

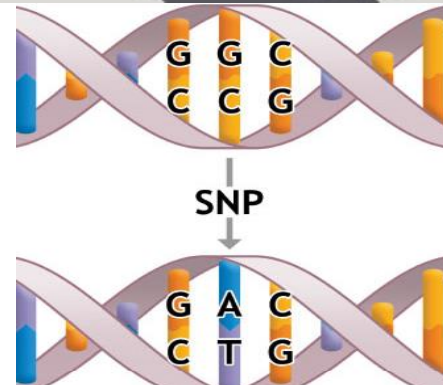
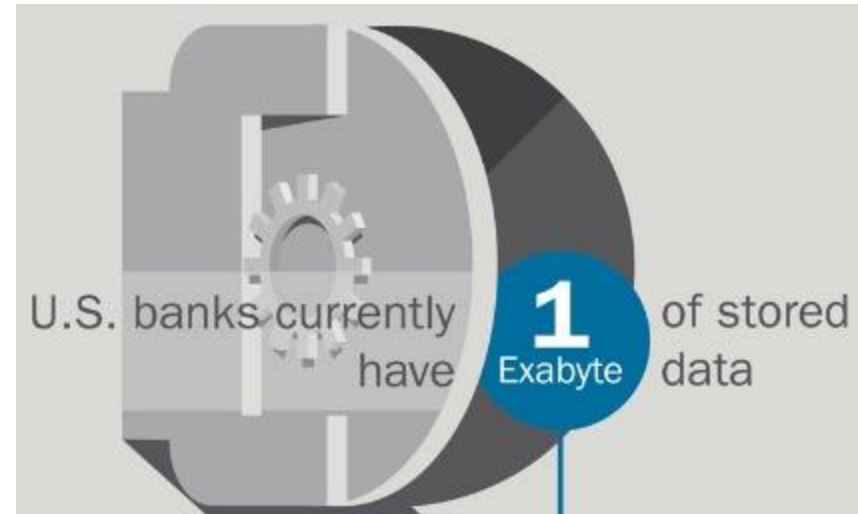
Just-In-Time Data Virtualization: Lightweight Data Management with **ViDa**

Manos Karpathiotakis*, Ioannis Alagiannis*, Thomas Heinis*[#],
Miguel Branco*, Anastasia Ailamaki*

Current data analysis does not scale

“Most firms estimate that they are only analyzing 12% of the data that they already have” [Forrester 2014]

- Growing data
- Growing heterogeneity
- Data movement regulations



Available data blocks business & scientific analytics

Discovering *disease signatures*

1 DATA FEDERATION

BEHAVIOR

NEURO-PSYCHOLOGY

BRAIN IMAGING

➔ DISEASE DEFINITION

➔ PHARMACOLOGY

➔ CLINICAL TRIAL

5 BIOLOGICAL SIGNATURE OF DISEASE

✗ Move data

✗ Copy data

✗ Transform data

2 DATA INTEGRATION

GENETICS

PROTEOMICS

KNOWLEDGE

SIMULATION

3 DATA MINING

4 CAUSAL MODELING

Clinical+Genetic+Imaging Data → Signature

Patients (CSV)

id	Protein : AACT	Age	Phenotype	...
1	1.4	45	Trauma	...
2	2	55	Chronic Symptoms	...
3	0.2	56

Brain_GrayMatter (Binary)

	0	1	...	n
0	0.45	0.75	...	0.1
1	0.33	0.3	...	0.38
...
m	0.12	0	...	0.47



BrainRegions (JSON)

```
[{"id": 1,
  "amygdala": {"X":15,"Y":20, "Vol": 0.5},
  "hippocampus": {"X":17, "Y":10, "Vol":0.2}},
 {"id": 2, ...},
 {"id": 3, ...}]
```

Signature:

age > 50

AND

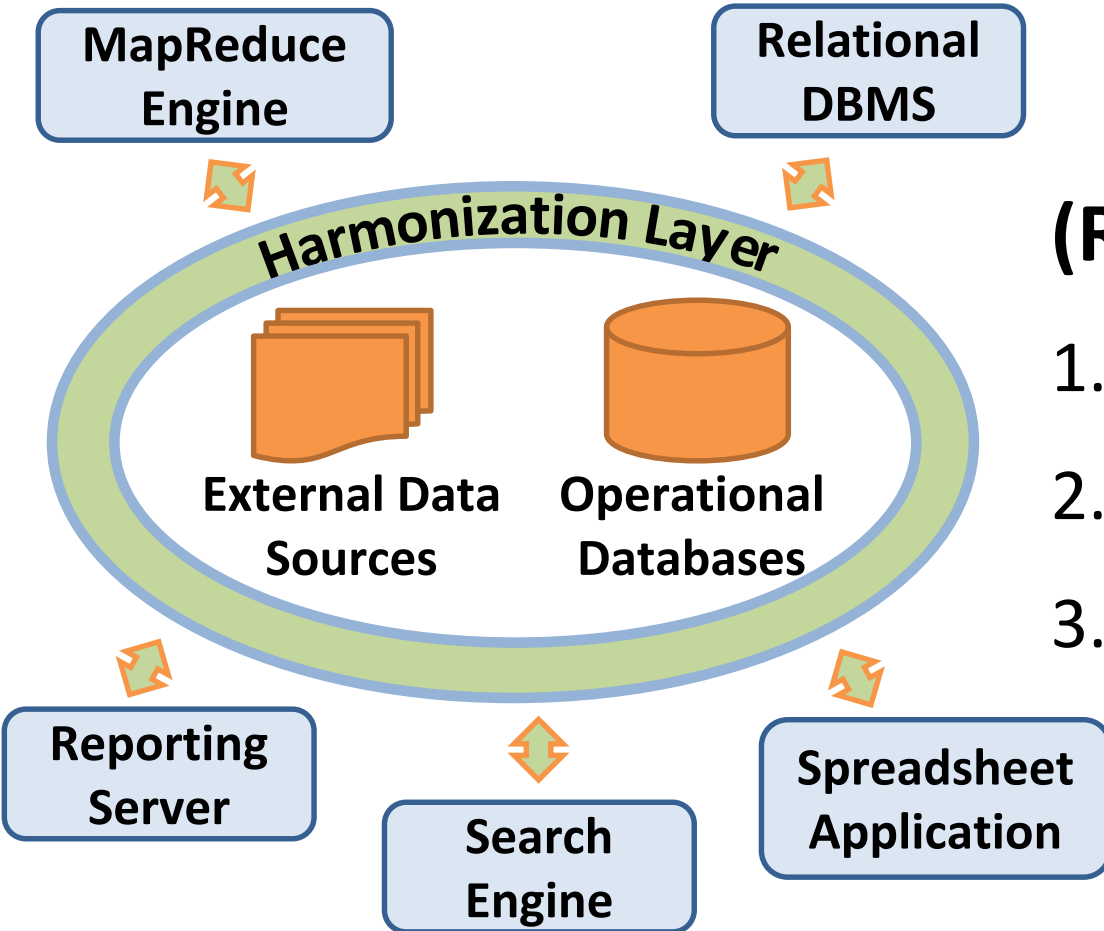
amygdala.Vol > 0.3

AND

AACT < 1

Challenge: Physical integration & diverse queries

Diverse applications over diverse datasets

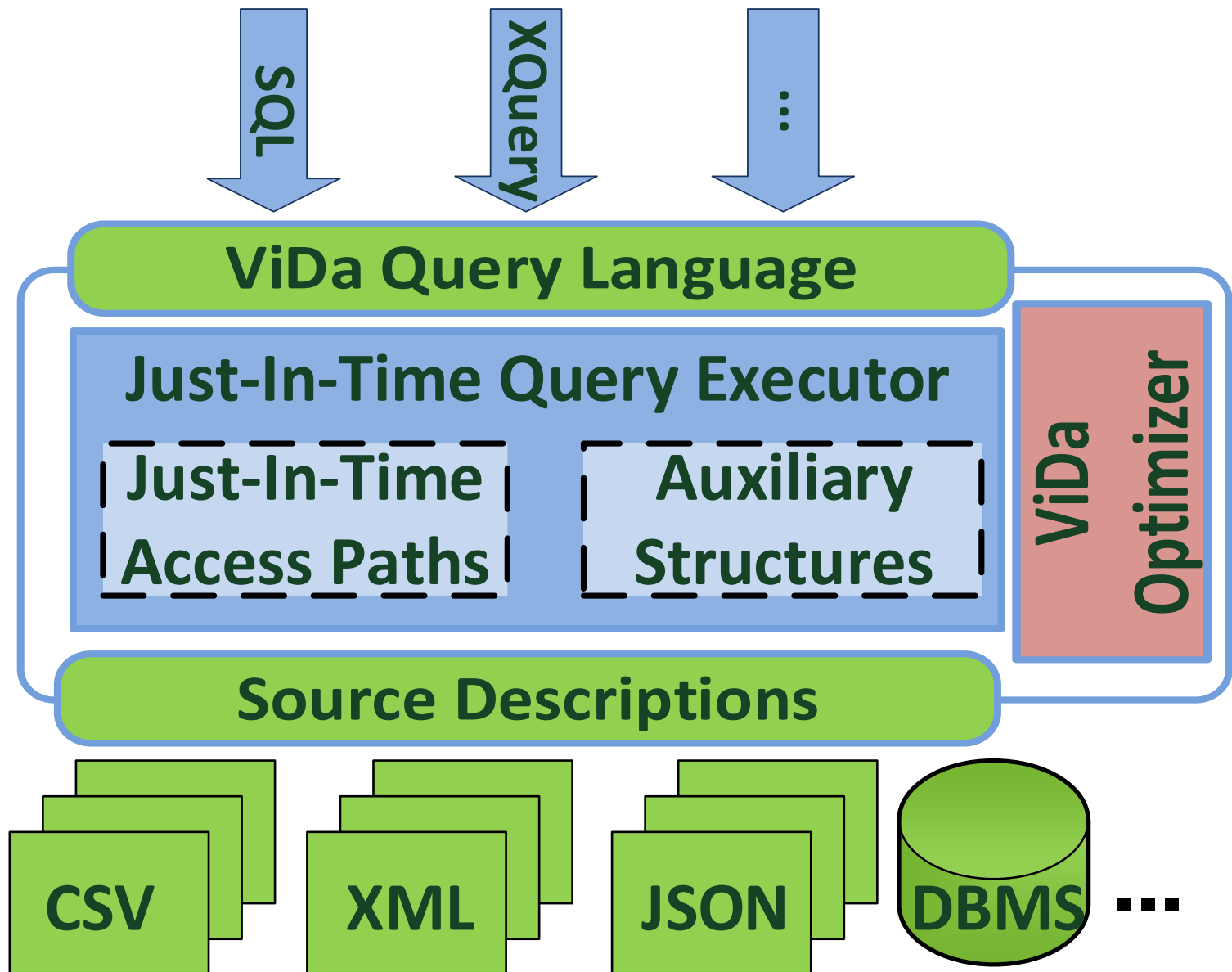


(Raw) Data:

1. "Golden" repository
2. Manipulate it freely
3. Adapt to it & to queries

Key: Data Virtualization
No Static Decisions!

ViDa Architecture



Queries over heterogeneous datasets

ViDa Query Language

Just-In-Time Query Executor

Just-In-Time
Access Paths

Auxiliary
Structures

ViDa
Optimizer

Source Descriptions

Queries translated to monoid comprehensions

Monoids:

- Abstraction for “aggregates” computation

Monoid Comprehensions*:

*Fegaras [TODS 2000]

- Operations between monoids

```
for {  
    p <- Patients, r <- BrainRegions,  
    p.id = r.id, r.amygdala.Vol > 0.2  
} yield list p.age
```

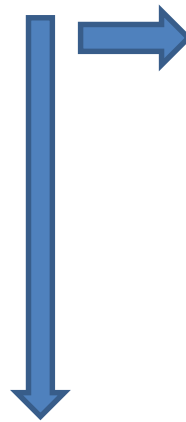
 **Sum/Bag/Set/Top-K/...**

Support multiple data models as input & output

“SQL++” → Comprehensions → Algebra

```
SELECT r.age
FROM Patients p
JOIN BrainRegions r
ON (p.id = r.id)
WHERE r.amygda.Vol > 0.2
```

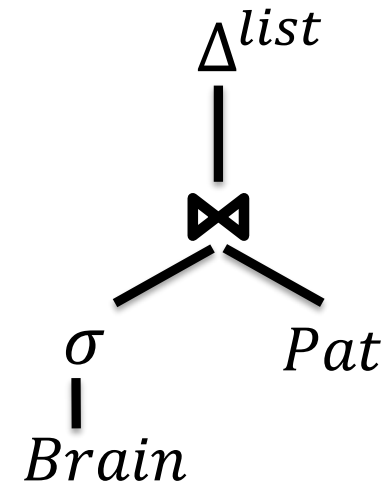
Internal Calculus



if-else
record construction
function application
(nested) comprehension
...

```
for {
  p <- Patients,
  r <- BrainRegions,
  p.id = r.id,
  r.amygda.Vol > 0.2
} yield list r.age
```

Optimizable
Algebra



Query execution in ViDa

ViDa Query Language

Just-In-Time Query Executor

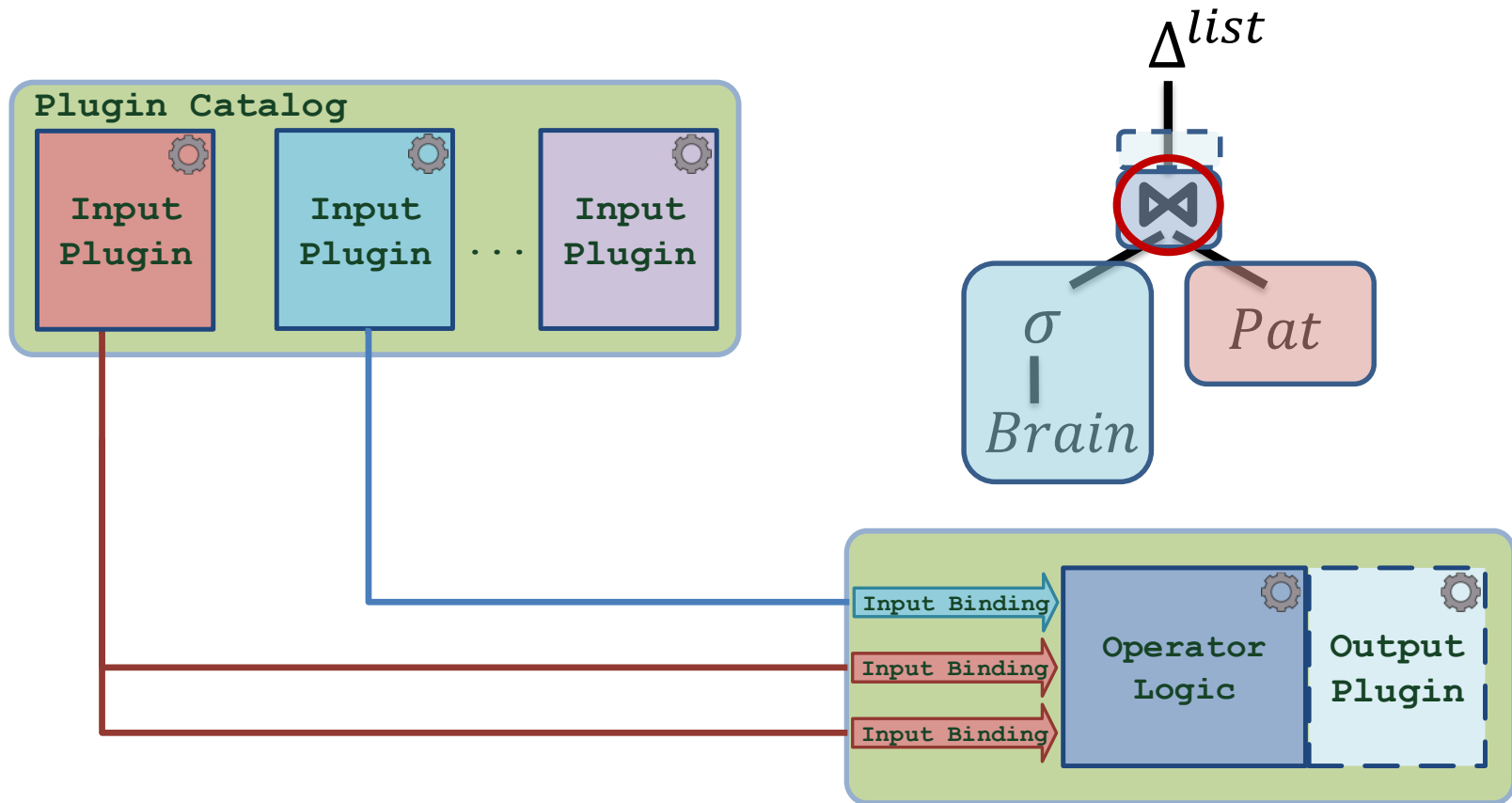
**Just-In-Time
Access Paths**

**Auxiliary
Structures**

ViDa
Optimizer

Source Descriptions

Creating a query executor *just-in-time*



Adapt to data and queries just-in-time

ViDa access paths

- Access paths generated *Just-in-time**

<u>id</u>	Protein: AACT	<u>age</u>	...
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- Adapting to schema of data

```

∀col:
  if col needed:
    if col isInt → readInt();
                  skipField();
                  readInt();
    ...           skipRest();
  
```

- File-format-specific opportunities
- Position caches for textual formats #
- Data caches

*RAW [VLDB 2014]

NoDB [SIGMOD 2012]

Reduce access costs by adapting to underlying data

Just-in-time operators

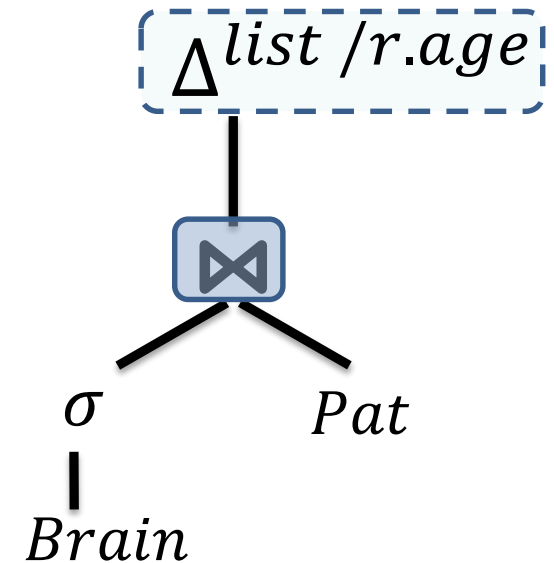
- Query operators generated *Just-in-time*

- “Hard-coded”, fine-grained operators

$\Delta_{\oplus/e}^p(X)$ \rightarrow `outputBindings(format);`

- Adapting data layout of caches to

- query requirements
- data format, model



Int	Int	JSON text	JSON text
Int	Int	BSON	..
Int	Int	start pos.	end pos.
...

Reduce processing costs by adapting to queries

Query optimization in ViDa

ViDa Query Language

Just-In-Time Query Executor

Just-In-Time
Access Paths

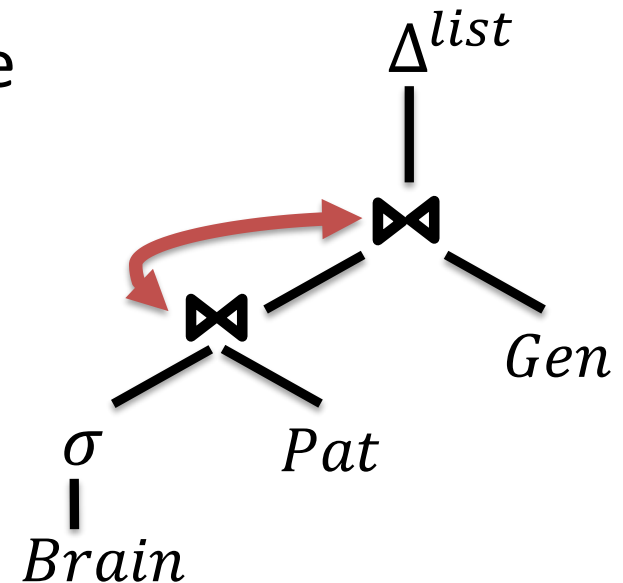
Auxiliary
Structures

ViDa
Optimizer

Source Descriptions

Optimizing a just-in-time database

- Choosing appropriate layout
- Lazy vs. Speculative Execution
- Fixing “wrong” decisions at runtime



Experimental Setup

- Intel(R) Xeon(R) CPU E5-2660 @ 2.20GHz
- 128 GB RAM
- 7500 RPM SATA

Relation name	Tuples	Attributes	Size	Type
Patients	41718	156	29 MB	CSV
Genetics	51858	17832	1.8 GB	CSV
BrainRegions	17000	20446	5.3 GB	JSON

```

SELECT val1, ..., valN
FROM Patients p
JOIN Genetics g ON (p.id = g.id)
JOIN BrainRegions b ON (g.id=b.id)
WHERE pred1 AND ... AND predN

```

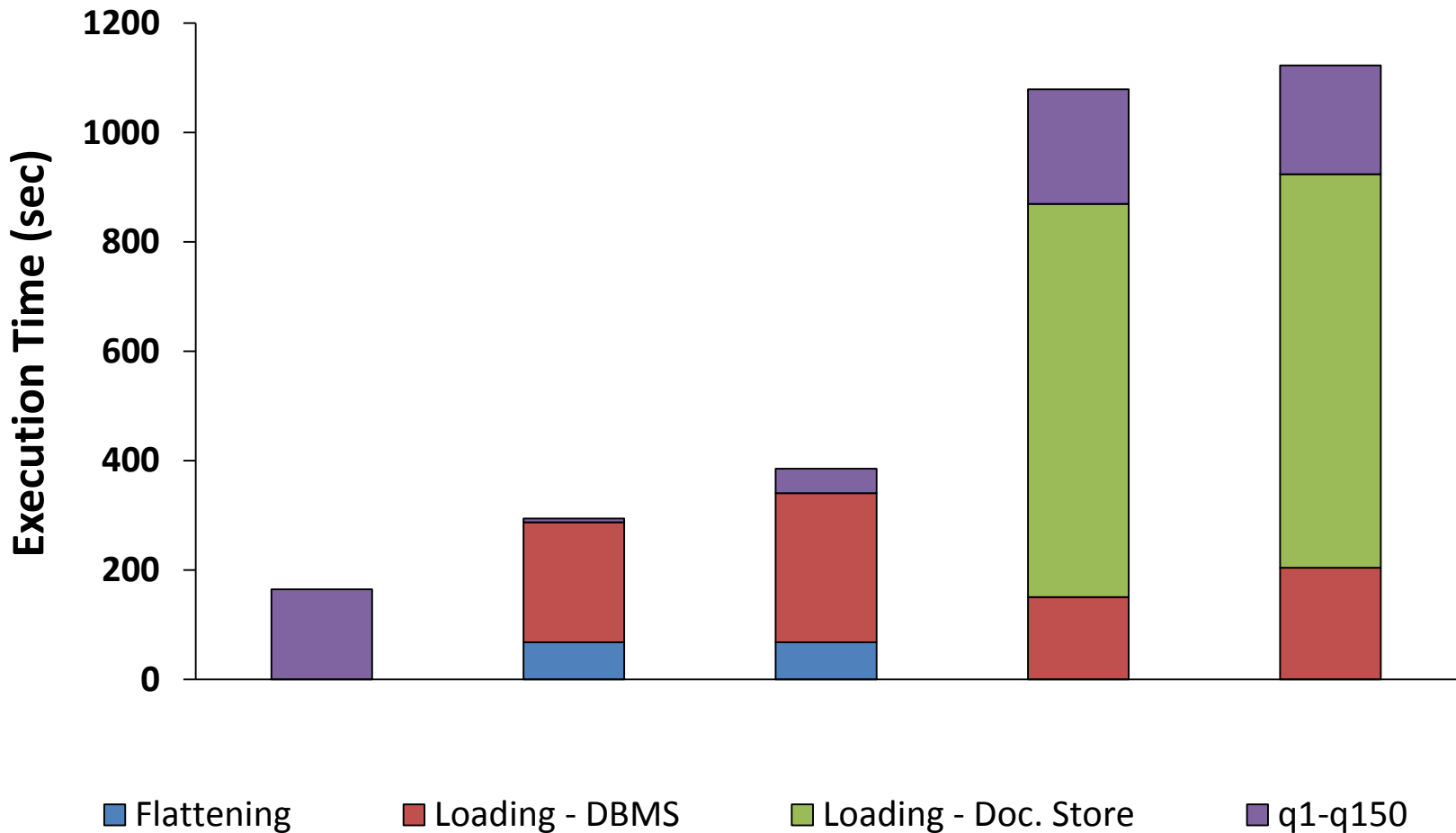
```

for { p <- Patients,
      g <- Genetics,
      b <- BrainRegions,
      p.id=g.id, g.id=b.id,
      pred1, ..., predN
} yield val1,...,valN

```


ViDa vs State-of-the-art

150 analytics queries on CSV & JSON data



ViDa: Competitive without loading/transforming

ViDa enables lightweight data management

- Decouple query language used from data layout
- Adapt to datasets and queries just-in-time
- Flexible and competitive with state of the art