

Scala Days

Gallia

*A schema-aware Scala library
for generic data transformation*

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Gallia Project



What: Gallia in a nutshell

Trivial example:

```
""{"first": "anthony", "last": "cros", "age": 39, "fit": true}""  
.read() // lazily + infers schema  
.nest("first", "last").under("name")  
.increment("age")  
.remove ("fit")  
.display() // trigger meta then data transformation
```

prints **schema**:

```
<root>  
  name  
    first _String  
    last  _String  
  age    _Int
```

prints **data**:

```
{ "name": {  
  "first": "anthony",  
  "last" : "cros" },  
  "age": 40 }
```

Gallia is "schema aware"

```
"""{"name": "anthony", "age": 39, "fit": true}"""  
  .read(  
    "name".string, "age".int, "fit".boolean)  
    // or via: .read[Person]  
    .toUpperCase("name")  
    .increment ("name") // nonsensical  
.remove ("fit") // ignored  
  .display()  
  // Meta error
```

- Before processing data (potential schema inference notwithstanding)
- For any level of nesting/multiplicity
- For any operation where such checks can be realized
(won't catch IOOB errors for instance)

How do I get started?

```
mkdir /tmp/sd23 && cd /tmp/sd23
```

```
echo 'libraryDependencies +=
```

```
  "io.github.galliaproject" %% "gallia-core" % "0.4.0" ' \  
  > build.sbt # 2.12 or 2.13 only
```

```
sbt console
```

```
-----  
scala> import gallia._
```

```
scala> """{"report": "TPS", "submitted": false}"""  
      .read().flip("submitted").display()
```

Main goals

1. Practicality
2. Readability
3. Scalability (optionally)

When should I use it?

Python pandas: small dataframes



Gallia: small and big data

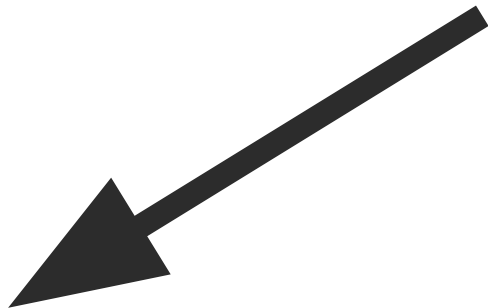


not necessarily
"framed" data
(think nesting)

Apache Spark: big dataframes

⇒ One-stop shop paradigm for data transformations*

Who's the team behind it?



*(hopefully I'm standing
somewhere down there)*

FOR NOW!

Why not Case Classes + Collections?

1. May require **lots** of *case classes* (see [DbNSFP](#) example on github)
 - Input, output, and **intermediate** case classes
 - Lots of **boilerplate** code
 - Lots of **naming**: naming things judiciously is **hard**
2. Transformation code only commits to schema elements used
 - For instance: `val f: HeadS => HeadS = _.remove("name").flip("fit")`
 - Only "commits" to there being:
 - "name" field (whose type is **irrelevant**)
 - "fit" field (**boolean**, because we flip it)
 - Great for **schema evolution** or **schema unification**
3. Data model may still be **changing**, or you may just be **poking around**

I/O Supported

Currently:

- {T,C}SV files: *plain*, *GZIP*, and *BZ2*
- JSON/jsonl : *plain*, *GZIP*, and *BZ2*
- Apache Avro and Parquet
- RDBMS: via JDBC
- MongoDB: read-only (for now)

In the future:

- Excel (yes, **lots** of research and clinical labs still rely on it)
- XML
- GraphQL, Sparql, Cypher (NEO4J), ..

Target selection

Choosing **what** to act on: its own meta-querying language

```
remove      (      "f1"  )
remove      (      "parent" |> "child"  )
remove      {      _.firstKey  }
remove      {      _.allBut ("f2", "f3")  }
remove      {      _.findKey(_.endsWith("1"))  }
remove      {      _.fullCustomKey { schema => [...] }  }
transform {  _.string("f1")          }.using([...])
transform {  _.string(_.firstKey)    }.using([...])
transform {  _.string(_.allkeys)     }.using([...])
```

Live coding session

Let's write some code!

More about scaling

(When Spark isn't available)

"Poor man's" scaling leveraging ***mergesort*** algorithm, think:

```
join -t$'\t' -o "1.1,2.6" -1 2 -2 7 \  
  <(sort -t$'\t' -k2,2 \  
    <(join -t$'\t' -o "1.8,2.7" -1 8 -2 8 \  
      <(sort -t$'\t' -k8,8 <(tail -n+2 file1.tsv)) \  
      <(sort -t$'\t' -k5,5 <(tail -n+2 file2.tsv)))) \  
  <(sort -t$'\t' -k7,7 <(tail -n+2 file3.tsv))
```

Scaling: Poor man's version

Invoke via the use of `.iteratorMode`:

```
"/my/big/file/input.jsonl.gz2"  
  .stream(  
    _ .iteratorMode.schema([...]))  
    .decrement("fanciness")  
    .groupBy([...])  
    [...]
```

***CAVEAT:** only works if **GNU sort** is available on your system
(never tested with Windows/Mac)*

Scaling with Gallia in practice

See example of real world usage: *GeneMania* dataset processing

- **Poor man**/mergesort: [GeneMania.scala](#)
- **Gallia+Spark** equivalent: [GeneManiaSparkDriver.scala](#)

They share **the exact same code** for the transformations, and differ only in their I/O

More features

See this [Towards Data Science](#) article which introduce:

- **Union Types:** minimal support
- **Metaschema:**
 - As a result of supporting union types
 - Could dogfood schema transformations
- **Cotransformations:**
 - Via intermediate case classes representing a **subset** of schema
 - Great for encapsulation
 - For ***M-to-N*** field transformations where ***M>1*** and ***N>1***
 - Example: [gist](#)

So, why should I use Gallia?

1. Most common/useful data operations
2. Readable DSL
3. Scaling is not an afterthought
4. Meta-awareness
5. Can process individual entities
6. Can process deeply nested entities of any multiplicity
7. Provides flexible target selection
8. Execution DAG can be optimized easily thanks to Gallia's abstractions

Conclusion

- Seeking **feedback** to decide on future **directions**
- Welcome comparisons with **existing tools**
 - What would the complex biomedical [data transformations](#) (e.g. *dbNSFP*) look like with ***pandas, Spark SQL***, etc?
 - Keeping in mind Gallia's **priorities!**
- Welcome **help** in general:
 - Terminology ("*deserialize1b*"...)
 - Documentation ("*deserialize1b*"???!!!!)
 - Optimization
 - Semantic information?

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Thanks!

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