

# Declarative Concurrent Programming with Chymyst

Sergei Winitzki

Scale by the Bay 2017

November 18, 2017

# What is “Chymyst”?

Chymyst = a Scala implementation of the “chemical machine” paradigm

- Reflexive Chemical Abstract Machine [Fournet & Gonthier 1996]
  - ▶ known as “join calculus” in the academic world
- it is a *declarative language* for concurrent & parallel computations
  - ▶ largely unknown and unused by the software engineering community
  - ▶ available as an open-source library & EDSL

# Concurrent & parallel programming is hard

Imperative concurrency is difficult to reason about:

- callbacks, threads, semaphores, mutex locks
- errors with shared mutable state
- hard to reason about states that mutate in parallel
- hard to test – non-deterministic runtime behavior!
  - ▶ race conditions, deadlocks, livelocks

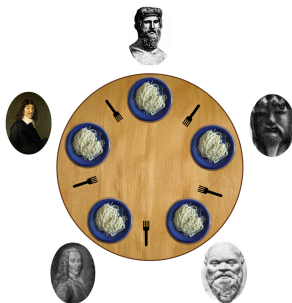
We can avoid this if we use declarative approaches:

- synchronous parallelism (parallel collections, Spark)
- asynchronous parallelism (`Future`, `async/await`)
- asynchronous streaming (Akka Streams)
- Actors (Akka)
- chemical machine (`Chymyst`)

# “Dining philosophers”

The paradigmatic example of concurrency

Five philosophers sit at a round table, taking turns eating and thinking for random time intervals



Problem: simulate the process, avoiding deadlock and starvation

Solutions: [Rosetta Code](#)

# Talk overview

How I learned to forget semaphores and to love concurrency

In this talk:

- Introduction to join calculus and “chemical” style of concurrency
- **Chymyst** -- a new Scala EDSL for join calculus
- Join calculus as an evolution of the Actor model
- Examples and demos

Not in this talk: Other approaches to declarative concurrency

- $\pi$ -calculus, PICT language (academic so far)
- Erlang’s message-passing  $\approx$  Akka’s “Actors”
- CSP / Go language
- STM (Haskell, Scala)

# Join Calculus: A New Hope

...and some new hype

Join calculus is ...

- ...a declarative language for general-purpose concurrency
- “What if Actors were auto-started, type-safe, and multiple-dispatch”
- No threads/semaphores/locks, no shared mutable state
- Concurrency is automatic and *data-driven*, not command-driven
  - ▶ Easier to reason about than any other concurrency formalism!

Metaphors for join calculus:

- “concurrent functions compute with concurrent data”
- “chemical soup with molecules and reactions”

# Concurrent data and concurrent functions

## Intuitions leading to join calculus

Message to auto-started actor  $\approx$  concurrent function call on data item  
What would it mean to make ordinary functions concurrent?

- Several functions should be able to run at once
- No shared state: Concurrent processes work on different data

This will be implemented if:

- Data items and functions are stored in a special “site”
- Each data item is labeled for specific concurrent function(s)
- Concurrent functions consume data from the site
- Computed results are emitted back to the site

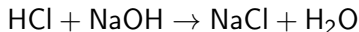
Operational semantics:

- Concurrent functions auto-start whenever input data is available
- Different instances of a conc. function consume separate data items

# Join Calculus: The Genesis

From real to abstract chemistry

Real chemistry:



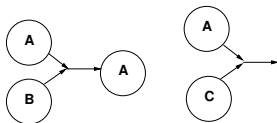
Abstract chemistry:

- Chemical “soup” contains instances of abstract “molecules”
- Combine certain sorts of molecules to start a “reaction”:

Abstract chemical laws:

$$a + b \rightarrow a$$

$$a + c \rightarrow \emptyset$$



- Program code defines molecules  $a$ ,  $b$ ,  $c$ , ... and chemical laws
- At initial time, the code emits some molecules into the “soup”
- The runtime system evolves the soup *concurrently* and *in parallel*

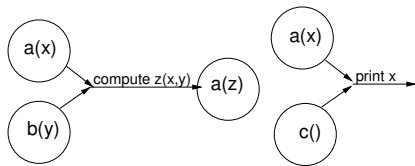


# Join Calculus in a Nutshell

“Better concurrency through chemistry”

Translating the chemical metaphor into practice:

- Each molecule carries a **value** (“concurrent data”)
- Each reaction computes a “molecule-set-valued” expression from input values
- Resulting molecules are emitted back into the soup
- Whenever input molecules are available, reactions start concurrently and in parallel



```
site(  
  go { case a(x) + b(y) =>  
    val z = f(x, y); a(z) },  
  go { case a(x) + c(_) =>  
    println(x) }  
)
```

When a reaction starts: input molecules disappear, expression is computed, output molecules are emitted

# Programs = chemical laws + initial molecules

First example: concurrent counter

We would like to decrement and increment concurrently

Chemical laws:

- $\text{counter}(n) + \text{decr}() \Rightarrow \text{counter}(n - 1)$
- $\text{counter}(n) + \text{incr}() \Rightarrow \text{counter}(n + 1)$

Initial molecule instances:

- $\text{counter}(0)$

“Data stays on the molecules”

We may emit  $\text{decr}()$  and  $\text{incr}()$  concurrently

# Chymyst: basic features

Molecule emitters and reaction definitions in the Scala DSL

Define **molecule emitters**:

```
val counter = m[Int]  
val decr = m[Unit]  
val incr = m[Unit]
```

Declare some **reactions** by pattern match on the molecule values:

```
val r0 = go { case counter(n) + decr(_) => counter(n-1) }  
val r1 = go { case counter(n) + incr(_) => counter(n+1) }
```

Activate a **reaction site**: `site(r0, r1)`

- For brevity, we can define reactions inline, within the `site()` call

# Chymyst: basic usage

## Operational semantics

Emit some molecules:

```
counter(10) // non-blocking side-effect  
incr() // ditto; we will have counter(11) later  
incr() // we will have counter(12) later
```

- Calling `counter(10)` returns `Unit` and emits a molecule as a side-effect
- This could be the state of the chemical soup at some point in time:
  - ▶ `counter(10) + incr() + incr()`

# Concurrent data and concurrent functions

## Chemical metaphor vs. concurrent terms metaphor

- Reaction consumes molecules  $\approx$  function consumes input values
- Reaction emits molecules  $\approx$  function returns result values
- Emit molecule with value  $\approx$  lift data into the “concurrent world”
- Define reaction  $\approx$  lift a function into the “concurrent world”
- Reaction site  $\approx$  container for concurrent functions and data items

# Chymyst: more features

## Blocking vs. non-blocking molecules

### Non-blocking molecules:

- emitter *does not wait* until a reaction starts with the new molecule

### Blocking molecules:

- emitter will block until a reaction starts and emits a “reply value”
- molecule implicitly carries a pseudo-emitter for “reply”
- when the “reply” is emitted, its value will be returned to caller
- Example:

```
val f = b[Int, String] // create blocking emitter
go { f(x, reply) + c(y) => reply(s"${x + y}") }
c(100) // non-blocking
val result: String = f(200) // blocking call, will get “300”
```

# Chymyst: examples I

## Counter with blocking access

Blocking molecule `getN` reads the value `x` in `counter(x)`:

```
val getN = b[Unit, Int]
// revise the join definition, appending this reaction:
... val r2 = go { case counter(x) + getN(_, reply) => reply(x) }
site(r0, r1, r2)
// Emit non-blocking molecules as before...
// Now emit the blocking molecule:
val x = getN() // blocking fetch, returns Int
```

Source code: [CounterSpec.scala](#)

# Definitions in local scopes

Chymyst = functional programming + join calculus

New molecules, reactions, and sites can be defined in *local scopes*

Emitters (`read: M[Int]`) can be molecule values too!

```
def makeCounter(init: Int): (M[Unit], M[M[Int]]) = {  
  val c = m[Int]  
  val decr = m[Unit]  
  val get = m[M[Int]]  
  site(  
    go { case c(x) + get(read) => c(x); read(x) },  
    go { case c(x) + decr(_) => c(x - 1) }  
  )  
  c(init) // emit initial molecule  
  (decr, get) // return emitters to the outside scope  
}  
  
// usage:  
val (decr, get) = makeCounter(100)  
val result = m[Int]  
get(result) // non-blocking fetch
```



# Chymyst: examples II

## Options, Futures, and Map/Reduce

Implement `Future` with blocking “`get`”:

```
go { case get(_, reply) => val x = f(); reply(x) }
```

Implement Map/Reduce:

```
go { case c(x) => d(x * 2) } // “map”  
go { case res(list) + d(s) => res(s :: list) } // “reduce”  
go { case get(_, reply) + res(list) => reply(list) }  
res Nil  
Seq(1,2,3).foreach(x => c(x))  
get() // this returned Seq(4,6,2) in one test
```

Source code: [FutureSpec.scala](#)

For more examples, see the [main repository](#) (first-of, barriers, rendezvous, critical sections, readers/writers, Game of Life, 8 queens, etc.)

# Chymyst: examples III

## Five Dining Philosophers

Philosophers 1, 2, 3, 4, 5 and forks f12, f23, f34, f45, f51

```
// ... definitions of emitters, think(), eat() omitted for brevity
site (
  go { case t1(_) => think(1); h1() },
  go { case t2(_) => think(2); h2() },
  go { case t3(_) => think(3); h3() },
  go { case t4(_) => think(4); h4() },
  go { case t5(_) => think(5); h5() },

  go { case h1(_) + f12(_) + f51(_) => eat(1); t1() + f12() + f51() },
  go { case h2(_) + f23(_) + f12(_) => eat(2); t2() + f23() + f12() },
  go { case h3(_) + f34(_) + f23(_) => eat(3); t3() + f34() + f23() },
  go { case h4(_) + f45(_) + f34(_) => eat(4); t4() + f45() + f34() },
  go { case h5(_) + f51(_) + f45(_) => eat(5); t5() + f51() + f45() }
)
t1() + t2() + t3() + t4() + t5()
f12() + f23() + f34() + f45() + f51()
```

Source code: [DiningPhilosophers.scala](#)

# From Actors to Join Calculus

“Chemical actors” are actors with new requirements:

- ① chemical actors are auto-started when messages arrive
- ② chemical actors may wait atomically for a *set* of different messages
- ③ messages carry statically typed values (“typed Akka”)

It follows from these requirements that...

- User code declares *computations* and not actor instances
- Auto-created actor instances must be stateless
- Message emitters are *specific to data*, not to actor instances:

```
// Akka
val a: ActorRef = ...
val b: ActorRef = ...
a ! 100
b ! 1;   b ! 2;   b ! 3
```

```
// Chymyst
go { case a(x) + b(y) => ... }
go { case b(y) + c(z) => ... }
a(100)
b(1); b(2); b(3)
```

- Multiple messages are automatically parallelized
- Blocking molecules  $\approx$  blocking-send: `actorRef ? 1`

# Join Calculus vs. Actor model

David vs. Goliath?

- reaction  $\approx$  actor
- emitted molecule  $\approx$  message sent to actor

Programming with actors:

- user code creates and manages explicit actor instances
- actors typically hold mutable state or mutate “behavior”
  - ▶ reasoning is about running processes *and* the data

Programming with reactions:

- processes auto-start when the needed input molecules are available
- many reactions can start at once, automatically parallel
  - ▶ reasoning is only about the data on present molecules

# Chymyst: examples IV

## Concurrent merge-sort: chemistry pseudocode

The `mergesort` molecule starts a “chain reaction”:

- receives the upper-level “`sortedResult`” molecule
- defines its own “`sorted`” molecules in *local scope*
- emits upper-level “`sortedResult`” when done

```
mergesort( (arr, sortedResult) ) ⇒  
  val (part1, part2) = arr.splitAt(arr.length/2)  
  sorted1(x) + sorted2(y) ⇒ sortedResult( arrayMerge(x,y) )
```

```
// Emit lower-level mergesort molecules:  
mergesort(part1, sorted1) + mergesort(part2, sorted2)
```

# Chymyst: examples IV

## Concurrent merge-sort: Chymyst code

```
val mergesort = m[(Array[T], M[Array[T]])]
site(
  go { case mergesort((arr, sortedResult)) =>
    if (arr.length <= 1) sortedResult(arr)
    else {
      val sorted1 = m[Array[T]]
      val sorted2 = m[Array[T]]
      site(
        go { case sorted1(x) + sorted2(y) =>
sortedResult(arrayMerge(x,y)) }
      )
      val (part1, part2) = arr.splitAt(arr.length/2)
      // Emit lower-level mergesort molecules:
      mergesort(part1, sorted1) + mergesort(part2, sorted2)
    }
  })
```

Source code: [MergeSortSpec.scala](#)

# Pipelined molecules: An automatic optimization

In join calculus: channels with *ordered* mailboxes

Reaction scheduler in Chymyst:

- Examines all present molecule instances and runs the next reaction
  - ▶ Is it sufficient to examine *only one* molecule instance?
    - ★ This could be true or false depending on the specific molecule
- If true, the molecule's instances are held in a queue ("pipelined")
  - ▶ Chymyst automatically makes *some* molecules pipelined

In a given chemical program, can we pipeline the molecule  $a(x)$ ?

- Consider the predicate  $f(x, y, z, \dots)$  for starting a reaction, e.g.:  
 $f(x, y, b) = \text{HAVE}(b(y)) \ \&\& \ x == 0 \ \&\& \ y > x$
- The predicate  $f(\dots)$  must be *factorizable* into a conjunction:  
 $f(x, y, z, \dots) = p(x) \ \&\& \ q(y, z, \dots)$ 
  - ▶ I have a proof that this optimization preserves semantics

# Everything you need to know about join calculus...

... but the [Wikipedia page](#) confused you, so you were afraid to ask

Academic descriptions of JC use the “message/channel” terminology

Chymyst	join calculus	code
molecule	message on channel	<code>a(123) // side effect</code>
emitter	channel name	<code>val a: M[Int]</code>
blocking emitter	blocking channel	<code>val q: B[Unit, Int]</code>
reaction	process	<code>go { case a(x) + ... }</code>
emitting a molecule	sending a message	<code>a(123) // side effect</code>
reaction site	join definition	<code>site(r1, r2, ...)</code>



# Join Calculus in the wild

- Previous implementations:
  - ▶ Funnel [M. Odersky et al., 2000]
  - ▶ Join Java [von Itzstein et al., 2001-2005]
  - ▶ JOCaml ([jocaml.inria.fr](http://jocaml.inria.fr)) [Fournet et al. 2003]
  - ▶ “Join in Scala” compiler patch [V. Cremet 2003]
  - ▶ Joins library for .NET [P. Crusso 2006]
  - ▶ ScalaJoins [P. Haller 2008]
  - ▶ Joinads (F#, Haskell) [Petricek and Syme 2011]
  - ▶ ScalaJoin [J. He 2011]
  - ▶ CocoaJoin (iOS), AndroJoin (Android) [S.W. 2013]
  - ▶ JEScala [G. Salvaneschi 2014]
- Chymyst -- a new JC implementation in Scala (this talk)
  - ▶ Better syntax, more checks of code sanity
  - ▶ (Some) automatic fault tolerance
  - ▶ Thread pool and thread priority control
  - ▶ Event monitoring and unit testing APIs

# Conclusions and outlook

- Chemical machine = declarative, purely functional concurrency
  - ▶ Similar to “Actors”, but easier to use and “more purely functional”
  - ▶ Short, declarative code implementing barriers, rendezvous, etc.
- A new open-source Scala implementation: **Chymyst**
  - ▶ Full-featured implementation of join calculus
  - ▶ Static DSL code analysis (with Scala macros)
  - ▶ Industry-strength features (thread priority control, pipelining, fault tolerance, unit testing and debugging APIs)
  - ▶ Extensive documentation: **tutorial book** and **draft paper**
- On the future roadmap:
  - ▶ Thread fusion for better performance
  - ▶ Full continuation-passing transformation to nonblocking code
  - ▶ Automatic backpressure (“reaction temperature”)
  - ▶ Automatic distributed runtime (“distributed soup”)
- Example code for **this talk**: [github.com/Chymyst/jc-talk-2017-examples](https://github.com/Chymyst/jc-talk-2017-examples)