In the turn-taking task, the conditions and appropriate actions which led to rewards were learnt by the monkeys. Both animals had to be clear whose turn it was because this condition would determine whether they made a choice action or not, and both animals monitored whether the actor's response was rewarded. Moreover, if the reward contingencies switched such that the actor's choice was unrewarded, both animals had to note this condition because it would mean the next turn-taker should alter their response from previous choices. Thus, it was crucial to distinguish whether it was the self or other's turn, and map which was the appropriate response in the current trial context.

Yoshida *et al.* [7] found that a small number (<5%) of partner neurons were selective for the target button colour — the goal of the partner's action in the current trial — while one-third encoded the spatial location of the goal. Importantly, some 40% of partner neurons also responded differently on error trials, compared to correct ones. Thus, apart from distinguishing self from other, activity within this population of neurons also held a rich set of information about current trial context.

Viewed from this perspective, partner neurons might be considered to be part of the neural system involved in encoding condition–action relationships which, in this particular paradigm, depended upon differentiating self from other, among other variables. An interesting question is whether the same neurons might encode different condition–action relationships if a single monkey was trained on a different protocol that did not require distinguishing self from other, or even turn-taking. Are these neurons part of a general purpose system that maps and remaps appropriate actions to different contexts, regardless of their social implications? Answering such a question would require an ambitious and challenging experimental design, but would seem to be crucial for a better theoretical understanding of the role of the pre-SMA.

Moreover, these findings highlight one of the challenges for 'social neuroscience'. Social behaviour requires understanding appropriate responses, conditional upon the current context, which often also depends upon previous contexts. Encoding such condition–action rules might be important for many aspects of an animal's survival and aren't necessarily specific to any 'social' brain system. Thus, distinguishing what is truly social in neural terms and what is built on underlying circuits that subserve more general brain functions is not always easy (see also [11]). In this regard, the research presented by Yoshida *et al.* [7] provides an important and provocative contribution, though one that raises as many questions as it answers.

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Climate: Baselines for the Biological Effects of Environmental Change

Establishing biological baselines requires access to organisms which lived earlier in, or before, the present episode of anthropogenic change. Specimens of a bryozoan collected on Scott's Antarctic expeditions, and subsequently, provide clear evidence of recent increases in growth rate after 80 years of constancy.

John A. Raven

Studies of how organisms have responded to the continuing environmental changes that began some two centuries ago require access to biological specimens that provide data from which growth rates (for example) can be estimated. One such source is organisms that are still alive, e.g. annual rings of trees with secondary thickening. Here the thickness of the rings indicates the growth rate of the tree, although not necessarily the environmental factor altering the growth rate. Similar principles apply to growth rings in the shells of long-lived bivalve molluscs. For organisms with shorter life-spans relative to the period under investigation, data are available from fossils in well-dated sediments,

e.g. foraminifera in marine sediments from which temperature can be recovered from the $^{18}O/^{16}O$ of the calcium carbonate skeleton over periods of millions of years.

However, some (relatively) short-lived organisms can potentially yield environmentally relevant data, even if they do not fossilize well or do not provide dateable fossils. Here we depend on specimens collected at a known date from a well described site, and subsequently kept under conditions which do not alter the property of interest. The work of Barnes *et al.* [1], as reported in a recent issue of *Current Biology*, uses material of the Antarctic perennial marine bryozoan *Cellarinella nuttii* collected on Scott's two expeditions in the early twentieth century, on subsequent expeditions, and from very recent collections to compute growth rates over the last 120 years.

The Bryozoa is a phylum in the Lophotrochozoa, which is one of the three main clades of the bilateralean metazoans [2–4]. Most Bryozoa are marine: they are colonial filter feeders, forming encrusting or erect colonies which range from ephemeral to perennial [4]. Despite being calcified, *C. nuttii* does not apparently yield fossils usable for growth rate analysis. However, collected specimens have clear anatomical indicators of the winter growth pause, so the extent of radial (as an increase in cross-sectional area) and elongation growth in the summer of a given calendar year can be assessed, provided the specimen has a known date of collection [1]. The specimens examined came from Scott's 1901 (Figure 1) and 1913 expeditions, the 1936 Discovery expedition, US collections from 1958 to 1972, and collections from 2004 onwards. The results show no significant change in growth rate from 1890 to 1970, but there has been an increase since the 1990s to twice the values found earlier.

The results are important in indicating a recent increase in carbon sequestration to the benthos [1], although care is needed in relating this to net storage of CO_2 from seawater and ultimately from atmospheric CO_2. This is because *Cellarinella* is calcified, and $CaCO_3$ precipitation generates CO_2 [5], counter to the CO_2 assimilation by phytoplankton which ultimately yields the organic matter in the bryozoans. Whether the growth and subsequent death of bryozoans brings about net CO_2 storage requires measurement of the $CaCO_3$ and the organic C contents of the animal as well as CO_2 losses in the food chain. Barnes *et al.* [1] suggest a plausible local mechanism for an increased food supply to the bryozoans by increased local planktonic primary productivity based on a recent increase in upwelling, despite the suggestion of a decrease in global marine primary productivity over the last century [6] and a decline in CO_2 sequestration by the Southern Ocean by physical and biological mechanisms over the last three decades [7].

As Barnes *et al.* [1] point out, the existence of the earliest specimens used in their analysis is a tribute to Scott's emphasis on science in his expeditions. Perhaps the best known of the scientific aspects is the collection of fertilized eggs of the emperor penguin *Aptenodytes forsteri* in the 'Winter Journey', vividly described in 'The Worst Journey in the World' [8]. The egg collection was motivated by the hypothesis that 'ontogeny recapitulates phylogeny' in relation to the possibility that penguins are close living relatives of ancestral birds. The results of the analysis of the eggs were not published until 1934 [9] and did not greatly illuminate the hypothesis. Subsequent work [10,11] resolved the issue in favour of the derived nature of penguins.

Another scientific contribution from Scott's second expedition was the collection of fossilized leaves of the Permian gymnosperm *Glossopteris*, the first time this Gondwanan species had been found in Antarctica [12]. It is said that the suggestion to Scott that *Glossopteris* should be sought in Antarctica on Scott's second expedition came from Dr Marie Stopes [12], who was later to become famous for her non-palaeobotanical work. However, when the expedition found *Glossopteris* it was apparently not identified as such [12].

The work of Barnes *et al.* [1] would not have been possible without well curated collections of dried or otherwise preserved biological specimens. Museums and herbaria house many specimens which can now be used to address problems not recognised, and/or using techniques not known, at the time of collection. A good example of the use of herbarium specimens is Woodward's [13] work on the change in stomatal density (number of stomata per unit area of leaf) of C_3 plants since pre-industrial times. This showed a decrease in stomatal density through the industrial period, which Woodward [13] related to increasing CO_2: similar effects are seen in fossils from the time of origination of stomata [14]. Decreases in stomatal density with increasing CO_2 for growth occurs at both the phenotypic and the genotypic level in C_3 plants [14,15], but with no significant effects in C_4 plants [15]. Recalling the *Glossopteris* collected on Scott's second expedition, suitable specimens of this genus can be used for estimating stomatal density [16] and also the natural abundance $^{13}C/^{12}C$ ratio which yields further information on the Permian palaeoatmosphere [17].

Figure 1. The RRS Discovery, built in Dundee for Scott's 1901 expedition, has been restored and is now berthed in Dundee. (Photo courtesy of Dundee Heritage Trust.)

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Host–Pathogen Interactions: Cheating the Host by Making New Connections

Dynamic signaling networks are required to perform complex cellular processes. Structural and functional data now indicate the intriguing possibility that extracellular bacterial pathogens use catalytic scaffolds to assemble unique supramolecular signaling networks that effectively subvert key cellular processes in the host.

Ivan de Curtis

Under appropriate environmental conditions, intracellular and extracellular pathogens may use a type III secretion system to deliver a pool of pre-formed effector proteins into the cytosol of host eukaryotic cells to subvert their molecular processes for the needs of the bacteria [1]. The nature of the bacterial effectors involved and the mechanisms that allow them to affect host signaling are only partially known. Several bacterial effectors have been identified for some intracellular pathogens, such as IcsA of *Shigella*, ActA of *Listeria*, and RickA of *Rickettsia*. These proteins target the host actin regulators N-WASP and Arp2/3 complex, which are required for the actin-based propulsion that facilitates bacterial survival in the host cytosol and invasion of adjacent cells [2]. Conversely, extracellular pathogens, including the closely related enterohemorrhagic *Escherichia coli O157:H7* (EHEC) and enteropathogenic *E. coli* (EPEC), do not enter the host cells, but intimately adhere to the host plasma membrane to drive changes in the host cytoskeleton. By formation of pedestals rich in filamentous actin (F-actin) under the host cell membrane, these food-borne pathogens induce striking lesions of the intestinal epithelium and thus trigger severe infantile diarrhea [3]. A study by Selyunin *et al.* [4], recently published in *Nature*, now provides new fascinating evidence on the ability of a single EHEC effector protein to organize supramolecular signaling networks by co-opting two different enzymes from the host cytosol.

Scaffolding proteins are known to assemble signaling networks to faithfully regulate cell behavior [5]. An important question is how can effectors from extracellular bacteria efficiently reorganize the host signaling networks according to the needs of the bacteria. Pathogens have already been shown to inhibit individual host enzymes [6]. Moreover, recently they were shown to provide scaffolding for the reorganization of host signaling networks. Alto *et al.* [7] demonstrated that the EPEC type III effector EspF interacts with two host proteins — the sorting nexin SNX9, which is involved in the formation of endocytic vesicles [8], and the actin polymerization promoter N-WASP. The assembly of this complex causes the remodeling of the eukaryotic endocytic membranes, as a consequence of the recruitment and activation of N-WASP–Arp2/3-mediated F-actin nucleation at these membranes. Interestingly, the SNX9 SH3 domain, which is responsible for EspF binding, can interact directly with N-WASP [9]. Therefore, the insertion of the bacterial EspF effector, by preventing the direct association between the two host proteins, may affect normal membrane traffic and actin reorganization, thus playing an important role in the pathogenesis.

Another example of reorganization of the host signaling networks is represented by the localized changes of the host cytoskeleton by EHEC type III effectors [10]. Type III secretion systems allow the intimate attachment of the bacterium to the host via the interaction of the bacterial outer-membrane protein intimin with the EHEC transmembrane effector Tir, which is inserted into the eukaryotic cell membrane [11] (Figure 1A). Tir then recruits host N-WASP, which interacts physically with, and is activated by, the proline-rich bacterial effector $EspF_U$. This complex affects the actin pool and thus reorganizes the cytoskeleton of the eukaryotic host cell, with ensuing formation of pedestals under the bacteria [12]. The EHEC effectors Tir and $EspF_U$ do not interact directly, but once translocated into the host cell they bind to distinct domains of the host adaptor protein IRSp53/IRTKS. The formation of this ternary complex is needed to activate N-WASP and to promote the vigorous