```bash
#!/usr/bin/bash

# set sample id
sampleid=$1

# set name of stage
stagename=$2

# set sample working directory. Example: /path/to/Y100
sampledir=$3
# if the directory does not exist, create a new one
if [ ! -d ${sampledir} ];then
    sudo mkdir -p ${sampledir}
fi


cd ${sampledir}

# set full path to the working directory for the stage. Example: /
path/to/Y100/ANNOTATE
stagedir=$4
# if the directory does not exist, create a new one
if [ ! -d ${stagedir} ];then
    sudo mkdir -p ${stagedir}
fi


# set full path to the input fasta file with all the contigs.
Example: /path/to/Y100/Y100_suspicious_contigs.fa
inputfile=$5
grep '>' < ${inputfile} > suspicious_contigs_titles.txt

# set database directory and name
db=/Users/helloalina/desktop/ncbi-blast-2.11.0+/bin/blastdb/testdb


# run blastn
source ~/opt/anaconda3/bin/activate bader
python /Users/helloalina/desktop/jhuardian_annotator.py --max_seqs 5
--queryfile ${inputfile} --outdir ${stagedir} --
blast_outputfile_basename results.xml --blastdb ${db} --blastcmd /
Users/helloalina/desktop/ncbi-blast-2.11.0+/bin/blastn --stage $
{stagename} --sample ${sampleid} --titles
suspicious_contigs_titles.txt

conda deactivate
```