Resource Summary Report

Generated by dkNET on Apr 16, 2025

Fluxus

RRID:SCR_008517
Type: Tool

Proper Citation

Fluxus (RRID:SCR_008517)

Resource Information

URL: http://fluxus-technology.com/sharenet.htm

Proper Citation: Fluxus (RRID:SCR_008517)

Description: DNA software and consultancy: The DNA Alignment software and Network software is used by biologists, anthropologists, medical researchers and students world wide. We carry out phylogeographic consultancy for US, UK and German clients, including legal medical work. We were involved in the tv projects The Real Eve (Discovery Channel) and Motherland (BBC). Our biotechnological director Dr Peter Forster is on the editorial board of the International Journal of Legal Medicine since 1999. Technology and sales consultancy: Clients include multinational corporations, research institutions, and medium to small businesses. Client quotes: Vorbildlicher Einsatz (Dr Stephan Hitzel, EADS, in CADplus 1/2003 journal, Cover Story). We have had an effective business relationship with Fluxus Technology since 1999, and their experience of the German market has proved to be invaluable as part of our operations supplying high end engineering software and consultancy services right across the engineering supply chain (Andy Chinn, Business Development Manager, ITI TranscenData, February 2006). Abstract. Indo-European is the largest and best-documented language family in the world, yet the reconstruction of the Indo-European tree, first proposed in 1863, has remained controversial. Complications may include ascertainment bias when choosing the linguistic data, and disregard for the wave model of 1872 when attempting to reconstruct the tree. Essentially analogous problems were solved in evolutionary genetics by DNA sequencing and phylogenetic network methods, respectively. We now adapt these tools to linguistics, and analyze Indo-European language data, focusing on Celtic and in particular on the ancient Celtic language of Gaul (modern France), by using bilingual GaulishLatin inscriptions. Our phylogenetic network reveals an early split of Celtic within Indo-European. Interestingly, the next branching event separates Gaulish (Continental Celtic) from the British (Insular Celtic) languages, with Insular Celtic subsequently splitting into Brythonic (Welsh, Breton) and Goidelic (Irish and Scottish Gaelic). Taken together, the network thus suggests that the Celtic language arrived in the British Isles as a single wave (and then differentiated locally), rather than in the traditional two-wave scenario (P-Celtic to Britain and Q-Celtic to Ireland). The phylogenetic network furthermore permits the estimation of time in analogy to genetics, and we obtain tentative dates for Indo-European at 8100 BC 1,900 years, and for the arrival of Celtic in Britain at 3200 BC 1,500 years. The phylogenetic method is easily executed by hand and promises to be an informative approach for many problems in historical linguistics.

Synonyms: Fluxus

Resource Type: software resource

Funding:

Resource Name: Fluxus

Resource ID: SCR_008517

Alternate IDs: nif-0000-30587

Record Creation Time: 20220129T080247+0000

Record Last Update: 20250410T065723+0000

Ratings and Alerts

No rating or validation information has been found for Fluxus.

No alerts have been found for Fluxus.

Data and Source Information

Source: SciCrunch Registry

Usage and Citation Metrics

We found 8 mentions in open access literature.

Listed below are recent publications. The full list is available at dkNET.

Brandt S, et al. (2024) The Phylogeography and Diversification of an Endemic Trapdoor Spider Genus, Stasimopus Simon 1892 (Araneae, Mygalomorphae, Stasimopidae) in the Karoo, South Africa. Ecology and evolution, 14(11), e70621.

Zhang L, et al. (2018) Interspecific Divergence of Two Sinalliaria (Brassicaceae) Species in Eastern China. Frontiers in plant science, 9, 77.

Ben Slimen H, et al. (2017) Selection on the mitochondrial ATP synthase 6 and the NADH

dehydrogenase 2 genes in hares (Lepus capensis L., 1758) from a steep ecological gradient in North Africa. BMC evolutionary biology, 17(1), 46.

Ishida Y, et al. (2013) Triangulating the provenance of African elephants using mitochondrial DNA. Evolutionary applications, 6(2), 253.

Boldt AB, et al. (2010) Phylogenetic nomenclature and evolution of mannose-binding lectin (MBL2) haplotypes. BMC genetics, 11, 38.

Chen X, et al. (2009) Molecular population genetics of human CYP3A locus: signatures of positive selection and implications for evolutionary environmental medicine. Environmental health perspectives, 117(10), 1541.

An P, et al. (2007) Polymorphisms of CUL5 are associated with CD4+ T cell loss in HIV-1 infected individuals. PLoS genetics, 3(1), e19.

Sengupta S, et al. (2006) Polarity and temporality of high-resolution y-chromosome distributions in India identify both indigenous and exogenous expansions and reveal minor genetic influence of Central Asian pastoralists. American journal of human genetics, 78(2), 202.