```
cwlVersion: v1.0
                                                                                                                                        cwlVersion: v1.0
cwlVersion: v1.0
                                                     class: CommandLineTool
                                                                                                                                       class: Workflow
class: CommandLineTool
                                                     doc: Spoa is a partial order aligment...
inputs:
                                                                                                                                       inputs:
                                                                                                 1. Community Maintained
  readsFA: File
                                                     inputs:
                                                                                                                                          pattern: string
                                                                                                    File Format Identifier
                                                       readsFA:
                                                                                                                                          sample data: File[]
                                                        type: File
baseCommand: spoa
                                                        format: edam:format 1929
                                                        doc: FASTA file containing a set of sequences...
                                                                                                                                        steps:
arguments: [ $(inputs.readsFA), -G, -g, '-6' ]
                                                                                                         2. Software Container
                                                     requirements:
                                                                                                                                          find matches:
                                                      InlineJavascriptRequirement: {}
outputs:
                                                                                                                                             run: grep.cwl
                                                     hints:
                                                                                                                    spoaGFA:
                                                                                                                                             in:
                                                       DockerRequirement:
    type: stdout
                                                        dockerPull: "quay.io/biocontainers/spoa:3.4.0--hc9558a2 0"
                                                                                                                                               pattern: pattern
                                                       ResourceRequirement:
                                                                                                                                               files: sample data
                                                        ramMin: $(15 * 1024)
                                                                                                                                             out: [ text matches ]
                                                        outdirMin: $(Math.ceil(inputs.readsFA.size/(1024*1024*1024) + 20))
                                                     baseCommand: spoa
                                                                                                   3. Dynamic Resource
                                                                                                                                          count lines:
                                                                                                       Requirements
                                                     arguments: [ $(inputs.readsFA), -G, -g, '-6' ]
                                                                                                                                             run: wc.cwl
                                                                                                                                             in:
                                                     stdout: $(inputs.readsFA.nameroot).g6.gfa
                                                                                                                                               file: find matches/text matches
                                                     outputs:
                                                                                                                                             out: [ lines ]
                                                       spoaGFA:
                                                        type: stdout
                                                                                                                                       outputs:
                                                        format: edam:format 3976
                                                        doc: result in Graphical Fragment Assembly (GFA) format
                                                                                                                                          number of matches:
                                                                                                                                             type: int
                                                     $namespaces:
                                                В
                                                                                                                                             outputSource: count lines/lines
                                                       edam: http://edamontology.org
```