

**A**

```
cwlVersion: v1.0
class: CommandLineTool

inputs:
  readsFA: File

baseCommand: spoa

arguments: [ $(inputs.readsFA), -G, -g, '-6' ]

outputs:
  spoaGFA:
    type: stdout
```

**B**

```
cwlVersion: v1.0
class: CommandLineTool

doc: Spoa is a partial order alignment...

inputs:
  readsFA:
    type: File
    format: edam:format_1929
    doc: FASTA file containing a set of sequences

requirements:
  InlineJavascriptRequirement: {}
hints:
  DockerRequirement:
    dockerPull: "quay.io/biocontainers/spoa:3.4.0--hc9558a2_0"
  ResourceRequirement:
    ramMin: $(15 * 1024)
    outdirMin: $(Math.ceil(inputs.readsFA.size/(1024*1024*1024) + 20))

baseCommand: spoa

arguments: [ $(inputs.readsFA), -G, -g, '-6' ]

stdout: $(inputs.readsFA.nameroot).g6.gfa

outputs:
  spoaGFA:
    type: stdout
    format: edam:format_3976
    doc: result in Graphical Fragment Assembly (GFA) format

$namespaces:
  edam: http://edamontology.org
```

1. Community Maintained  
File Format Identifier

2. Software Container



3. Dynamic Resource  
Requirements