

AAConWSClientExample.java

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package compbio.ws.client;

import java.io.ByteArrayInputStream;
import java.io.FileNotFoundException;
import java.io.IOException;
import java.util.List;
import java.util.Set;

import compbio.data.msa.Annotation;
import compbio.data.sequence.FastaSequence;
import compbio.data.sequence.Score;
import compbio.data.sequence.SequenceUtil;
import compbio.metadata.JobSubmissionException;
import compbio.metadata.Preset;
import compbio.metadata.PresetManager;
import compbio.metadata.ResultNotAvailableException;
import compbio.metadata.UnsupportedRuntimeException;
import compbio.metadata.WrongParameterException;
import compbio.runner.conservations.AACon;

/**
 * AAConWS client example
 */
public class AAConWSClientExample {

    /**
     * Input sequences. For the simplicity keep them in the class
     */
    static final String input = ">Foo      \r\n"
        + "MTADGPRELLQLRAAVRHRPQDFVAWMLLADAELGMGDTTAGEMAVQRGLLALHPGHPEAV\r\n"
        + "ARLGRVVRWTQQRHAEAAVLLQQASDAAPEHPGIALWLGHAELEDAGQAEAAAAAYTRAHQL\r\n"
        + "LPEEPYITAQLLNWRRRLCDWRALDVLSAQVRAAVAQVGVAVEPFAFLSEDASAAEQLAC\r\n"
        + "ARTRAQAI AASVRPLAPTRVRSKGPLRVGFVSNVGFAGHPTGLLTVALFEALQRRQPDLM\r\n"
        + "HLFATSGDDGSTLRTRLAQASTLHDVTALGHLATAKHIRHHGIDLLFDLRGWGGGRPEV\r\n"
        + "FALRPAPVQVNWLAYPGTSGAPWMDYVLGDAFALPPALEPFYSEHVLRLQGAQFQPSDTSR\r\n"
        + "VVAEPPSRTQCGLPEQGVVLCFNNYSYKLNQSMARMLAVLREVPDSVLWLLSGPGEADA\r\n"
        + "RLRAFAHAQGVDAQRLVFMKPLPHPQYLARYRHADLFLDTHPYNAHTTASDALWTGCPVL\r\n"
        + "TTPGETFAARVAGSLNHHGLGDEMNVADDAAFVAKAVALASDPAALTALHARVDVLRRES\r\n"
        + "GVFEMDGFADDFGALLQALARRHGWLGI\r\n"
        + "\r\n"
        + ">Bar      \r\n"
        + "-----MGDTTAGEMAVQRGLLALH-----\r\n"
        + "-----QQRHAEAAVLLQQASDAAPEHPGIALWL-HAELEDAGQAEAAAA-YTRAHQL\r\n"
        + "LPEEPYITAQLLN-----AVAQVGVAVEPFAFLSEDASAAE----\r\n"
        + "-----SVRPLAPTRVRSKGPLRVGFVSNVGFAGHPTGLLTVALFEALQRRQPDLM\r\n"
        + "HLFATSGDDGSTLRTRLAQASTLHDVTALGHLATAKHIRHHGIDLLFDLRGWGGGRPEV\r\n"
        + "FALRPAPVQVNWLAYPGTSGAPWMDYVLGDAFALPPALEPFYSEHVLRLQGAQFQPSDTSR\r\n"
        + "VVAEPPSRTQCGLPEQGVVLCFNNYSYKLNQSMARMLAVLREVPDSVLWLLSGPGEADA\r\n"
        + "RLRAFAHAQGVDAQRLVFMKPLPHPQYLARYRHADLFLDTHPYNAHTTASDALWTGCPVL\r\n"
        + "TTPGETFAARVAGSLNHHGLGDEMNVADDAAFVAKAVALASDPAALTALHARVDVLRRES\r\n"
        + "GVFEMDGFADDFGALLQALARRHGWLGI\r\n"
        + "\r\n"
        + ">Noname      \r\n"
        + "-MTADGPRELLQLRAAVRHRPQDVAWMLLADAELGMGDTTAGEMAVQRGLLALHPGHPEAV\r\n"
        + "ARLGRVVRWTQQRHAEAAVLLQQASDAAPEHPGIALWLGHAELED-----HQL\r\n"
        + "LPEEPYITAQLDVLSAQVR-----AAVAQVGVAVEPFAFLSEDASAAEQLAC\r\n"
        + "ARTRAQAI AASVRPLAPTRVRSKGPLRVGFVSNVGFAGHPTGLLTVALFEALQRRQPDLM\r\n"
        + "HLFATSGDDGSTLRTRLAQASTLHDVTALGHLATAKHIRHHGIDLLFDLRGWGGGRPEV\r\n"
        + "FALRPAPVQVNWLAYPGTSGAPWMDYVLGDAFALPPALEPFYSEHVLRLQGAQFQPSDTSR\r\n"
        + "VVAEPPSRTQCGLPEQGVVLCFNNYSYKLNQSMARMLAVLREVPDSVLWLLSGPGEADA\r\n"
        + "RLRAFAHAQGVDAQRLVFMKPLPHPQYLARYRHADLFLDTHPYNAHTTASDALWTGCPVL\r\n"
        + "TTPGETFAARVAGSLNHHGLGDEMNVADDAAFVAKAVALASDPAALTALHARVDVLRRES\r\n"

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AAConWSClientExample.java

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+ "I-----";

public static void main(String[] args) throws UnsupportedOperationException,
    JobSubmissionException, WrongParameterException,
    FileNotFoundException, IOException, ResultNotAvailableException,
    InterruptedException {

    /*
     * Annotation interface for AAConWS web service instance
     */
    Annotation<AACon> client = (Annotation<AACon>) Jws2Client.connect(
        "http://www.compbio.dundee.ac.uk/aacon", Services.AAConWS);

    /* Get the list of available presets */
    PresetManager presetman = client.getPreset();

    /* Get the Preset object by preset name */
    Preset preset = presetman.getPresetByName("Complete conservation");

    /*
     * Load sequences in FASTA format from the file You can use something
     * like new FileInputStream() to load sequence from the file
     */
    List<FastaSequence> fastalist = SequenceUtil
        .readFasta(new ByteArrayInputStream(input.getBytes()));

    /*
     * Submit loaded sequences for an alignment using preset. The job
     * identifier is returned by this method, you can retrieve the results
     * with it sometime later.
     */
    String jobId = client.presetAnalyze(fastalist, preset);

    /* This method will block for the duration of the calculation */
    Set<Score> result = client.getAnnotation(jobId);

    /*
     * This is a better way of obtaining results, it does not involve
     * holding the connection open for the duration of the calculation,
     * Besides, as the University of Dundee public server will reset the
     * connection after 10 minutes of idling, this is the only way to obtain
     * the results of long running task from our public server.
     */
    // while (client.getJobStatus(jobId) != JobStatus.FINISHED) {
    // Thread.sleep(1000); // wait a second, then recheck the status
    // }

    /* Output the alignment to standard out */
    Score.write(result, System.out);

    /* Alternatively, you can record retrieved alignment into the file */
    // FileOutputStream out = new FileOutputStream("result.txt");
    // Score.write(result, out);
    // out.close();
}
}

```