Enabling Java string-bioinformatics libraries in Kawa Scheme

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Motivation

- Integration of a well-established JVM implementation of Scheme, viz. Kawa
- Cater to existing Java libraries (particularly bioinformatics)
- Java libraries are decorated with special annotations to indicate they should be used in the Kawa environment
- Annotated Java functions are presented in a natural way in the Kawa Scheme environment

- Java is a mature and robust programming environment
- Tools and libraries for use in bioinformatics
- Particular libraries of string-bioinformatics algorithms
- Java-based tools provide
 - Strong typing
 - Portability
 - The Java Virtual Machine features (garbage collection, etc.)

- Java is not convenient for prototyping
- Interactive development is new
- REPL (Read-Evaluate-Print-Loop) just recently added in Java 9
- The new jshell for Open JDK 11 is Very good!

- Subset of the Lisp programming language
- Runs on the JVM via Kawa
- Convenient for rapid prototyping
- Scheme is an attractive choice because
 - Well-studied and mature language
 - Enables programming in diverse styles in particular functional-style programming

Technique

- Java string-bioinformatics libraries are decorated with a special annotation that indicates they are to be made available in Kawa
- Annotations in Java are simply tags containing meta-data that begin with the @ symbol

- At compile time, descriptive information is extracted from the source code and stored in XML files
- XML files are bundled with other artifacts within jar files
- Function descriptive information is extracted from the accompanying Javadoc
- Annotation syntax allows supplying alternative documentation
- Documentation is made available to the Kawa REPL

Deterministic

- Value returned by a function depends only on the values of its argument
- The result cannot depend on any state
- May not depend on any external input from I/O devices

Side-effect free

- Execution does not cause any observable side effect or output
- side-effect-free function must not mutate objects or output to $\ensuremath{I/O}$ devices.

- Existing Java string-bioinformatics libraries
 - Directly modified by adorning functions with annotations
 - Indirectly supported by wrapping them with the introduction of a language-bridge library

Annotation Tooling

- The Processor class provides a mechanism to process annotated classes
- Most implementations extends the AbstractProcessor class
- Processing takes place using a sequence of rounds
- The user defined processor is specified using the @AutoService(Processor.class) annotation

- Data is stored in XML using the JAXB-API
- For example, Java comment objects are converted into XML
- A fully qualified XML file is created for every class that contains @KawaFunction annotated methods

- Initialization of the KawaServer includes searching the annotation processor classpath for annotation XML files
- Function aliasing is performed on the discovered @KawaFunction annotated methods
- By default, long packaging namespace prefix removed
- The newly created alias is available in the default namespace kjava

Kawa-Scheme Annotations

- 1 @Retention(RUNTIME)
- 2 @Target(METHOD)
- 3 **public** @interface KawaFunction { /* ... */ }
 - 1. @Retention specifies the annotation is available at runtime
 - 2. The @Target indicates that this annotation may only be used with Java methods

@KawaFunction Annotation Expanded

public @interface KawaFunction {

```
1
 2
 3
 4
 5
 6
 7
 8
 9
10
11
12
13
14
```

}

```
String namespace() default "kjava";
/* Grabs the surrounding Javadoc by default */
String description() default "";
```

/* Returns the same result given the
 same argument value(s). */
boolean deterministic() default false;

/* No semantically observable side effect or output */
boolean sideEffectFree() default false;

Kawa-Scheme Programming

- Create on the Java side when application initializes
- Use the KawaServer class to initialize a Kawa telnet server in a separate Java thread.
- Care must be taken to ensure that client model modification does not interfere with native Java library states.

- **REPL** created from telnet connection (default port 5146)
- **rlwrap** program provides typical shell experience
- Emacs is excellent for Scheme programming

Conclusion

- Test with a broader set of string-bioinformatics libraries
- Expand on the type interaction of the two language environments
 - Support function preconditions and postconditions
 - Investigate functional, multi-threaded applications

- Java libraries decorated with annotations
- Library provides natural functional-style programming
 environment
- Provide Kawa Scheme integration with existing Java string-bioinformatics libraries