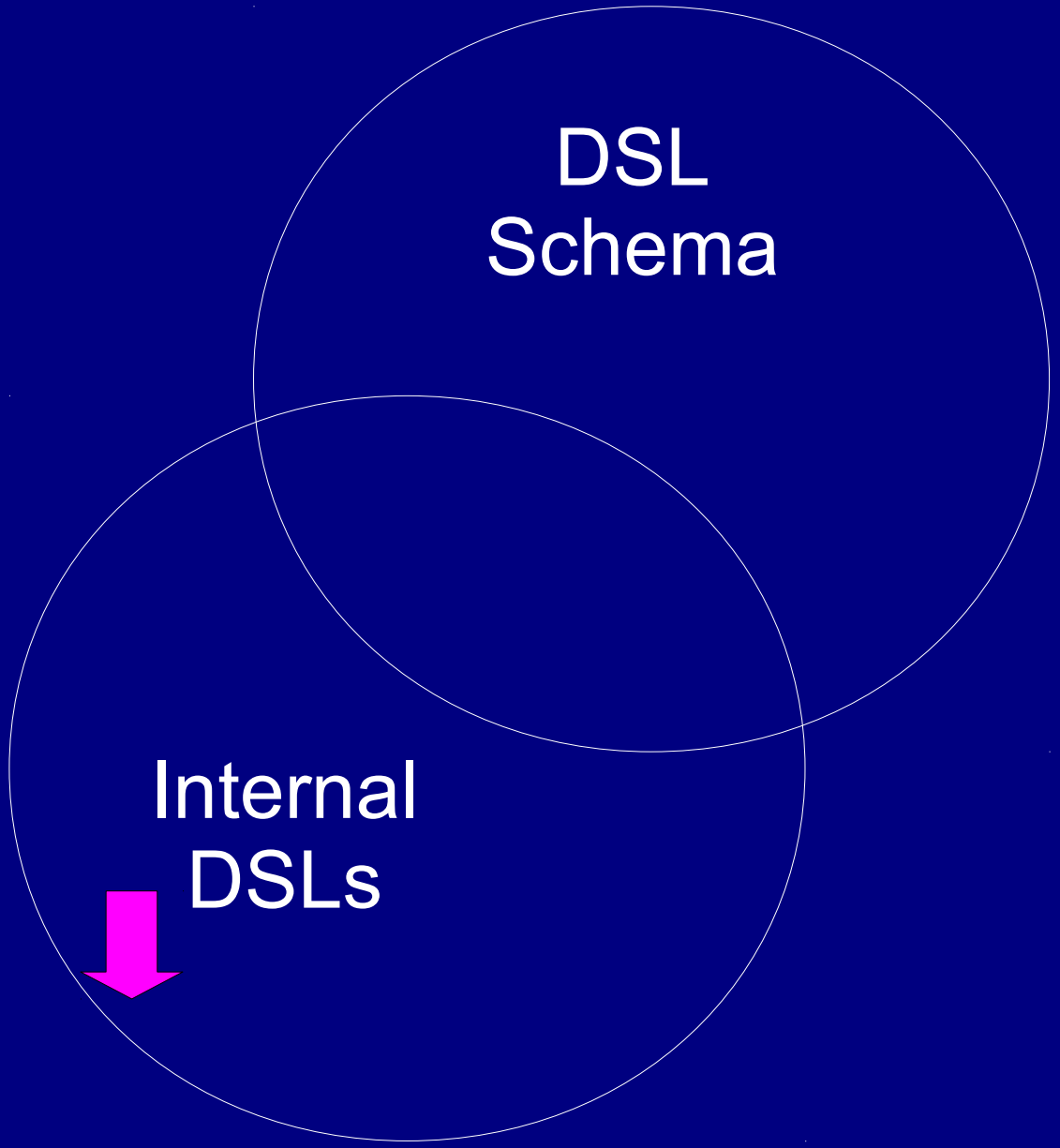

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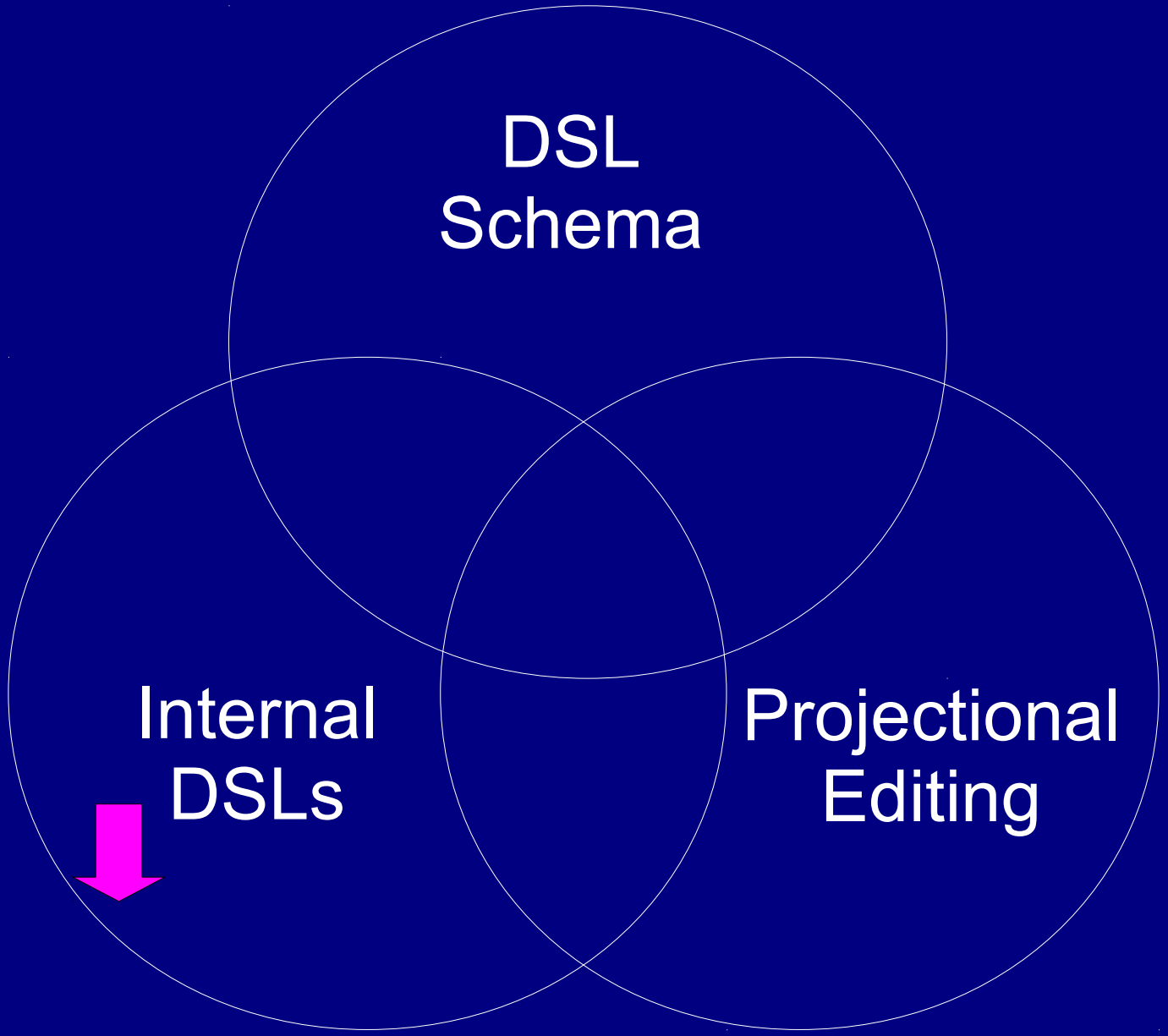

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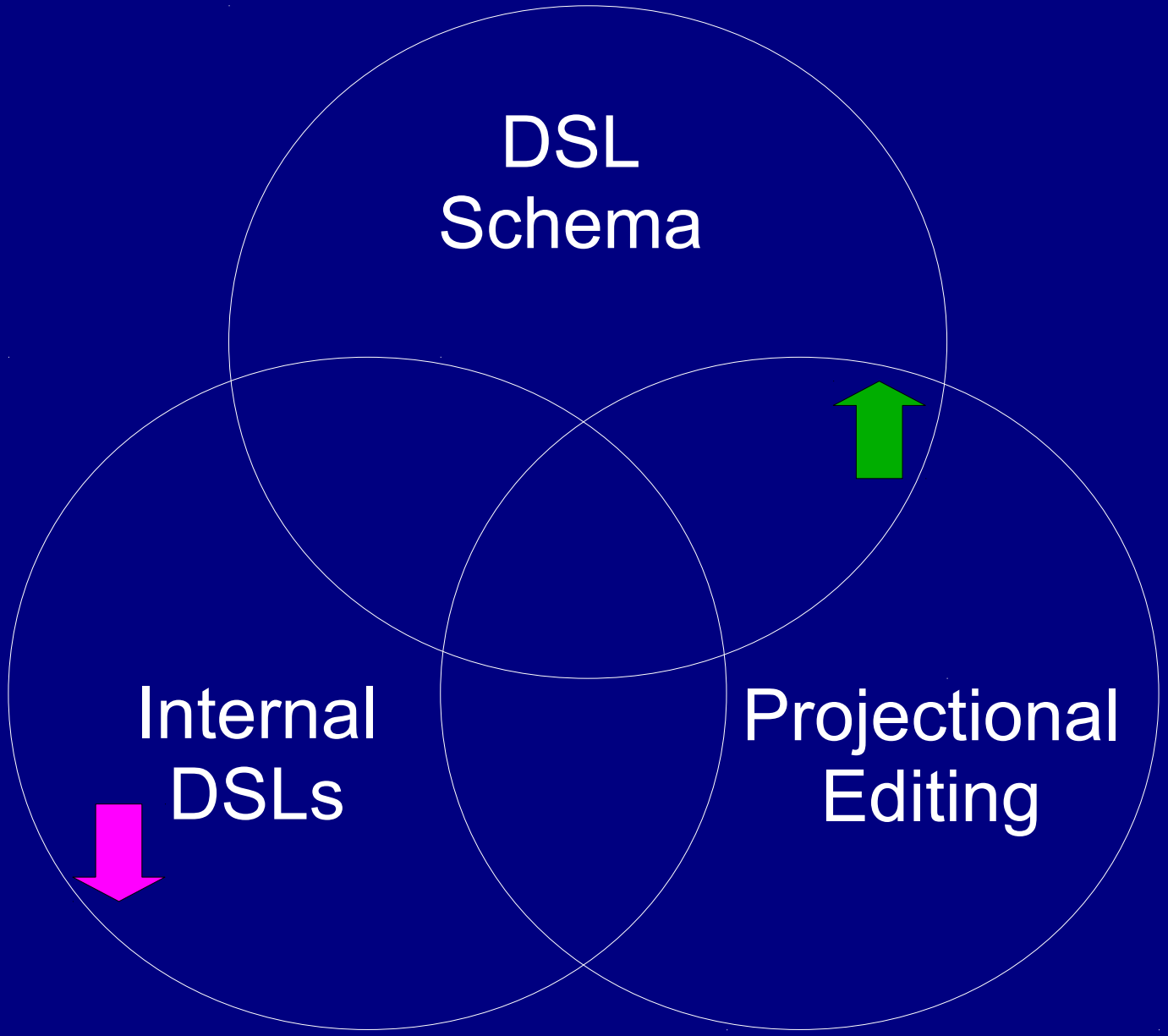

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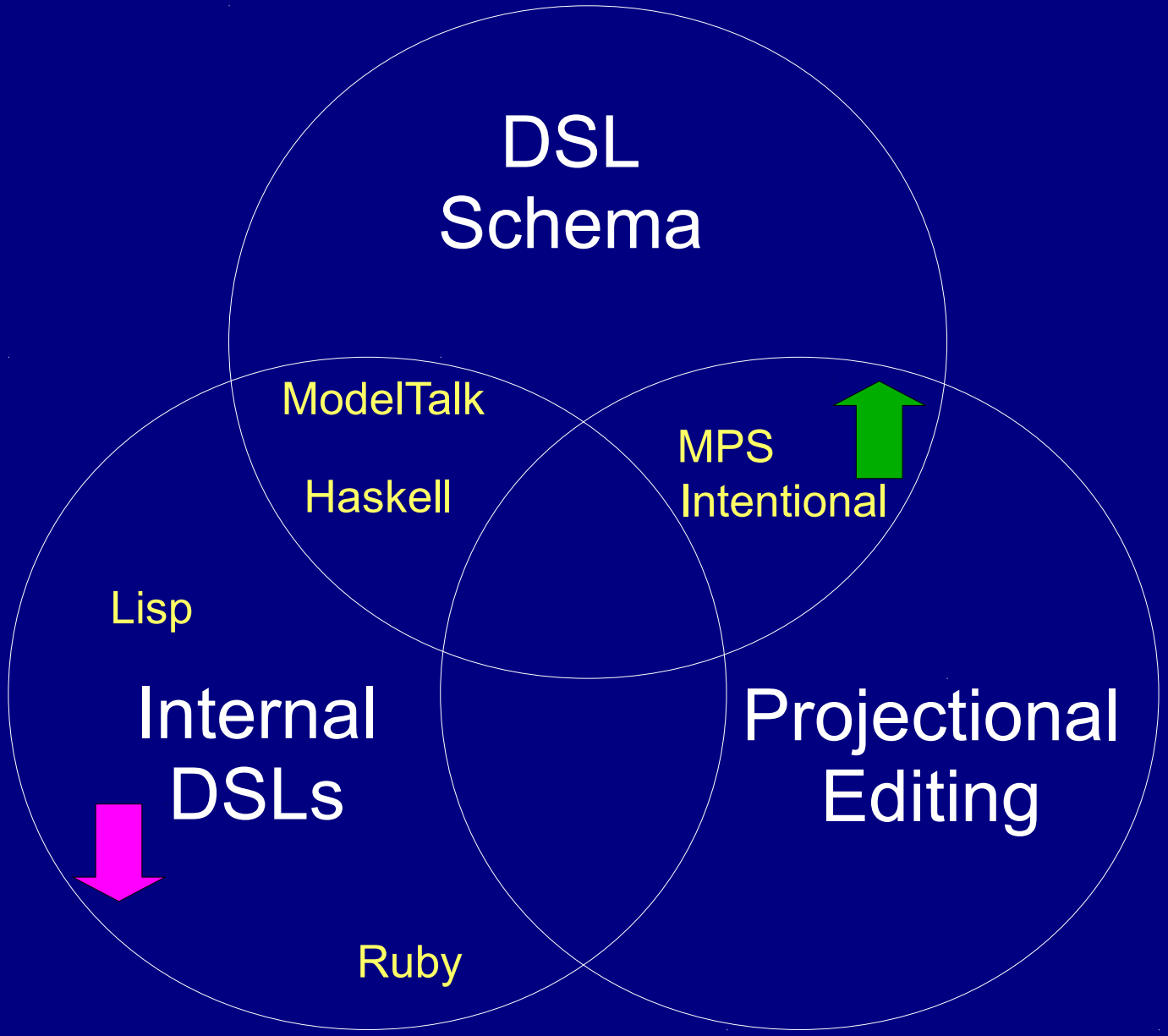

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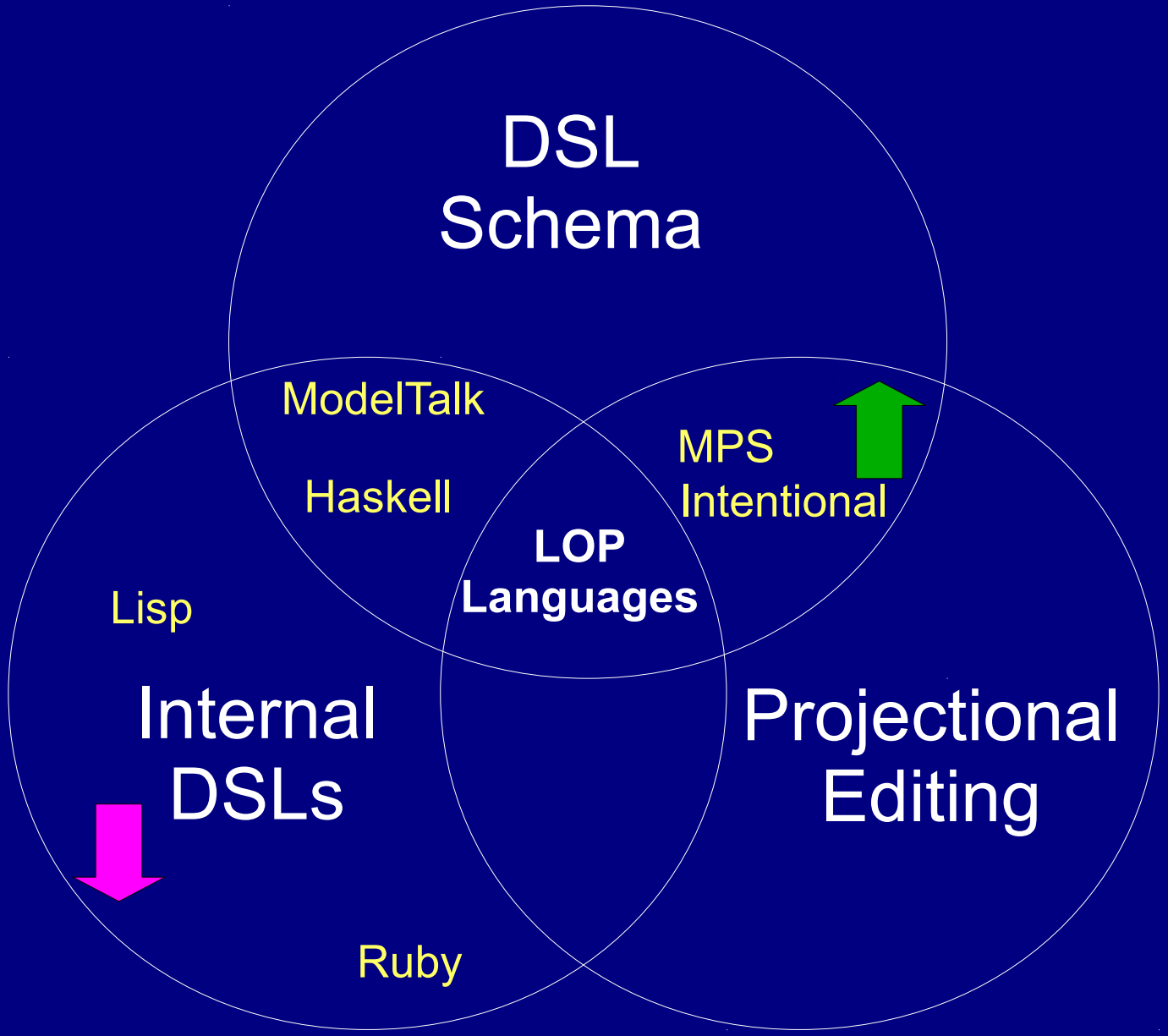
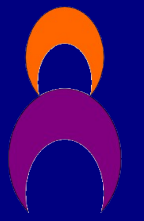


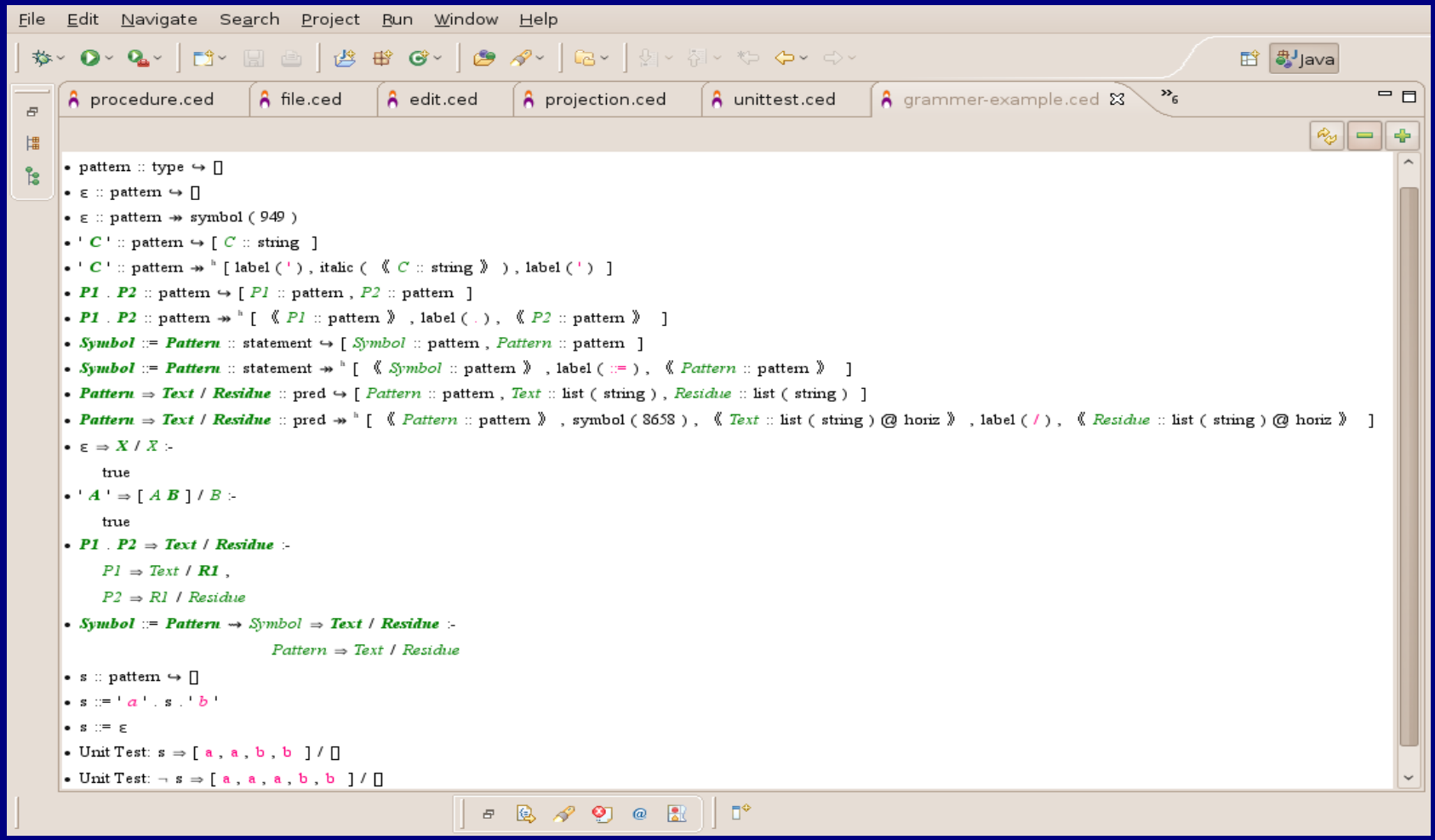
Cedalion: An LOP Language



- **Logic Programming Language**
  - Hosts internal DSLs
- **Uses Projectional Editing**
  - As a way to provide syntactic freedom
- **Statically Typed (Type Inference)**
  - As a way to define schema
- **Open-source:**
  - http://cedalion.sf.net

Cedalion standing on the shoulders of Orion;
Nicolas Poussin, 1658

Cedalion in Action



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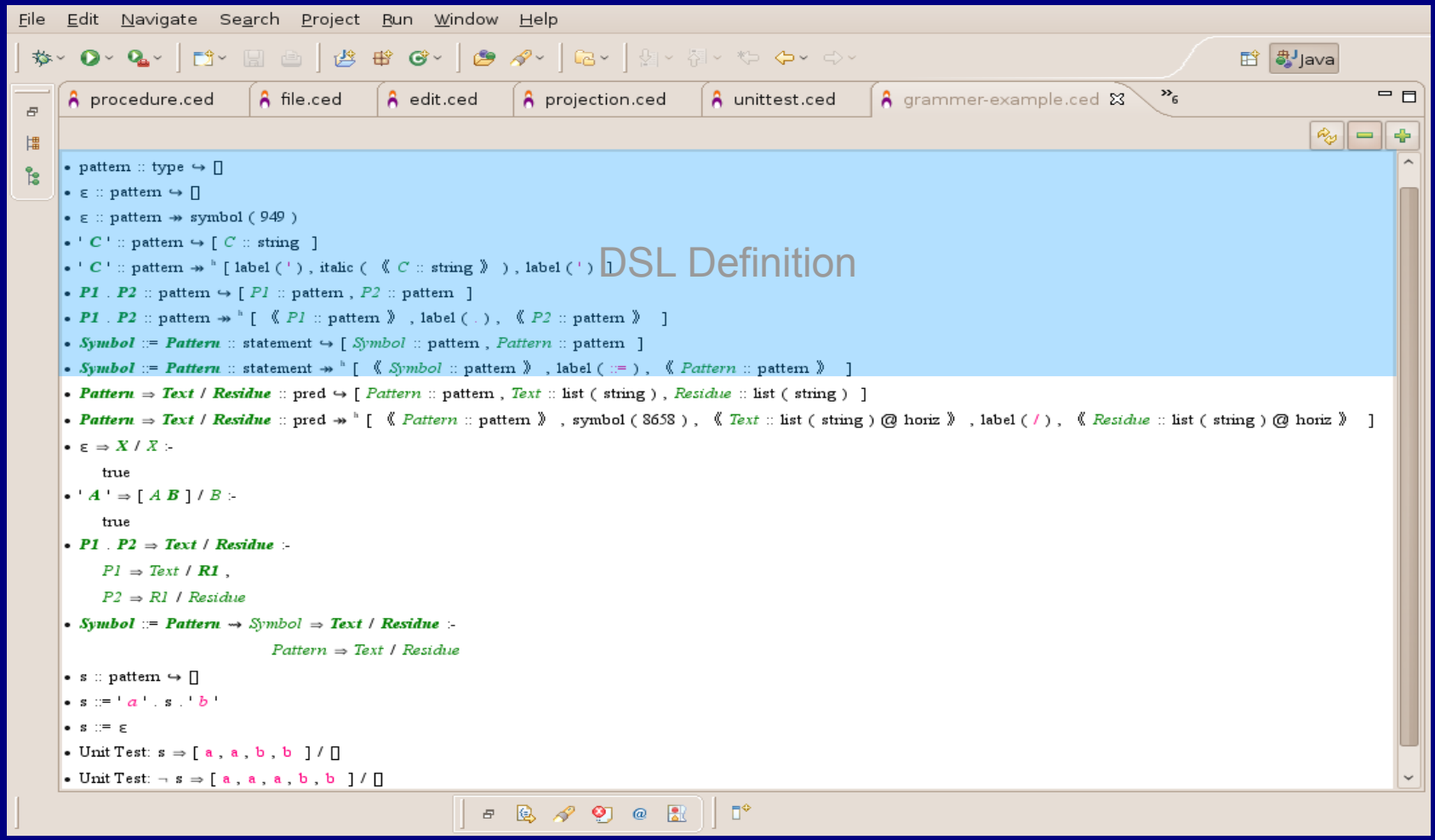

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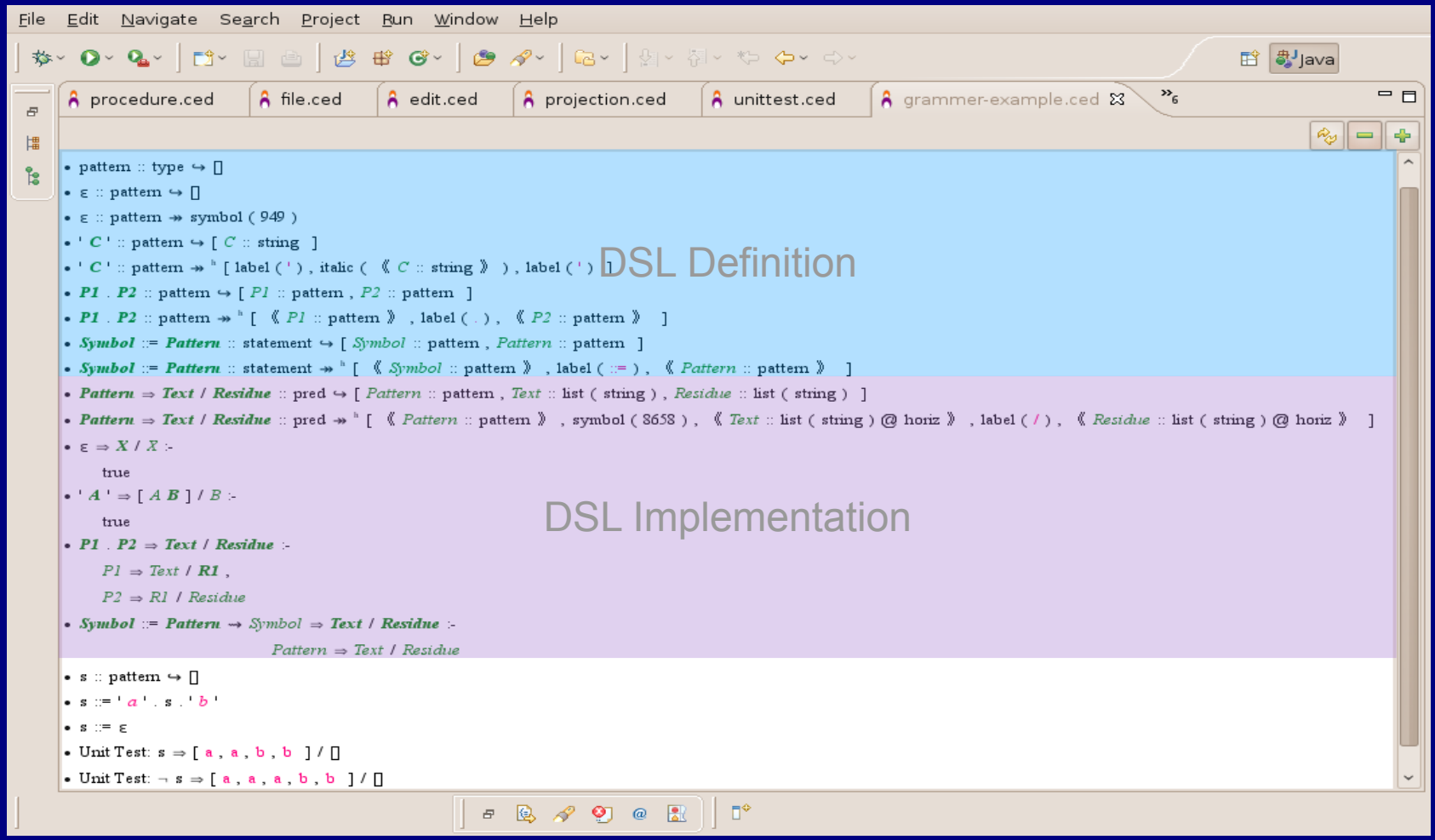

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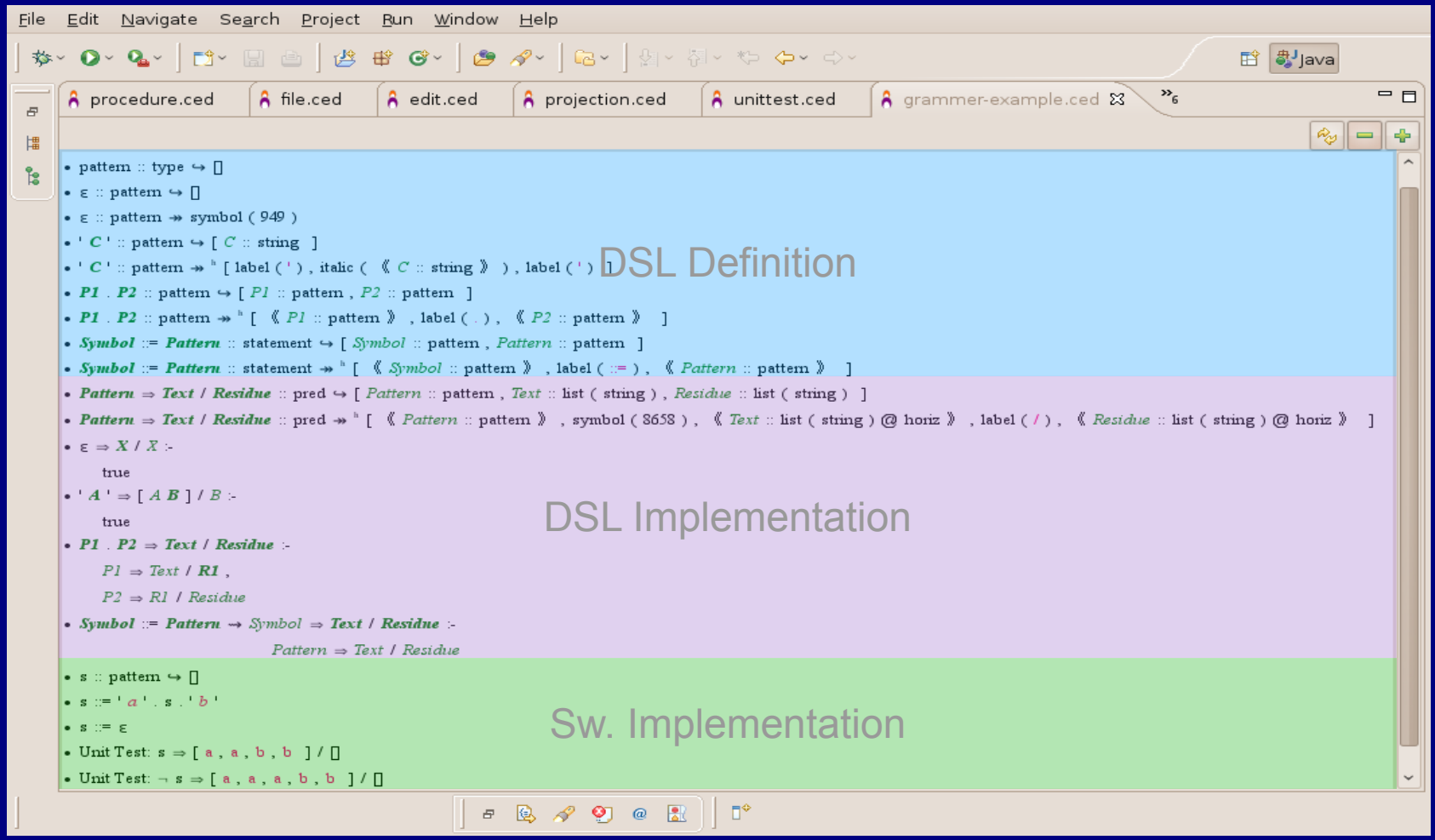


Cedalion Case Studies

- BNF Grammar for Parsing + Evaluation.
- Functional Programming.
- Process Calculus (CCS) + Modal Logic (HML).
- DNA Sequence Sets

::= λ

P<a>[b]

Related Work

- **Language Oriented Programming**
  - [Ward, 1994] Language-oriented programming. Software-Concepts and Tools, 15(4):147–161, 1994
  - [Fowler, 2005] Language workbenches: The killer-app for domain specific languages. 2005.
- **Language Workbenches**
  - [Dmitriev, 2004] Language oriented programming: The next programming paradigm. JetBrains onBoard, 1(2), 2004.
  - [Simonyi, Christerson, and Clifford, 2006] Intentional software. ACM SIGPLAN Notices, 41(10):451–464, 2006.
- **Internal DSLs**
  - [Hudak, 1996] Building domain-specific embedded languages. ACM Computing Surveys (CSUR), 28(4es), 1996.

Conclusion

- **Contributions**
  - LOP Languages
  - Cedalion
- **Future Work**
  - Theory
    - Further investigate the properties of LOP Languages.
    - Prove Cedalion type-system correctness.
  - Practice
    - Make Cedalion “ready for prime-time”.
    - Provide more validation by real life examples.

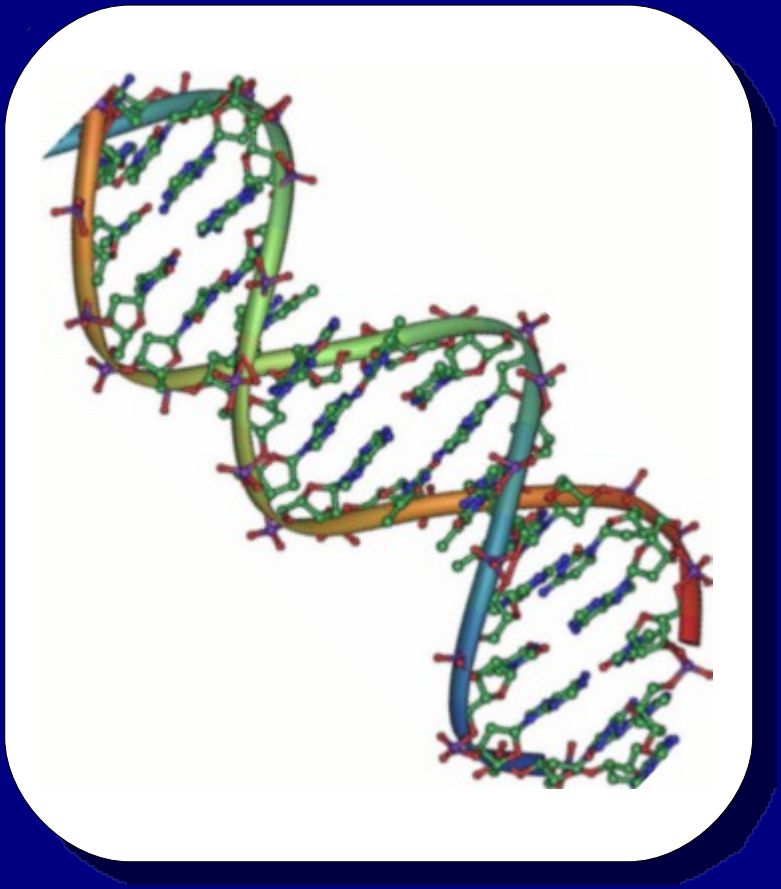
Case Study

DNA Sequence Sets
for
DNA Microarray Design

Joint work with Itai Beno,
Faculty of Biology,
Technion – Israel Institute of Technology

What is DNA?

- Deoxyribonucleic acid.
- A double-helix consisting of nucleotides.
- Four types, abbreviated A,T,C,G.
- Stores the “machine code” of life.
- ~3GBase (~750MB) is the size of the worlds most amazing “software”...



DNA and Cancer Research

- DNA anomalies play a significant role in the formation of Cancer.
- Studying these anomalies is critical in the search for effective treatment for Cancer.
- Certain proteins which participate in cancerous processes interact with DNA.
- These interactions are of extreme importance to this field.

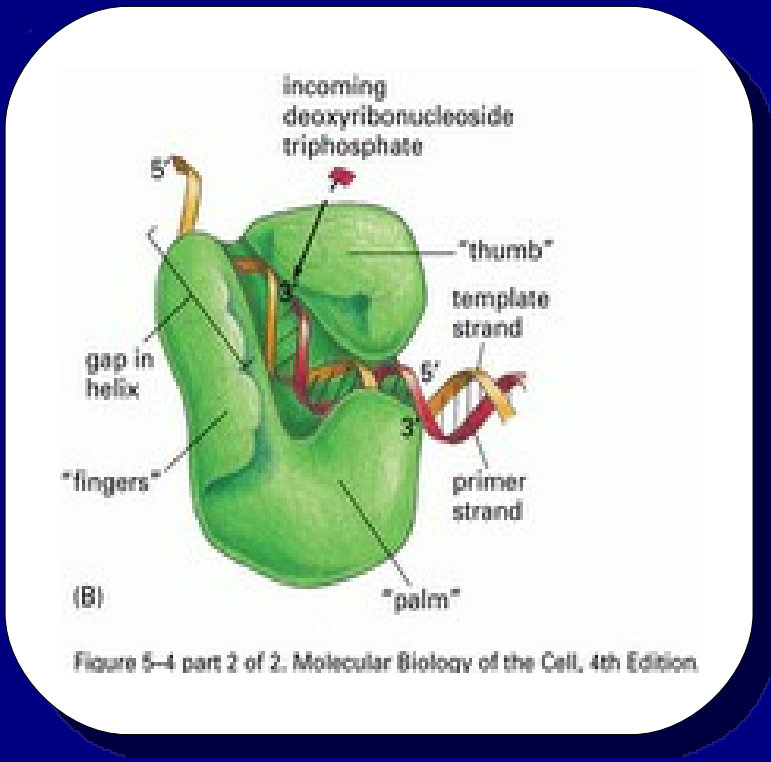
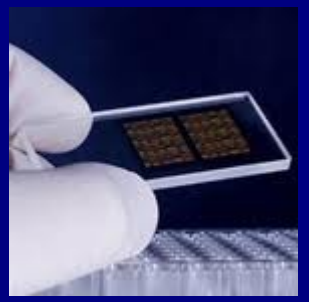
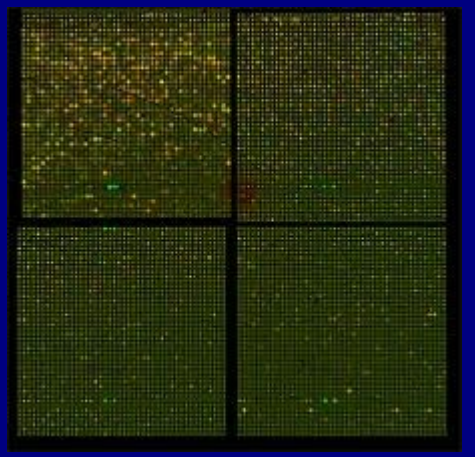


Figure 5–4 part 2 of 2. Molecular Biology of the Cell, 4th Edition.

DNA Microarray

- Finding a sequence with certain qualities requires multiple experiments.
- A DNA Microarray is a device containing $O(10^5)$ microscopic spots, each containing a different DNA sequence (multiple instances).
- Microarrays can be custom-made for specific experiments.
- Biologists provide the manufacturer a list of all sequences need to be produced.





Case-Study Goals

- **Produce a list of O(10^5) DNA sequences that reflect the desired design.**
- **Do this "LOP Style":**
  - Microarray specification is done by biologists (non-programmers).
  - These biologists should use a DSL developed for this purpose.
  - All "programming" should be restricted to the DSL and its runtime environment, and should be agnostic of the actual Microarray design.

Before Cedalion...

- The biologist performing this experiment has a programming day-job...
- Programmed ~500 LOC in Java to express a simple design.
- ✔ Runs fast (few seconds).
- ✗ This code must change to accommodate any change to the microarray design.

With Cedalion...

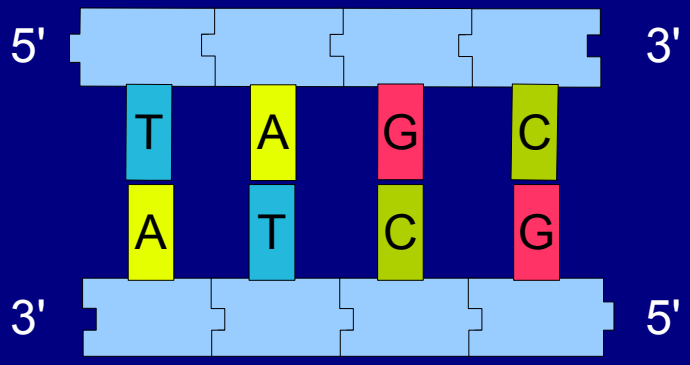
- A DSL was provided to express sets of DNA sequences.
- A microarray design can be defined using sets of sequences, with a name and quantity for each.
- A microarray design can be generated into files containing all sequences in the set.
- A 30 LOC Perl-script decimates the sequence files to form the desired output.

DSL for DNA Sequence Sets

- A/T/C/G: Singleton sets of a single nucleotide.
- N:=A∪T∪C∪G
- X.Y: The set consisting of an element of X concatenated to an element of Y.
- X^n: A singleton set containing the empty sequence if n=0, or $X.X^{n-1}$ otherwise.
- Y=[X]: Evaluates to the members of X. Y is bound to a singleton set containing that member, e.g., $Y=[N^2].Y$

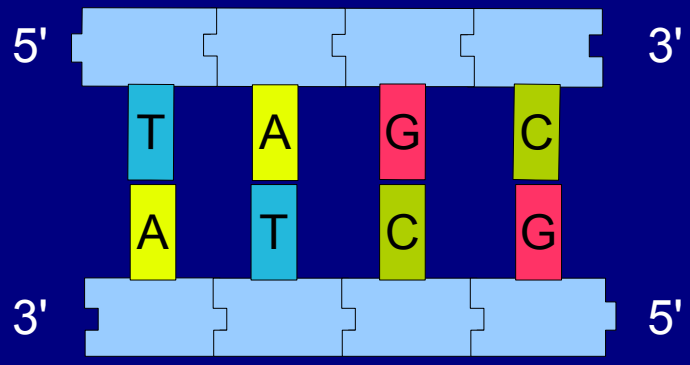
DSL for DNA Sequence Sets

- X^{inv} : The members of X in inverse order.
- X^{conj} : The members of X, with all nucleotides replaced by their conjugates: A⇔T; C⇔G.
- $X^{comp} := (X^{conj})^{inv}$



Restricting a Set

- Double-stranded DNA is redundant.
- For each sequence **S**, **S** and $\mathbf{S}^{comp}$ represent the same double-stranded DNA.
- restrict(**X**): Contains all members of **X**, taking only the "smaller" of two sequences representing the same DNA.
- uniformRestrict(**X**): Same as restrict(**X**), but taking either the smaller of the greater, at coin-toss.



Generating a Microarray

- A microarray has a **name** (base file name) and a list of **sections**.
- Each section consists of a **name**, a **set of sequences** and a **quantity** – how many sequences we wish to select.
- A context-menu-entry allows the generation of the microarray files, containing all possibilities.
- Running the Perl script in the target directory creates the final, decimated files.

Exercise

- **Build a microarray design.**
- **All sequences will start with ACCGGT and end with TTTTT.**
- **The middle part consists of a sequence followed by its conjugate.**
- **The basic sequence consists of the following:**
  - Experiment: A sequence of 5 bases, with either A or T in the middle. Select 100.
  - Control: A sequence of 5 bases, with either C or G in the middle. Select 20.

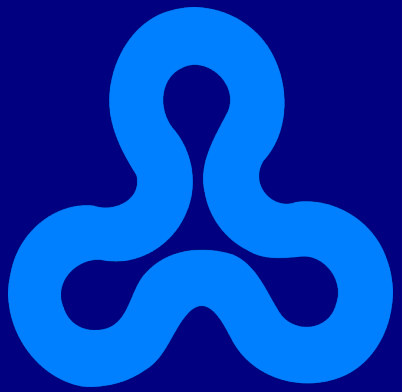
Case-Study Results

- With some assistance, the biologist was able to specify the microarray design using Cedalion.
- The design was changed twice before reaching the final version. Non of the changes required “programming”.
- Unit-tests were used to assure that the constant parts of the DNA sequences do not contain “interesting” features.

Case-Study: Conclusion

- **The microarray design produced by Cedalion was submitted to the manufacturer.**
- **Pros:**
  - ✔ Specification was done by non-programmer.
  - ✔ Modifications to the design were straight-forward.
- **Cons:**
  - ✗ Runtime performance is bad: x10 to x100 slower then the hand-written Java implementation (6 minutes for ~500,000 sequences).

Thank You!



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