**Supplementary Methods:**

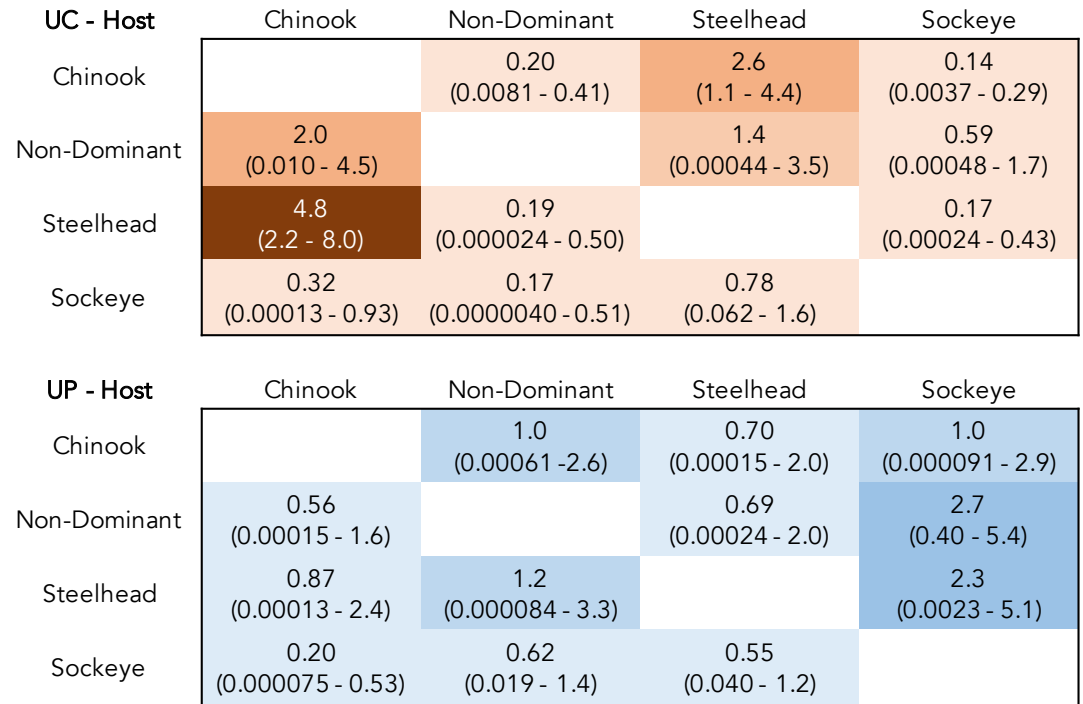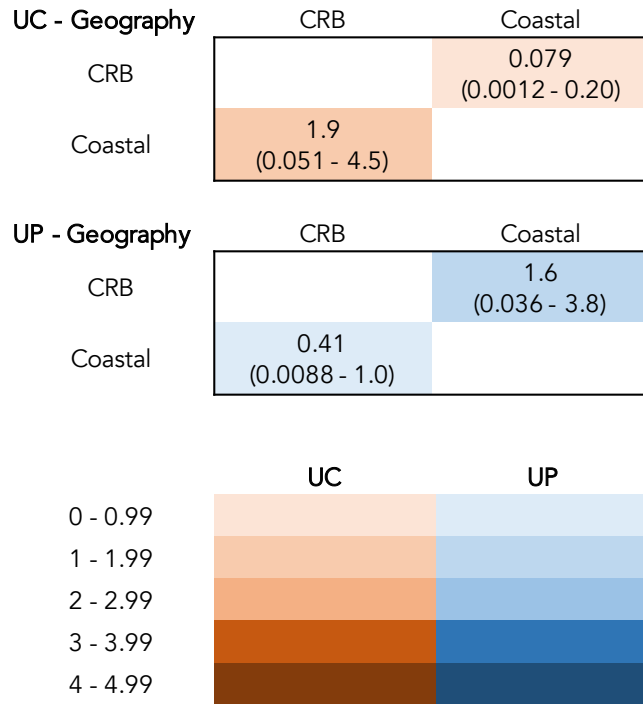*Generation of equitably subsampled dataset*

To assess the robustness of our phylogeographic analysis to sampling biases we subsampled the primary events dataset ($n = 619$) to create a more equitable distribution of the number of samples per year per host per geographic range. Using a Python script we binned samples of like year, host, and geography. For bins with less than 5 events, all events were selected into the subsampled events dataset. For bins with greater than 5 events we randomly selected 5 events for the subsampled dataset. Supplemental Table 1 compares the number of events by geography and by host between the two datasets.

Supplemental Table 1: Comparison of numbers of events between the primary dataset and the subsampled dataset by geographic range and by host species. Steelhead trout includes steelhead trout and rainbow trout (both *O. mykiss*). Sockeye salmon includes sockeye salmon and kokanee salmon (both *O. nerka*).

	Primary Dataset (n=619)	Subsampled Dataset (n=380)
Geography		
Coastal watersheds	131	114
Columbia River Basin	488	266
Ratio	1 to 3.73	1 to 2.33
Host		
Chinook salmon	295	119
Steelhead trout	163	117
Sockeye salmon	123	107
Ratio	2.40 to 1.33 to 1	1.11 to 1.09 to 1
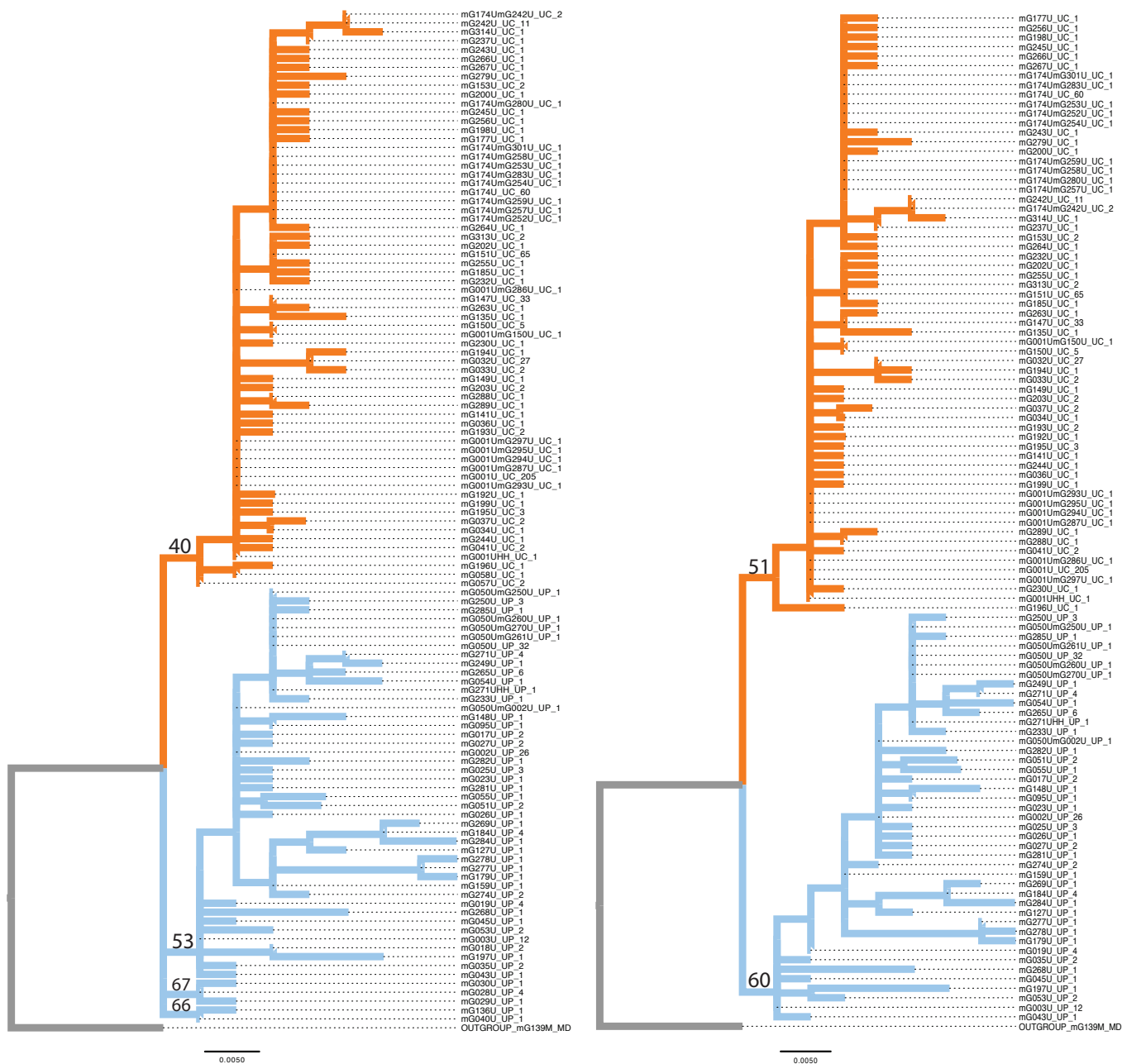
Supplemental Figure 1: Impact of removing wandering taxa from the maximum likelihood phylogenetic analysis. The tree on the left represents all 114 unique genotypes. The tree on the right has 8 wandering taxa removed, increasing the bootstrap support on the UC basal node from 40 to 51 and on the primary UP basal node from 53 to 60. UC viruses are colored orange, UP viruses are colored blue, and the outgroup is colored grey.

UC - Geography

	CRB	Coastal
CRB		0.079 (0.0012 - 0.20)
Coastal	1.9 (0.051 - 4.5)	

UP - Geography

	CRB	Coastal
CRB		1.6 (0.036 - 3.8)
Coastal	0.41 (0.0088 - 1.0)	

	UC	UP
0 - 0.99		
1 - 1.99		
2 - 2.99		
3 - 3.99		
4 - 4.99		

UC - Host

	Chinook	Non-Dominant	Steelhead	Sockeye
Chinook		0.20 (0.0081 - 0.41)	2.6 (1.1 - 4.4)	0.14 (0.0037 - 0.29)
Non-Dominant	2.0 (0.010 - 4.5)		1.4 (0.00044 - 3.5)	0.59 (0.00048 - 1.7)
Steelhead	4.8 (2.2 - 8.0)	0.19 (0.000024 - 0.50)		0.17 (0.00024 - 0.43)
Sockeye	0.32 (0.00013 - 0.93)	0.17 (0.0000040 - 0.51)	0.78 (0.062 - 1.6)	

UP - Host

	Chinook	Non-Dominant	Steelhead	Sockeye
Chinook		1.0 (0.00061 - 2.6)	0.70 (0.00015 - 2.0)	1.0 (0.000091 - 2.9)
Non-Dominant	0.56 (0.00015 - 1.6)		0.69 (0.00024 - 2.0)	2.7 (0.40 - 5.4)
Steelhead	0.87 (0.00013 - 2.4)	1.2 (0.000084 - 3.3)		2.3 (0.0023 - 5.1)
Sockeye	0.20 (0.000075 - 0.53)	0.62 (0.019 - 1.4)	0.55 (0.040 - 1.2)	

Supplemental Figure 2: Mean estimated transition rates (in events per lineage per year) and 95%HPDs based on ancestral state reconstruction for geographic range and host species for UC viruses (orange) and UP viruses (blue). For geographic range CRB denotes the Columbia River Basin and coastal denotes the coastal watersheds geographic range. For host, Sockeye includes both sockeye and kokanee salmon, and Steelhead includes both steelhead and rainbow trout. Non-dominant includes coho salmon, chum salmon, and Atlantic salmon. Transition direction is from the row trait to the column trait (e.g. the transition rate of UC viruses from the Columbia River Basin to coastal watersheds is 0.079 events per lineage per year).
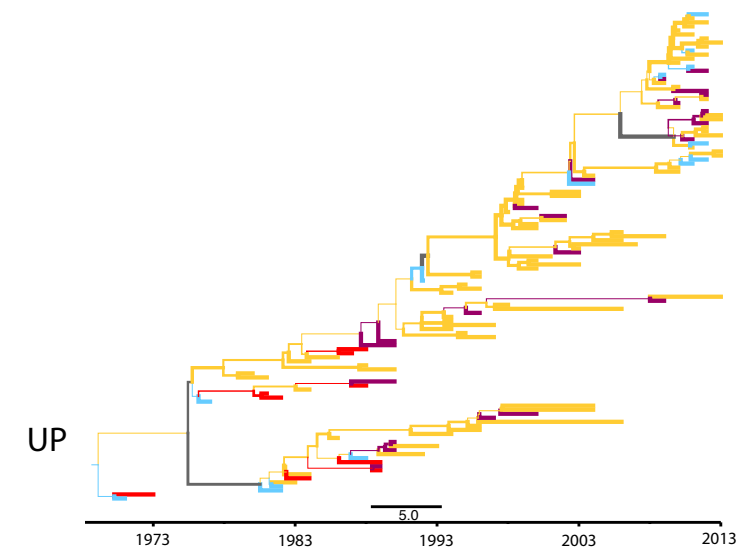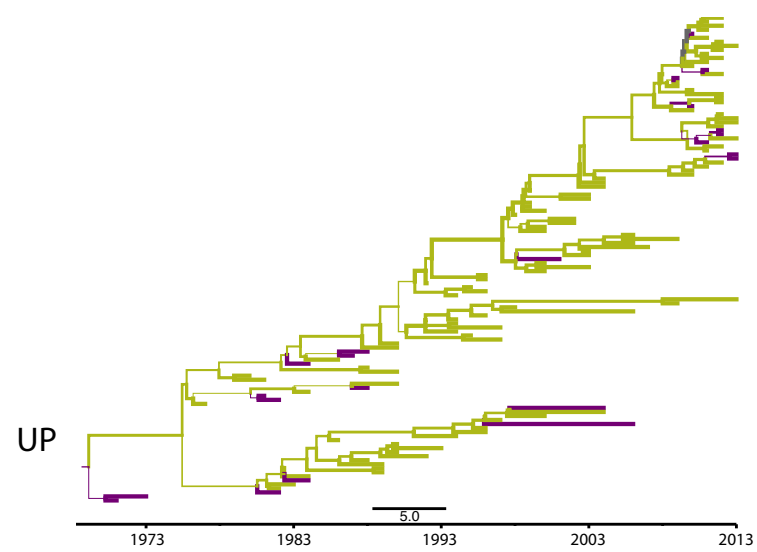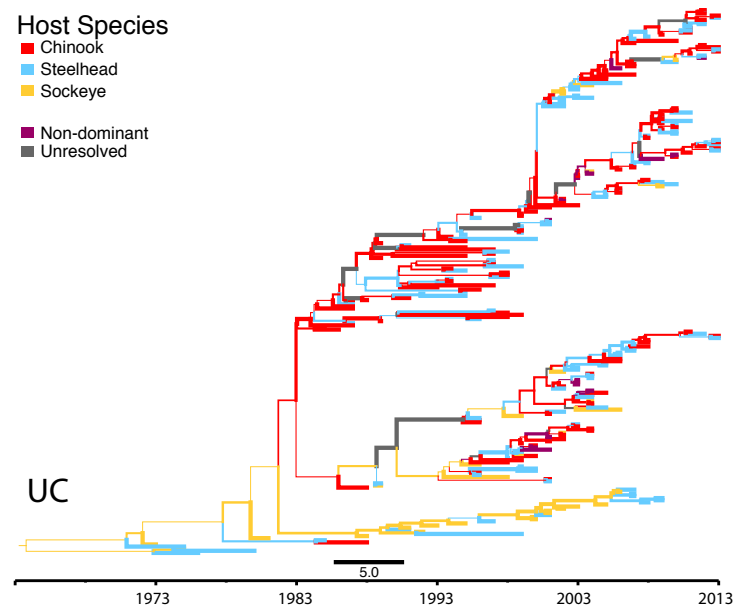
Geographic Range
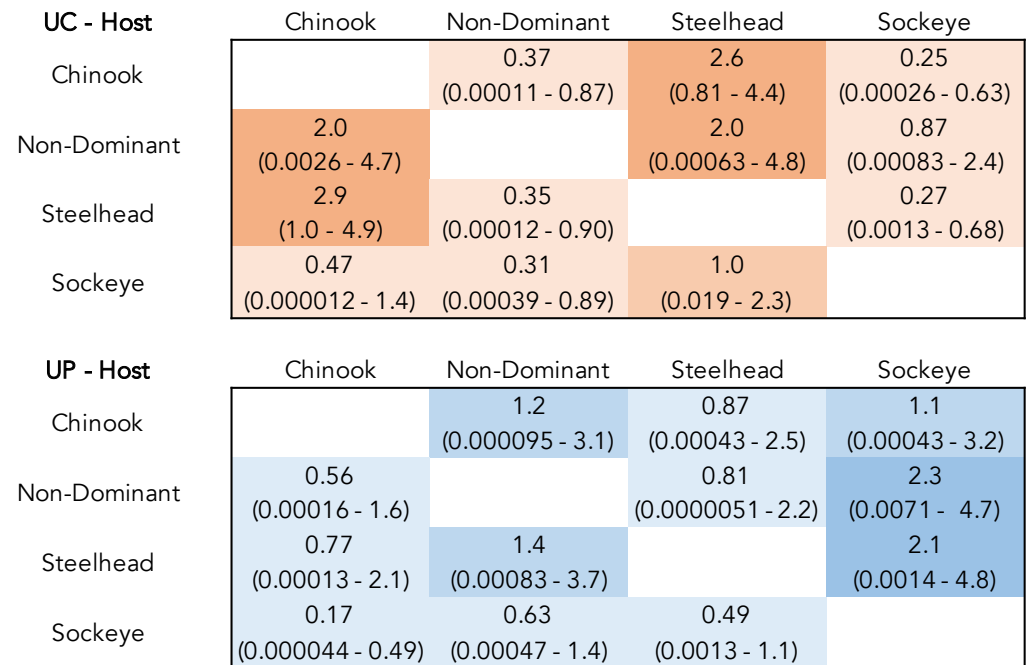- Columbia River Basin
- Coastal watersheds
- Unresolved
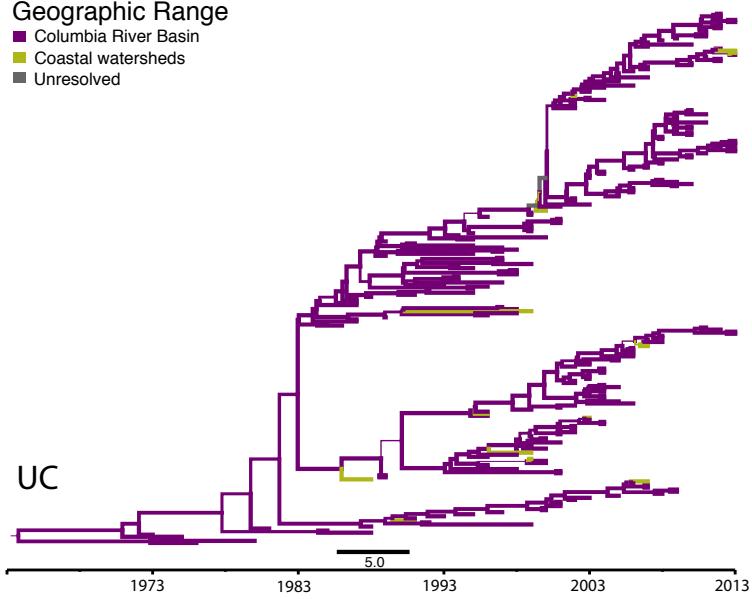
Host Species
- Chinook
- Steelhead
- Sockeye
- Non-dominant
- Unresolved

Supplemental Figure 3: Coalescent phylogenetic trees reconstructed from the equitably subsampled events dataset showing ancestral geographic range on the left and ancestral host on the right. Steelhead includes steelhead and rainbow trout and sockeye includes both sockeye salmon and kokanee salmon. Non-dominant includes coho salmon, chum salmon, and Atlantic salmon. Line weights are scaled according to the probability of being in that state; thicker lines indicate a higher probability.

UC - Geography

	CRB	Coastal
CRB		0.13 (0.0020 - 0.33)
Coastal	1.9 (0.048 - 4.6)	

UP - Geography

	CRB	Coastal
CRB		1.7 (0.034 - 3.8)
Coastal	0.37 (0.0047 - 0.91)	

	UC	UP
0 - 0.99		
1 - 1.99		
2 - 2.99		
3 - 3.99		
4 - 4.99		

UC - Host

	Chinook	Non-Dominant	Steelhead	Sockeye
Chinook		0.37 (0.00011 - 0.87)	2.6 (0.81 - 4.4)	0.25 (0.00026 - 0.63)
Non-Dominant	2.0 (0.0026 - 4.7)		2.0 (0.00063 - 4.8)	0.87 (0.00083 - 2.4)
Steelhead	2.9 (1.0 - 4.9)	0.35 (0.00012 - 0.90)		0.27 (0.0013 - 0.68)
Sockeye	0.47 (0.000012 - 1.4)	0.31 (0.00039 - 0.89)	1.0 (0.019 - 2.3)	

UP - Host

	Chinook	Non-Dominant	Steelhead	Sockeye
Chinook		1.2 (0.000095 - 3.1)	0.87 (0.00043 - 2.5)	1.1 (0.00043 - 3.2)
Non-Dominant	0.56 (0.00016 - 1.6)		0.81 (0.0000051 - 2.2)	2.3 (0.0071 - 4.7)
Steelhead	0.77 (0.00013 - 2.1)	1.4 (0.00083 - 3.7)		2.1 (0.0014 - 4.8)
Sockeye	0.17 (0.000044 - 0.49)	0.63 (0.00047 - 1.4)	0.49 (0.0013 - 1.1)	

Supplemental Figure 4: Mean estimated transition rates (in events per lineage per year) and 95%HPDs based on ancestral state reconstruction for geographic range and host species for the subsampled events dataset. Rates from UC viruses are shown in orange and UP viruses in blue. For geographic range CRB denotes the Columbia River Basin and coastal denotes the coastal watersheds geographic range. For host, Sockeye includes both sockeye and kokanee salmon, and Steelhead includes both steelhead and rainbow trout. Non-dominant includes coho salmon, chum salmon, and Atlantic salmon. Transition direction is from the row trait to the column trait.

Supplemental Table 2: Contingency table displaying numbers of IHNV events by host species and geographic range of detection.

		Geographic Range	
		Coastal	Columbia River Basin
Host Species	Chinook salmon	8	287
	Steelhead trout	18	145
	Sockeye salmon	84	39

Supplemental Table 3: Comparison of the descriptive ability of different logistic models of subgroup (UC or UP). Predictors of interest are 1) host species modeled as a categorical variable with three levels (sockeye salmon, steelhead trout, and Chinook salmon), 2) geographic range modeled as a binary variable (Columbia River Basin or coastal watersheds), and 3) an additive model including both host and geographic range. Despite high correlation between host and geography, the model with both predictors fits the best, as assessed by minimizing the Akaike information criterion (Akaike 1974).

Model	AIC
Subgroup ~ Host	356.12
Subgroup ~ Geographic Range	292.80
Subgroup ~ Geographic Range + Host	247.15

References

Akaike, H. (1974) "A New Look at the Statistical Model Identification." *IEEE Transactions on Automatic Control* 19 (6): 716–23. doi:10.1109/TAC.1974.1100705.