Organism	Pubmed ID	Citation	Distance	Clustering	Software
M. tuberculosis	22984400	PLoS One. 2012;7(9):e41991	Categorical	Bayesian (& MST)	MrBayes3 (& BioNumerics)
S. Enteritidis	23096767	Trop Anim Health Prod. 2012 Oct 25	Categorical	Not specified	BioNumerics
L. interrogans	23122311	Biomed Environ Sci. 2012 Oct;25(5):542-8	Categorical	UPGMA	BioNumerics
Y. pestis	23079835	Genet Mol Res. 2012 Sep 25;11(3):3414-24	Categorical	UPGMA	MEGA
A. baumannii	22984530	PLoS One. 2012;7(9):e44597	Clustering performed but no methods specified		
C. difficile	23052318	J Clin Microbiol. 2012 Dec;50(12):4078-82	Consecutive episodes with sum of tandem repeat differences ≤ 2 were defined as relapses, ≥ 3 were defined as reinfections.		
S. aureus	23078039	Clin Microbiol Infect. 2012 Sep 15	NA; 2 isolates		
S. Typhimurium	23153086	Commun Dis Intell. 2012 Mar 31;36(1):101-6.	NA; all strains differed by ±1 at single locus		
S. Enteritidis	23091125	Poult Sci. 2012 Nov;91(11):2727-35	NA; closely related defined as different at only one locus		BioNumerics
S. aureus	23100339	J Clin Microbiol. 2012 Oct 24	NA; compared only within-patient pairs		
L. monocytogenes	22997210	Clin Infect Dis. 2012 Oct 19	NA; identical patterns		
E. coli	23129461	Eur J Clin Microbiol Infect Dis. 2012 Nov 6	NA; not compared		
C. burnetii	22988998	BMC Vet Res. 2012 Sep 18	NA; small number of profiles, compared manually		

C. burnetii	23040417	Int J Med Microbiol. 2012 Nov;302(6):253-6	Not specified	Minimum spanning	Not specified
S. Enteritidis	23035725	Foodborne Pathog Dis. 2012 Oct;9(10):885-95	Not specified	UPGMA	BioNumerics (assumed as data was processed in BioNumerics)
Aspergillus flavus	23028503	PLoS One. 2012;7(9):e44204	Not specified; assume categorical based on ref. 18	UPGMA, Minimum spanning tree	BioNumerics (assumed as data was processed in BioNumerics)
S. pneumoniae	23088225	BMC Microbiol. 2012 Oct 22;12(1):241	Simple	Minimum spanning	BioNumerics
B. henselae	22956995	PLoS One. 2012;7(8):e43621	Simple	NJ (note also did MST with single-locus rule)	R (MST in BioNumerics)
S. enterica serovar 4,[5],12:i:-	22995432	Euro Surveill. 2012 Sep 13	Single or double LV rules	Minimum spanning	BioNumerics (assumed as data was processed in BioNumerics)

Table 1. Summary of 19 studies reporting MLVA data, published in a 4-month period (August – November 2012)

Clustering using categorical distance: 4
Clustering using simple distance: 3
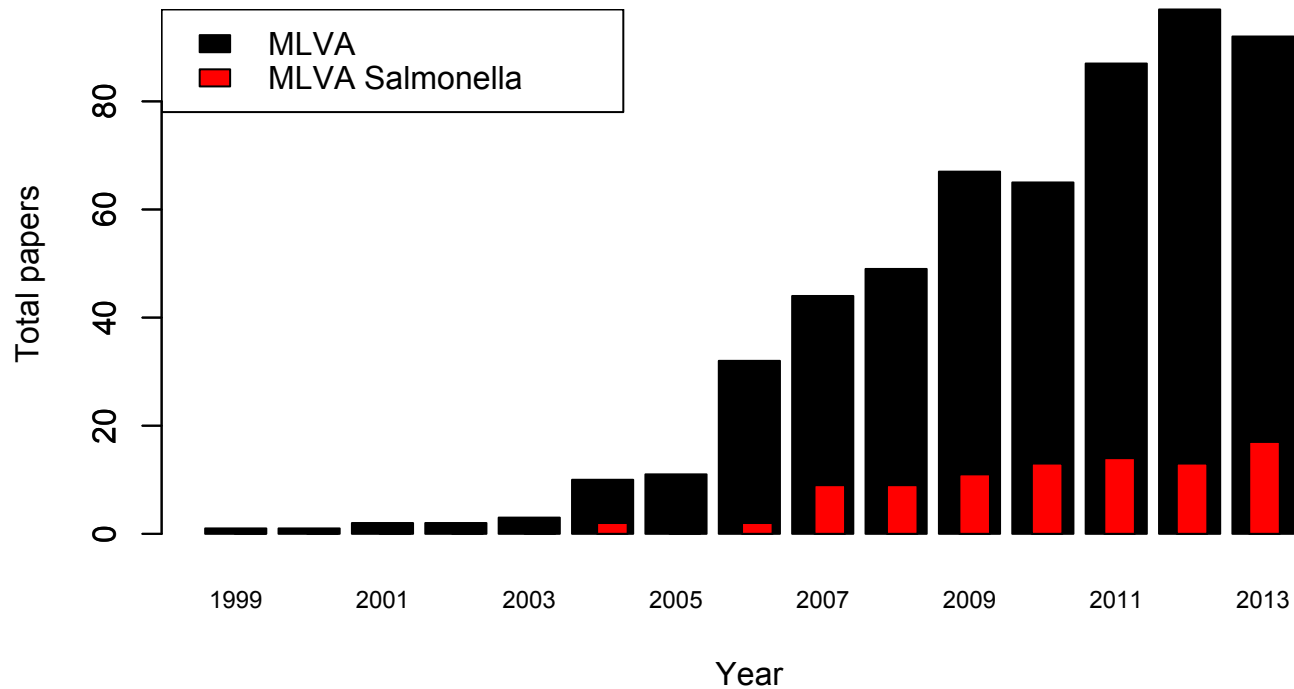Clustering results reported but no methods specified: 4

Figure 1. MLVA papers published (up to November 4, 2013)
PubMed search was conducted using the search term 'mlva and 'mlva salmonella'. For 'mlva', 563 results were returned starting in 1999 (a single paper from 1978 described a different use of the abbreviation and was excluded). For 'mlva salmonella', a total of 90 results were returned starting in 2004. Results were downloaded in CSV format, year was extracted from the 'Create date' field in Excel. Total publication counts per year are shown.