

# Gene Normalizer: A Tool to Resolve Genetic Ambiguity Through Data Harmonization



Anastasia Bratulin<sup>1</sup>, James Stevenson<sup>2</sup>, Kori Kuzma<sup>2</sup>, Matthew Cannon<sup>2</sup>, Wesley Goar<sup>2</sup>, Alex Wagner<sup>2</sup>

The Ohio State University, Columbus, OH, <sup>2</sup>The Steve and Cindy Rasmussen Institute for Genomic Medicine, Nationwide Children's Hospital, Columbus, OH

## **Problem 1: Alias-Gene Intersections**

# Alias-Gene Intersections describe when the same gene symbol is used in a primary gene symbol category as well as an alias category for two distinct genes.

	HGNC Gene Symbol	Aliases	
n	NRAS	NS6, CMNS, KRAS N-ras, NCMS, NRAS1, ALPS4	
/ IS	KRAS	NS, NS3, OES, CFC2, RALD, K-Ras, KRAS1, KRAS2	

Source	Total # of gene records	# of records with alias- gene intersections
Ensembl	40354	266 (0.6%)
HGNC	43164	483 (1.1%)
NCBI Gene Info	75346	2394 (3.2%)

Figure 1. Alias-Gene Intersection illustration using two genes.

**Figure 2.** Evidence of Alias-Gene Intersections across three different sources.

# **Problem 2: Alias-Alias Intersections**

Alias-Alias				
Intersections				
describe when the				
same gene				
symbol is used in				
the alias category				
for multiple				
distinct genes.				

	HGNC	Aliases
	Gene Symbol	
3	IGHM	AGM1, MU, VH
		10111/04
7	IGHV6-1	IGHV61, VH
	SLC7A4	HCAT3, CAT-4, VH

Source	Total # of gene records	# of records with a shared alias
Ensembl	40354	3075 (7.6%)
HGNC	43164	2084 (4.83%)
NCBI Gene Info	75346	2957 (3.92%)

**Figure 3.** Alias- Alias Intersection illustration using three genes.

**Figure 4.** Evidence of Alias-Alias Intersections across three different sources.

### Alias-Alias Intersection Distribution per Data Source

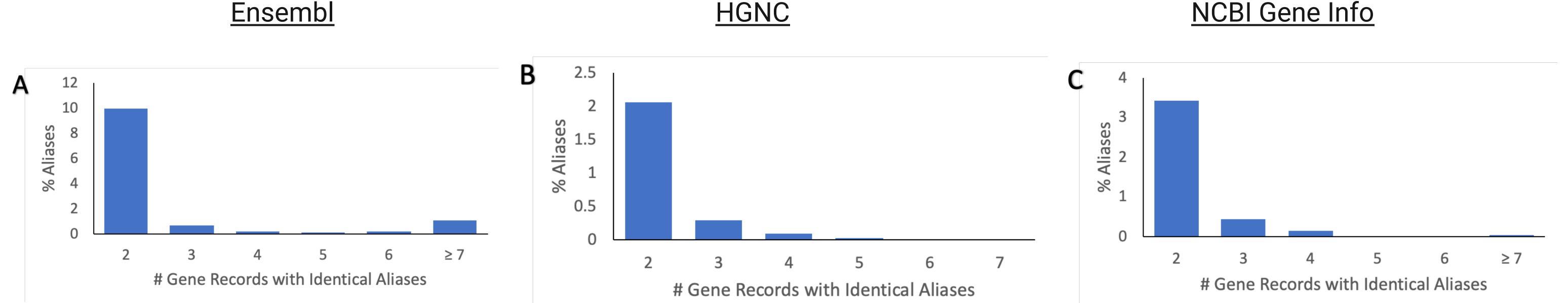


Figure 5. Percentage of aliases in each source that are shared amongst two gene records or more.

### **Future Directions: Gene Normalizer**

Using policies that prioritize the gene symbol category (Problem 1) and identify aliases that are family groups (Problem 2), allows the Gene Normalizer to systematically blend data from different sources into one cohesive construct.

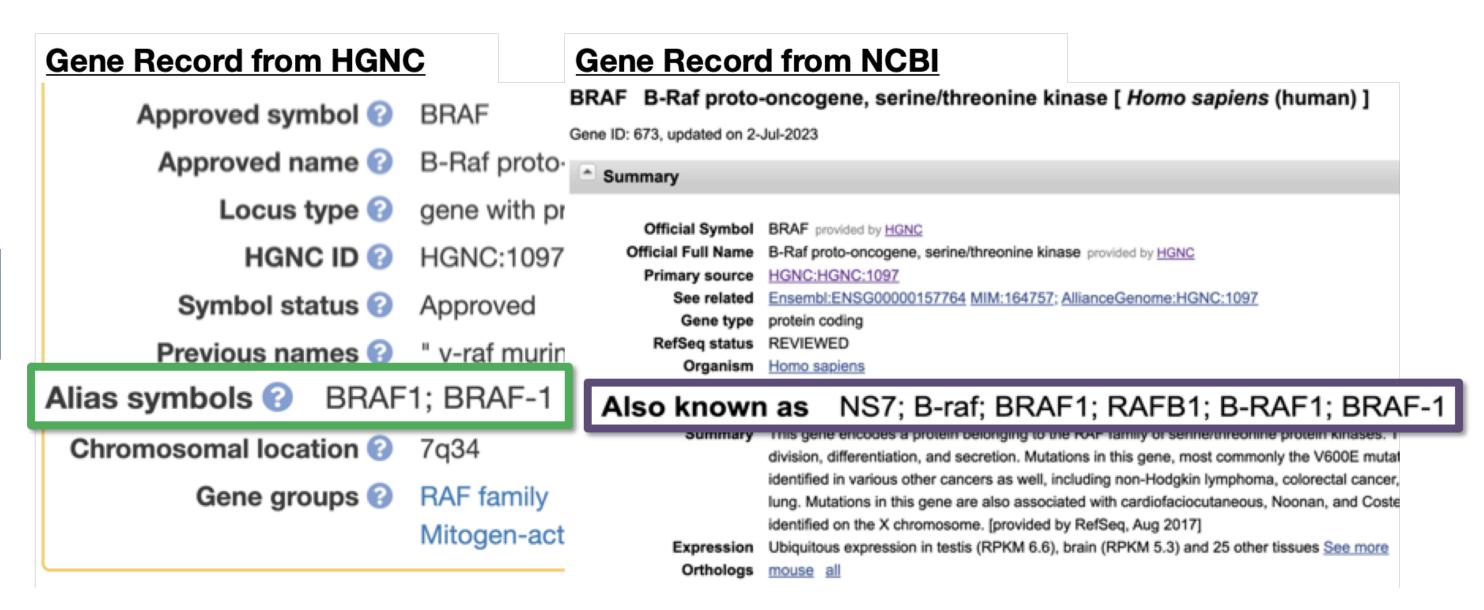
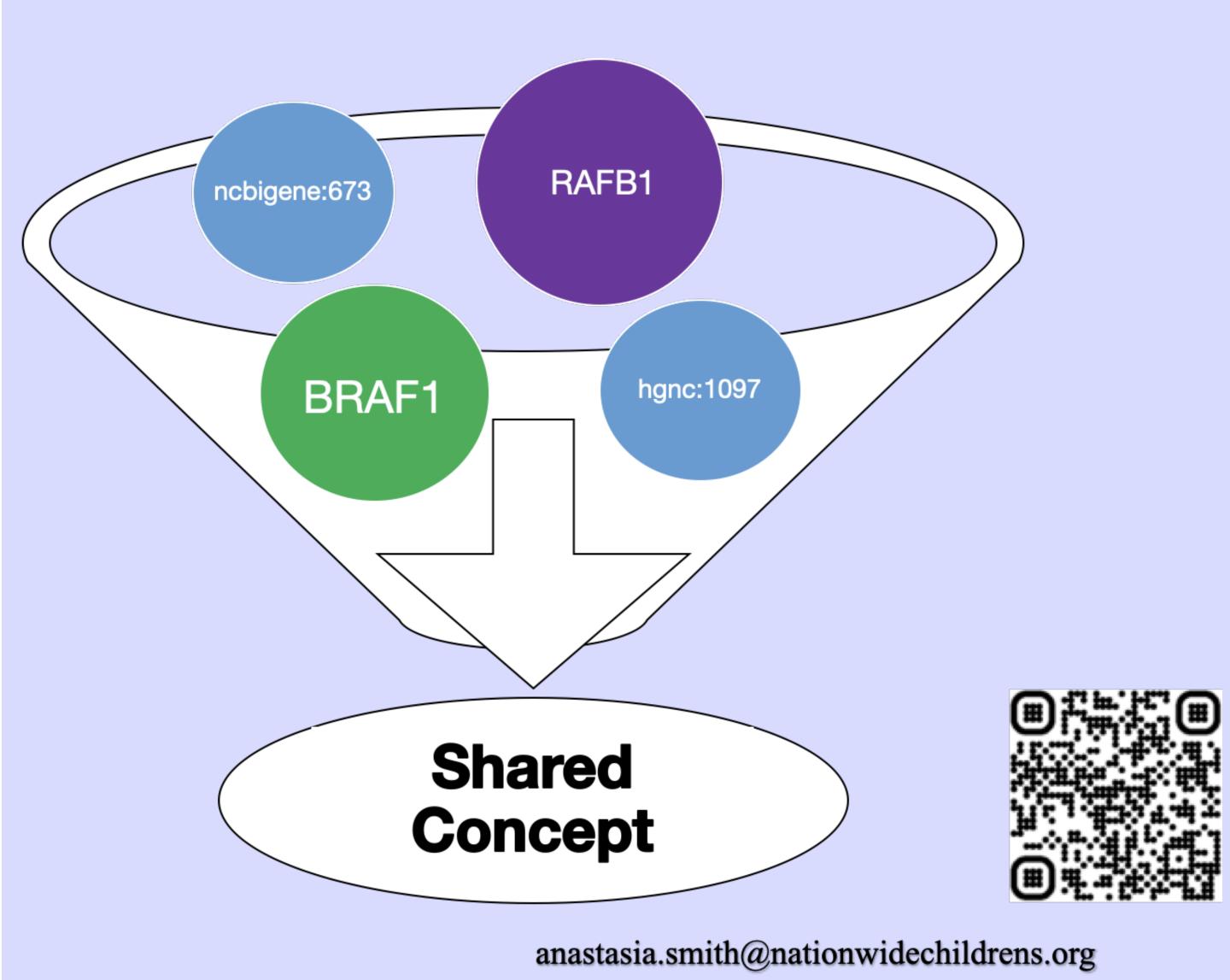


Figure 6. Gene records from different sources.



**Figure 7.** The Gene Normalizer - identifying a shared concept supports a publicly accessible normalization service at <u>normalize.cancervariants.org/gene</u>