

The **Whisky** application can be downloaded from:

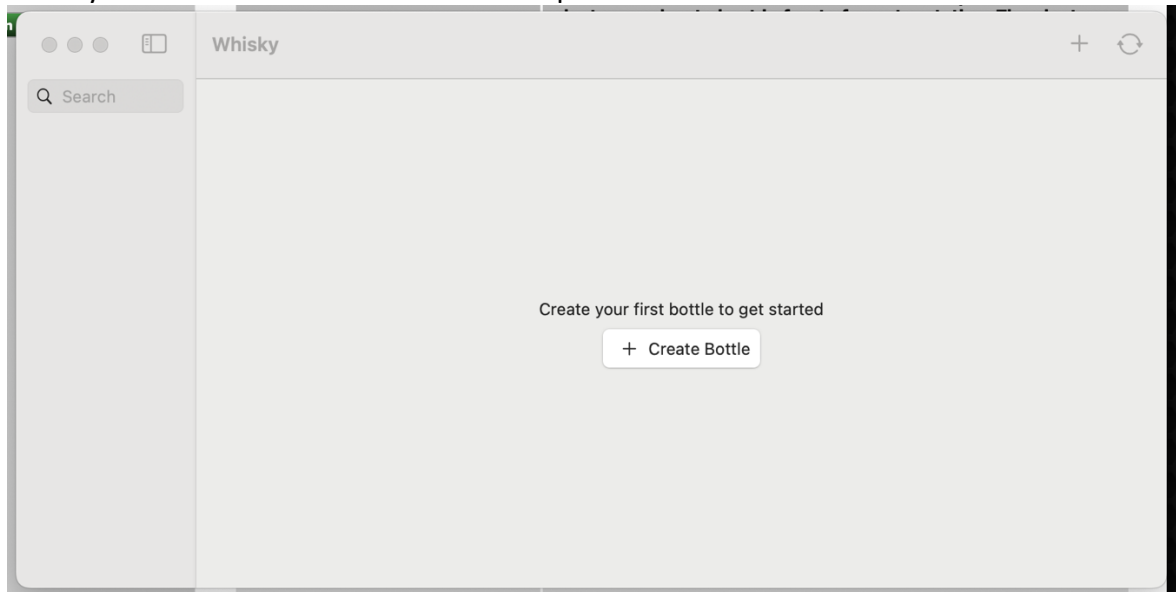
<https://getwhisky.app/>

Tested confirmed features:

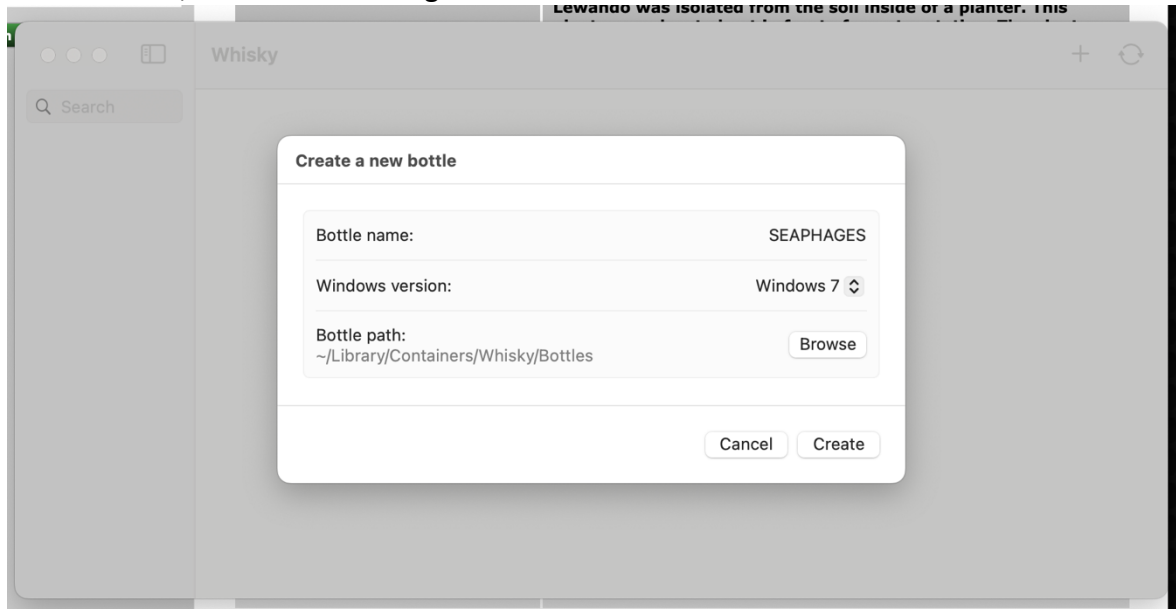
- Preferences are saved between launches
- Auto update to 2705
- Gene starts called the same way
- BLAST connections work
- Fasta/dnam5 files can be easily saved and are accessible directly through **Finder** for sharing (**Open C: drive** on startup screen)
- Maximum RAM usage at 900MB, Maximum disk usage below 1.4GB

Double click the Whisky.zip to extract then double click the Whisky application to start. Allow opening if you get a security warning and follow auto install instructions for any dependencies Whisky finds are missing (~30-60s).

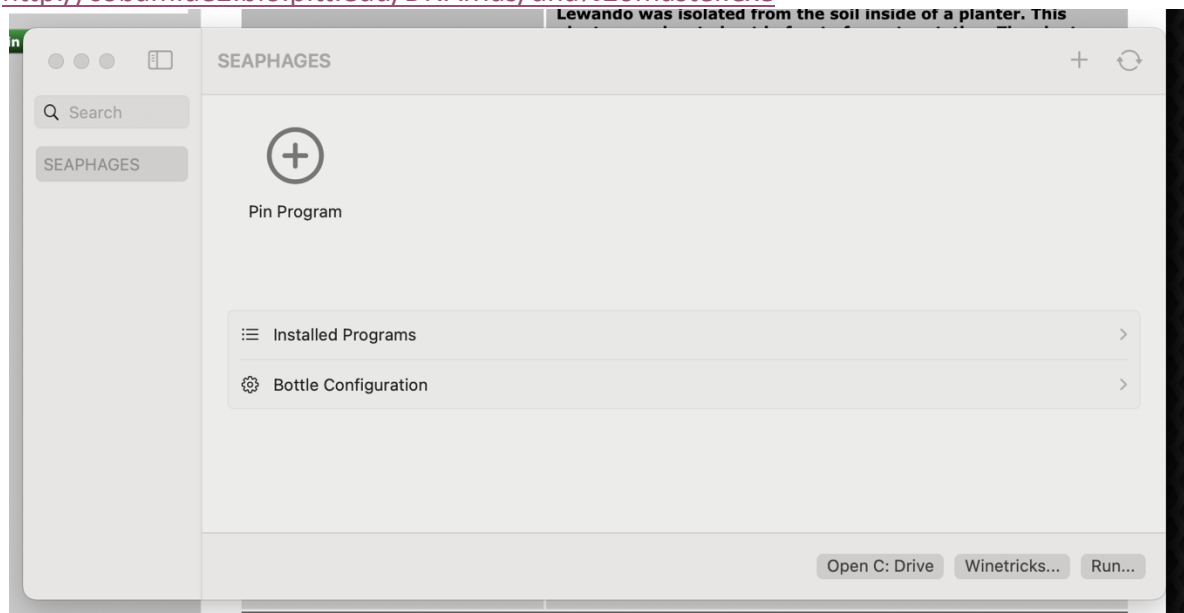
Whisky start screen after auto-install of dependencies



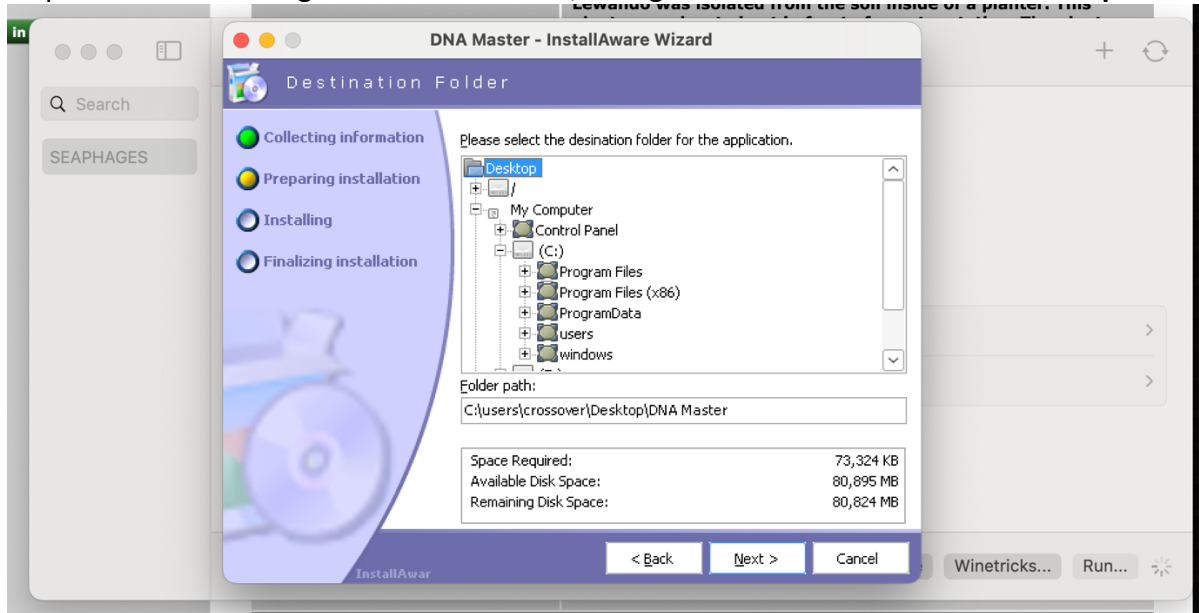
Create Bottle, name it something familiar and select **Windows 7** as the Windows version:



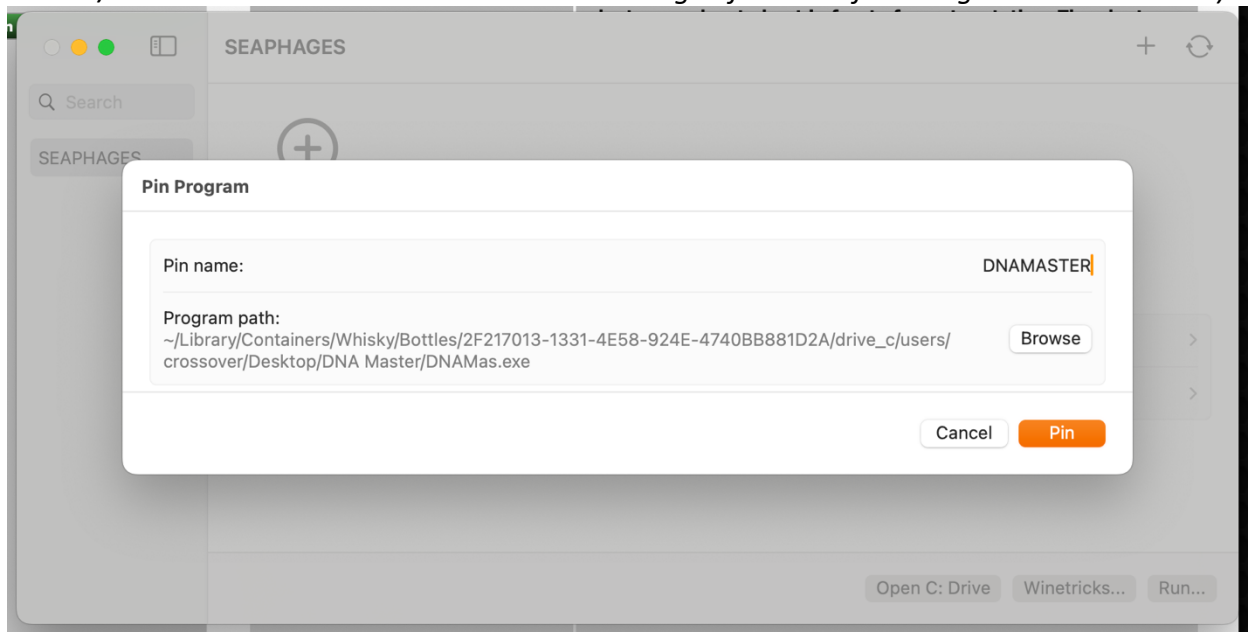
The first initialization can take a minute or two. Then select **Run...** and point the software to the **dna master.exe installer** (not the DNAMas.exe re use to run the software later.) available at <http://cobamide2.bio.pitt.edu/DNAMas/dna%20master.exe>



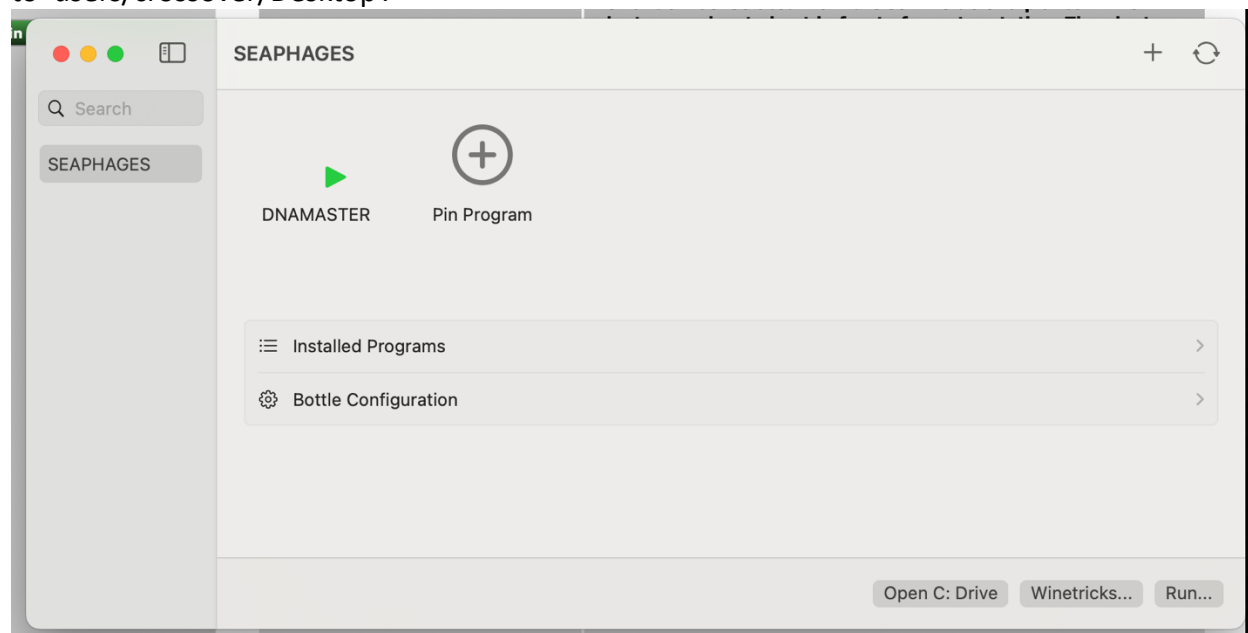
As per the installation guide on SEAPHAGES, change the destination folder to **Desktop**.



After install, you can use the **Pin Program** option to make the software easier to access. Label the Pin name and navigate to the **Desktop/DNA Master** folder if you followed the instructions in the last step. (*note: the path shown below has a unique bottle ID which will be different on different systems but the overall structure of Library/Containers/Whisky/Bottles/*****/drive_c/users/crossover/Desktop/DNA Master/DNAMas.exe should be the same when using default and following these instructions.*)



Once this is done, it allows us to double click the new pin **DNAMASTER** (or right click and select **Run...**) to start DNAMaster. Files can be saved and read from anywhere on the Mac, if using the **Desktop** folder from the app, the easiest way to access it is to click **Open C: Drive** and navigate to 'users/crossover/Desktop'.



From there, follow the guide to set up **Preferences**

For comparison, I followed the equivalent steps in a Dell Latitude 5420 running Windows 11 and we get the same gene starts and BLAST results to confirm everything is working (shown below)

Features and BLAST on Windows for phage Lewando

Score	Description	Accession	GI	Length	Max Score
383	hypothetical protein SEA_LEWANDO_9 [Arthrobacter phage Lewando]	WNN94513	116	383	
165	hypothetical protein PBL_SPORTO_10 [Arthrobacter phage Sporto]				
157	hypothetical protein PBL_STAYER_9 [Arthrobacter phage Stayer] > gblQ				
144	hypothetical protein PP914_gp021 [Arthrobacter phage Qui] > gblQED11				
115	gp018 [Rhodococcus phage ReqPoco6] > gbADD81016.11 gp018 [Rhx				
104	hypothetical protein HwC78_gp14 [Gordonia phage Avazak] > gblQIGJ8				
106	hypothetical protein SEA_GIANTSBBANE_9 [Arthrobacter phage Giantst				
103	hypothetical protein SEA_CATERPILLAR_10 [Arthrobacter phage Cater				
103	hypothetical protein SEA_MEDIUMFRY_10 [Arthrobacter phage Mediu				

High-Scoring Pair (HSP)

Query	Target	Positives	Identity	Similarity	% Aligned	Gaps
1 - 116	1 - 116	116	116	100.0	100.0	0

Raw BLAST Output:

```

1  MDMEEALND FLMHYGVKGM KWKGHASKAD YKSSVKSHRK ELYKGVGVQV
1  |||
1  MDMEEALND FLMHYGVKGM KWKGHASKAD YKSSVKSHRK ELYKGVGVQV
51  KSKTQXXXXX XXXXXXXXXX XXXXXXXXXX GAGYSKSKSX XXXXXXXXXX
51  |||
51  KSKTQGVFAV AGTLLGGGAG SATVGVQSHR GAGYSKSKSL ANGLLGGAG
101  XXIAIEVKAR RNAAED
  
```

Features and BLAST on Whisky for phage Lewando

DNA Master

File Tools Window Help

Extracted from FastA Library Lewando.fasta

Overview Features References Sequence Documentation

Sort By Index

Select Features Direct SQL

Type is All

Name like

GenelD =

Locus like

Start >

Length >

Regions >

% GC <

CAI >

EC# like

Product like

Function like

FeatureID =

Tag like

☐ Hide Ignored Fea

Select All Featu

Name	5' End	Length
1	334	294
2	733	378
3	1292	150
4	1530	981
5	2510	165
6	2667	372
7	3011	513

There are no BLAST results for this feature

QBLAST against public database via NCBI server

Blast this gene Blast ALL Genes Clear All

Local Blast against DNA Master database

Blast this gene Blast ALL Genes

BLAST search for 5419 - 5769 (9)

Retrieve XML Results Text Results Save to Database

Score	Description
383	hypothetical protein SEA_LEWANDO_9 [Arthrobacter phage Lewando]
165	hypothetical protein PBL_SPORTO_10 [Arthrobacter phage Sporto]
157	hypothetical protein PBL_STAYER_9 [Arthrobacter phage Stayer] >gbIQ
144	hypothetical protein PP914_gp021 [Arthrobacter phage Qui] >gbIQED11
115	gp018 [Rhodococcus phage ReqiPoco6] >gbADD81016.1 gp018 [Rho
104	hypothetical protein HWC78_gp14 [Gordonia phage Avazak] >gbIQGJ8
106	hypothetical protein SEA_GIANTSBBANE_9 [Arthrobacter phage Giantsb
103	hypothetical protein SEA_CATERPILLAR_10 [Arthrobacter phage Cater
103	hypothetical protein SEA_MEDIUMFRY_10 [Arthrobacter phage Medium

BLAST Hit

Accession WNN94513

GI

Length 116

Max Score 383

HSP Coverage Map

High-Scoring Pair (HSP)

Bit Score	Score	E-Value	Query	Target	Positives	Identity	Similarity	Gaps
152.141	383	8.4E-45	1 - 116	1 - 116	116	116	100.0	0

% Aligned 100.0

1 MDMMNEEALND FLMHYGVKCM KWGKHASKAD YKSSVKSHRK ELYKGVCGQV

1 |||

1 MDMMNEEALND FLMHYGVKCM KWGKHASKAD YKSSVKSHRK ELYKGVCGQV

51 KSKKQVGVFAV AGTLLGGCAG SATVGVQHMIR GAGYSKCKSL AMGLLGCAF

51 |||

51 KSKKQVGVFAV AGTLLGGCAG SATVGVQHMIR GAGYSKCKSL AMGLLGCAF

101 XOXIAIEVKAR KHAKED

Peak Hours

1 - 50000 Position: 39877

☒ Controls >> Map ☒ Map >> Controls

87 Features Live

55075

Accession ☐ Favorite Genome Recent Genome Recent File ☐ ATG ☐ OD 9 Events Start DNA Master as specified above