Title

The dopamine circuit as a reward-taxis navigation system

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Abstract

Research on certain circuits in simple organisms, such as bacterial chemotaxis, has enabled the formulation of mathematical design principles, leading to ever more precise experimental tests, catalyzing quantitative understanding. It would be important to map these principles to the far more complex case of a vertebrate behavioral circuit. Here, we provide such a mapping for the midbrain dopamine system. Dopamine transmission plays a key role in learning, motivation, and movement, but its systems-level function is not fully understood. We develop a minimal mechanistic model of the dopamine circuit based on physiological and behavioral data, and show that it can be mapped mathematically to the bacterial chemotaxis circuit. Just as chemotaxis robustly climbs attractant gradients, the dopamine circuit performs 'reward-taxis' where the attractant is the expected value of reward. The reward-taxis mechanism is based on a circuit feature called fold-change detection, where the circuit outputs the temporal logarithmic derivative of expected reward. The model can explain the general matching law, in which the ratio of responses to concurrent rewards goes as the reward ratio to the power β. It provides an accurate mechanistic value for β as the average gain/baseline ratio of the dopaminergic neurons. Reward-taxis provides testable etiologies for specific dopamine-related disorders.

Introduction

Foundational work in the field of systems biology showed how, once a biological circuit is well characterized in terms of components and behavior, general mathematical principles can be formed which not only shed light on the original circuit but can generalize to explain many other circuits. It is important to explore whether these principles apply also to a vertebrate behavioral circuit. To do so, it is ideal to begin with a well-characterized circuit in terms of neuronal dynamics, physiology, and behavior. A good candidate for such a circuit is the midbrain dopamine circuit.

Dopamine transmission in the midbrain participates in at least two major biological functions. The first role is the control of movement and motivation (Niv *et al*, 2007; Mazzoni *et al*, 2007; Dudman & Krakauer, 2016; da Silva *et al*, 2018; Shadmehr & Ahmed, 2020). Dopamine transmission regulates movement initiation and vigor on a sub-second level as shown in freely behaving mice (da Silva *et al*, 2018), and defects in dopamine transmission underlie the movement difficulties in Parkinson's disease (Meder *et al*, 2019).

The second role of dopamine is encoding *reward prediction errors* (Schultz *et al*, 1997). Reward prediction errors are the difference between the experienced and predicted rewards. They play a key role in a specific method of reinforcement learning called temporal difference learning (TD learning) (Schultz *et al*, 1997; Sutton & Barto, 1998; Glimcher, 2011; Steinberg *et al*, 2013). In addition to rapid responses encoding reward prediction errors, dopamine also slowly ramps up when approaching a reward (Howe *et al*, 2013; Hamid *et al*, 2016; Mohebi *et al*, 2019). Importantly for the present study, a recent experiment demonstrated that dopaminergic ramps represent a temporal derivative-like computation on expected reward (Kim *et al*, 2020). Kim et al. used virtual reality to manipulate the rate of change of expected reward as mice moved towards a target, and found that mice responded to the temporal derivative of expected reward, rather than to its absolute value.

To better understand the dopamine circuit on the system level, it is important to unify, in a single conceptual framework, both its reward-derivative and its motion control functions (Berke, 2018; Shadmehr & Ahmed, 2020). Why does dopamine play two important roles at the same time: invigorate movements and encode the derivative of expected reward? Theoretical studies have analyzed this question from the perspectives of learning (Friston, 2010; Bogacz, 2020) and cost-benefit theories (Yoon *et al*, 2018; Shadmehr & Ahmed, 2020). Here, we consider the function of the circuit from the point of view of navigation, a connection anticipated by early work on TD learning (Montague *et al*, 1995).

For this purpose, we develop a mechanistic model of the dopamine circuit, and show that it can be mathematically mapped to the navigational circuit that guides bacterial chemotaxis, a foundational circuit in systems biology. We show that experimental observations on dopaminergic regulation can be explained by a circuit property known as fold-change detection *(FCD)*, in which the output of the circuit responds to *relative* rather than absolute changes in the input (Shoval *et al*, 2010; Adler & Alon, 2018). FCD was discovered in bacterial chemotaxis and was then found to be widespread in sensory and navigational circuits (Adler & Alon, 2018). In the case of dopamine, the input to the circuit is expected reward. Additionally, just as chemotaxis controls bacterial runs and tumbles, we build on measurements of animal movement to propose a model where high dopamine results in prolonged bouts of vigorous and correlated movements ("runs") whereas low dopamine causes pauses and slow reorientations ("tumbles"). This model for dopaminergic regulation of movement indicates how the two roles of dopamine, reward-derivative and motion-regulator, combine to provide a robust navigation system that climbs reward gradients. We call this the 'reward-taxis' model for the dopamine system. The model provides a mechanistic explanation for the well-established generalized matching law of behavior, predicts search dynamics that are invariant to the scale of the rewards, and provides testable etiologies for specific dopamine-related disorders.

Results

Dopamine release as fold-change detection of expected reward

We begin by developing a minimal model for midbrain dopamine regulation by environmental cues (Figure 1A). Consider a behaving animal exploring an open field for a reward of magnitude u, such as a food or drink. For simplicity, we assume a uniform response amongst all dopaminergic neurons. In reality, there are important heterogeneities between and within midbrain structures, and some dopaminergic neurons may be specialized to specific cues (Eshel *et al*, 2016; Parker *et al*, 2016; da Silva *et al*, 2018; Lee *et al*, 2019; Engelhard *et al*, 2019). If the animal is familiar with the environment, dopamine release d will increase as the animal observes cues that indicate closer proximity to the reward (Howe *et al*, 2013; Hamid *et al*, 2016; Kim *et al*, 2020). This is due to the increase in expected reward R, which decays with distance from the target (Howe *et al*, 2013; Gershman, 2014; Kim *et al*, 2020). Here expected reward is defined based on TD learning: the expected temporally discounted sum of present and future rewards (see Methods).

How does dopamine release, d, depend on expected reward, R? Recordings from VTA dopaminergic neurons in mice reveal a sublinear relationship between the magnitude of

received rewards u and the dopaminergic response above its baseline, $\Delta d(u)$ (Eshel *et al*, 2015, 2016) (Figure 1B). The sublinear relationship indicates that dopamine neurons may be (at least in some magnitude range) responding to the logarithm of expected reward, i.e., that: $\Delta d(u) = \mu \log(R(u))$, where $R(u) = au + b$ is the expected reward, where a is a scaling factor and b is a magnitude-independent component of the expected reward. The parameter μ is the gain of the dopaminergic response. Logarithmic responses are consistent with widespread logarithmic coding in the brain (Dehaene, 2003; Nieder & Miller, 2003; Shen, 2003; Dehaene *et al*, 2008; Nieder & Dehaene, 2009; Laughlin, 1989) as well as with economic notions of utility (Bernoulli, 1968; Rubinstein, 1977).

To test this, we fit the function $\mu \log(au + b)$ to the average dopaminergic response to a variable water reward in mice (Eshel *et al*, 2016), finding an excellent fit ($r^2 = 0.999$), with a gain of $\mu = 4.94 \pm 0.45$.

In addition to activation by expected reward, dopaminergic neurons in the VTA are inhibited by the output g of adjacent GABAergic neurons, and this inhibition is subtractive (Eshel *et al*, 2015, 2016). We therefore propose the following minimal description of dopamine release:

$$d = C + \mu \log R - \alpha g \quad [1]$$

where C is the baseline activity of the dopaminergic neurons when $\log R = g = 0$, μ is the gain, R is perceived expected reward, and α is the effectiveness of inhibition by the GABAergic output g. Since our model focuses on the regulation of behavior, rather than on learning or representation, we will assume that the log-transformed expected reward $\log R$ is an input signal that is provided to the circuit. Additionally, while subtractive inhibition was established for VTA dopaminergic neurons, we assume that similar regulation is shared among all midbrain dopaminergic neurons.

To complete the model requires a minimal description of the dynamics of GABAergic output g. The mechanisms of interaction between GABAergic and dopaminergic neurons are complex, and there are many local and remote interactions (Morales & Margolis, 2017; Cox & Witten, 2019). However, there are several experimental observations that impose constraints on these interactions (Figure 1CDE). First, upon presentation of a reward-predicting cue - equivalent to a step increase in *R(t)* - dopamine rapidly increases and then drops and adapts precisely to its baseline on a sub-second timescale (Schultz *et al*, 1997; Tobler *et al*, 2005; Cohen *et al*, 2012) (Figure 1C). Second, dopamine responses are scaled relative to the expected reward baseline: when the expected reward is of magnitude u and the received reward is of magnitude λu for a constant λ, dopamine responses are nearly identical and independent of u

(Tobler *et al*, 2005) (Figure 1D). Third, dopamine release represents a temporal-derivative-like computation of *R(t)* (Kim *et al*, 2020) (Figure 1E). Finally, GABAergic activity tracks *R(t)* (Cohen *et al*, 2012) (Figure 1C).

These experimental observations are the hallmarks of a circuit feature known in systems biology as *fold-change detection (FCD)* (Shoval *et al*, 2010; Adler & Alon, 2018) (Figure 1A). FCD is a property where the circuit output depends only on relative changes in the input, rather than absolute changes. FCD circuits output the temporal (logarithmic) derivative of low-frequency input signals, whereas high frequency inputs are normalized by their baseline (Tu *et al*, 2008; Adler *et al*, 2014; Lang & Sontag, 2016).

FCD circuits are ubiquitous in biological sensing, as reviewed in (Adler & Alon, 2018). They can be implemented by a handful of specific feed-forward and feedback mechanisms (Adler *et al*, 2017). In all FCD mechanisms, a slow internal variable (g) encodes the background input level and acts to normalize the output accordingly. Taken together, the FCD property can explain all of the experimental observations on dopamine responses described in Figure 1.

Since we do not know the exact mechanistic implementation of the FCD property in the dopamine circuit, we will make the simple assumption of a negative feedback loop, and choose the simplest design that provides FCD. In this design, inhibitory neuron activity g is given by an integral-feedback equation with respect to dopamine release d:

$$\dot{g} = \omega\left(\frac{d}{d_0} - 1\right) \quad [2]$$

Or, more generally, $\dot{g} = F(d)$ where $F(d)$ increases with d and has a single zero at $d = d_0$. This feedback loop generates exact adaptation of d: the only steady state solution is $d = d_0$. d_0 is the homeostatic activity level of dopaminergic neurons, which is about ~5 spikes/s in mice (Robinson *et al*, 2004; Eshel *et al*, 2016). The parameter ω determines the adaptation time of the dopaminergic neurons after a change in R(t). This timescale is on the order of hundreds of milliseconds. For the GABAergic neurons, after a step change in *R(t)*, the firing rate in the model increases proportionally to the logarithm of *R(t)*, such that $g = \frac{C - d_0 + \mu \log R}{\alpha}$ (this is because GABAergic output integrates dopaminergic activity). Taken together, Eqs. 1-2 provide a minimal model for dopamine responses to expected reward inputs *R(t)*.

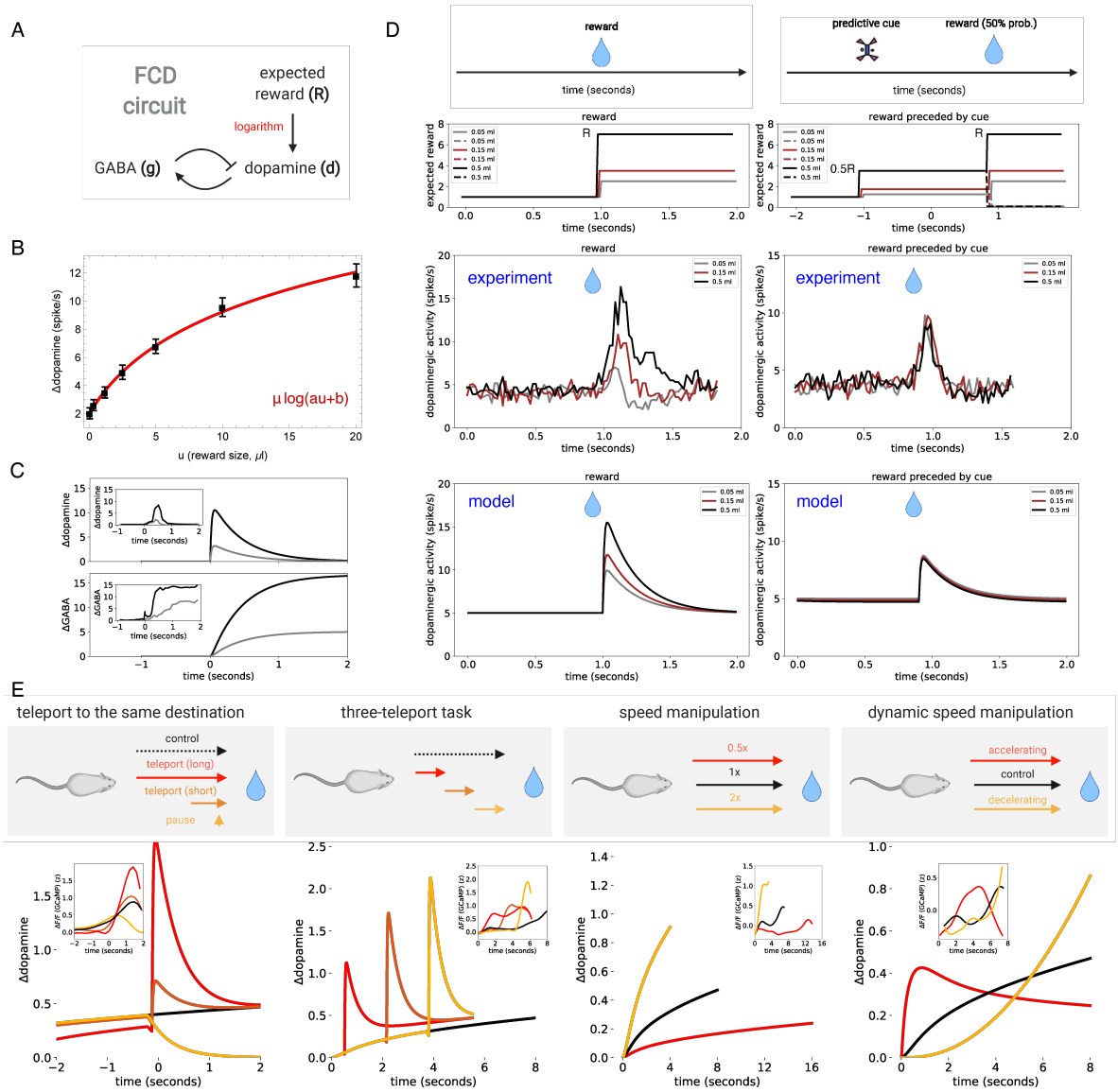


Figure 1. Dopamine responses as fold-change detection of expected reward. (A) Minimal circuit for dopamine responses. Dopamine *(d)* is activated by the logarithm of expected reward ($\log R$) and is inhibited by negative feedback from GABAergic input (g). See *Methods* for equations and parameters. (B) The response of VTA dopaminergic neurons in mice (n=5) to a water reward of variable volume (black squares, mean ± SEM, taken from Figure 1C in (Eshel *et al*, 2015)) is well-described by the logarithmic relation $\Delta d = \mu \log(au + b)$ ($r^2 = 0.999$, best-fit parameters $a = 0.5 \pm 0.1, b = 1.5 \pm 0.05, \mu = 4.9 \pm 0.45$, N=7 reward magnitudes). (C) Simulation of dopamine and GABA responses to a step increase in expected reward input which corresponds to the presentation of a reward-predicting cue. The step is given by $R(t) = R_0 + \lambda\theta(t - t_0)$ where $\theta(t - t_0)$ is a unit step function, $R_0 = 1$ and $\lambda = 7$ for the black line (large reward) and $\lambda = 1.8$ for the gray line (small reward). *Insets.* Average change in firing rates from dopaminergic (type I) and GABAergic (type II) VTA neurons, in response to reward-predicting cues for a small reward (gray) or a large reward (black). Data from Figure 2D of (Cohen *et al*, 2012). (D) Population responses of dopaminergic neurons of two Macaque monkeys to variable size liquid reward, either without a preceding cue (left panels, n=55 neurons), or with a preceding visual cue that predicts reward delivery with 50% probability (right panels, n=57 neurons). *Upper.* The expected-reward input following the reward-predicting cue is $R = 0.5(b + \lambda u)$ (where λ is proportional to reward magnitude), which is doubled following reward delivery, $R = b + \lambda u$, where u is the reward magnitude (we use $b = 2$ and $\lambda = 10ml^{-1}$). *Middle.* Experimentally measured average dopaminergic responses, adapted from Fig. 2A and Fig. 4B of (Tobler *et al*, 2005). When the reward is delivered without a cue, dopaminergic responses increase with reward magnitude (left panel). When it is given after a cue that predicts reward delivery with 50% probability, dopaminergic responses to reward delivery are identical (right panel), as predicted by the FCD property. This is despite the 10-fold difference in reward magnitude. *Lower.* Simulations of the dopamine model capture the experimentally observed dynamics. (E) Dopamine output to movement in a reward gradient given by $R(x) = e^{-\gamma x^h}$, with $h = 1.5, x_0 = 1, v_0 = 1$ and $\gamma = 0.04$, and perturbations as described

in Figure 2 of (Kim *et al*, 2020). *Insets.* Corresponding dopaminergic outputs from mice (left to right: n=11, n=11, n=15, n=5) VTA neurons measured by calcium imaging, from Figure 2CGKO in (Kim *et al*, 2020), smoothed using a Savitzky–Golay filter. All simulations were performed with the parameters provided in Table 1.

A reward-taxis model for dopamine regulation of behavior

To link the dopamine circuit to animal behavior, we provide an additional equation as a minimal model for dopamine control of motion. The equation is motivated by the well-established role of dopamine in the regulation of action vigor and locomotor activity (Niv *et al*, 2007; Beierholm *et al*, 2013; Panigrahi *et al*, 2015; Ek *et al*, 2016; da Silva *et al*, 2018).

We focus on stochastic exploratory motion, as opposed to directed and deliberate motion along a specific path. We therefore model movement as a random-walk process, which is a standard approach for modelling animal movement (Blackwell, 1997; Codling *et al*, 2008; Smouse *et al*, 2010; Mwaffo *et al*, 2015; Hanks *et al*, 2015; Michelot *et al*, 2019). While the model is presented in the context of physical spatial motion of an animal, it can be readily generalized to other aspects of behavior, as we will detail below.

We assume that the navigating animal can be in one of two states – arrested or moving. We also assume that when the animal is moving, it runs in a straight line, and when the animal is arrested, it chooses its subsequent movement direction at random (allowing the new direction to be correlated with the previous direction does not affect the conclusions). Such a model can capture, for example, the swimming behavior of zebrafish (Budick & O'Malley, 2000; Mwaffo *et al*, 2015), or the movement of mice in an open field (da Silva *et al*, 2018). The random walk has two parameters: movement speed v (units of length/time), and run duration, which is exponentially distributed with mean ϕ (units of time).

Dopamine increases movement vigor, which may be due to increasing v or increasing ϕ. In zebrafish, the dopamine agonist apomorphine increased the speed of swimming bouts at low doses (higher v), and the duration of swimming bouts (higher ϕ) at high doses (Ek *et al*, 2016). In a recent study, da Silva et al. performed sub-second measurements of SNc dopaminergic neurons in freely behaving mice in an open field (da Silva *et al*, 2018). The neuronal measurements were coupled with high-resolution motion measurements. Dopamine activity prior to movement increased the probability and vigor of subsequent movement (da Silva *et al*, 2018). Both these effects may again manifest in higher movement speed v, or in correlated movement patterns that correspond to higher ϕ.

Based on these observations, we propose two possibilities for dopamine regulation of movement. In the first possibility, dopamine increases run duration:

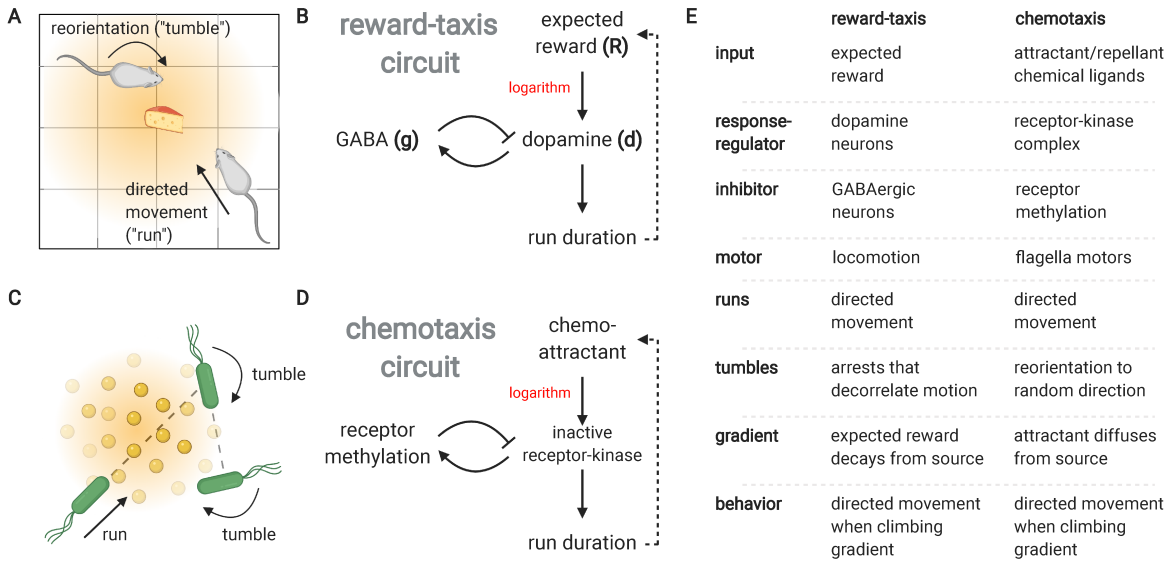
208 $$\phi(d) = \tau \frac{d}{d_0} \quad [3]$$

209 Where τ is the average run duration in an environment without reward cues. Dopamine d in
210 Eq. 2 corresponds to the (normalized) dopaminergic activity in the brain, so loss of
211 dopaminergic neurons (as occurs in Parkinson's disease) reduces d proportionately, which
212 effectively reduces run duration τ. We assume a linear relation between run duration and d,
213 which is consistent with the gradual increase in movement vigor with dopaminergic activity
214 (see Fig. 1j-k in da Silva et al. (da Silva *et al*, 2018)). The important aspect is that high
215 dopamine results in directed motion, whereas low dopamine decorrelates motion.
216 We can also consider an alternative model where dopamine increases running speed:

217 $$v(d) = v_0 \frac{d}{d_0} \quad [4]$$

218 In this case, loss of dopamine neurons effectively decreases the average running speed v_0. Such
219 a speed-control model provides the same conclusions as a run-duration-control model with Eq.
220 3 (Methods). However, in order to emphasize the analogy with chemotaxis, we use Eq. 3. Note
221 that in both cases, we focus on the sub-second regulation of movement parameters by
222 dopamine, as observed by da Silva et al. (da Silva *et al*, 2018).
223 Eqs. 1-3 define a biased random walk that is guided by the gradient of the logarithm of the
224 expected reward (Figure 2B), which we call *reward-taxis*.
225 This biased random walk is analogous to bacterial chemotaxis: bacteria such as *E. coli* use a
226 run-and-tumble navigation strategy to climb gradients of chemical attractants (Figure 2CDE)
227 (Berg & Brown, 1972; Tu *et al*, 2008; Shoval *et al*, 2010; Sourjik & Wingreen, 2012). The
228 chemotaxis signaling network is based on an FCD circuit that controls run duration (Shoval *et*
229 *al*, 2010; Lazova *et al*, 2011). It therefore maps onto dopamine release dynamics, where
230 expected-reward inputs play the role of chemoattractant concentration in chemotaxis. Both
231 systems respond to relative input levels. They both respond to the derivative of low-frequency
232 input components and respond proportionally to high-frequency input components (Tu *et al*,
233 2008), and show exact adaptation to step changes in input. Thus, the dopamine circuit can allow
234 animals to climb gradients of reward expectation.
235 The reward-taxis model was presented for whole-body spatial movement, but its assumptions
236 are general and may potentially extend to other aspects of behavior. One such aspect is
237 *hippocampal replay*, the activation of hippocampal place cells during sharp-wave ripples
238 (Gomperts *et al*, 2015; Ólafsdóttir *et al*, 2018; Stella *et al*, 2019). Hippocampal replay consists
239 of a firing sequence of neurons that represents temporally compressed motion trajectories (Lee

& Wilson, 2002; Pfeiffer & Foster, 2013; Ólafsdóttir *et al*, 2018). It can occur either during sleep or rest ("offline") or when the animal is awake and engaged in a task ("online"). Online replay plays an important role in planning and navigation (Pfeiffer & Foster, 2013). The activation of the place neurons corresponds to stochastic movement trajectories with a characteristic speed (Davidson *et al*, 2009) that are biased towards the location of rewards (Pfeiffer & Foster, 2013); when foraging is random, the trajectories are diffusive, resembling Brownian motion (Stella *et al*, 2019). Hippocampal activity during online replay is tightly coordinated with reward-associated dopamine transmission (Gomperts *et al*, 2015). To map reward taxis to hippocampal replay requires that dopamine transmission modulate the stochastic trajectories of hippocampal replay, for example through the modulation of reorientation frequency.



	reward-taxis	chemotaxis
input	expected reward	attractant/repellant chemical ligands
response-regulator	dopamine neurons	receptor-kinase complex
inhibitor	GABAergic neurons	receptor methylation
motor	locomotion	flagella motors
runs	directed movement	directed movement
tumbles	arrests that decorrelate motion	reorientation to random direction
gradient	expected reward decays from source	attractant diffuses from source
behavior	directed movement when climbing gradient	directed movement when climbing gradient

Figure 2. Dopamine regulation of behavior in the model is analogous to bacterial chemotaxis. (A) The behavior of an animal in an open field is modelled as a series of directed movements (runs). The direction of each run is chosen at random (or, more generally, stops between runs decorrelate motion direction), and the duration of each run increases with dopamine level. (B) Dopamine is controlled by an FCD circuit activated by expected reward. (CD) The reward-dopamine-behavior circuit is analogous to the chemotaxis circuit that underlies bacterial navigation towards chemo-attractants. Bacterial motion is composed of a series of runs. The direction of each run is randomized by tumbling events, and run duration increases with the inactivation of a receptor-kinase complex, which is controlled by an FCD circuit activated by chemoattractant concentration. (E) Table detailing the mapping between the dopamine system and the chemotaxis system.

Reward-taxis quantitatively provides the matching law of operant behavior

We next ask how the reward-taxis model compares with features of animal behavior. We find that the model provides the *general matching law of operant behavior*, one of the best-established behavioral phenomena (Herrnstein, 1970; Baum, 1974, 1981; Baum *et al*, 1999; Lau & Glimcher, 2005; McDowell, 2013). If an animal has a choice of two rewards with

expected magnitude r_1, r_2 at two locations x_1, x_2, the long-term average of its response rates (the relative amount of time it chooses each reward (Baum & Rachlin, 1969)) $P(x_1), P(x_2)$ goes as a power β of the ratio of rewards:

$$\frac{P(x_1)}{P(x_2)} = \left(\frac{r_1}{r_2}\right)^{\beta} \quad [5]$$

The matching law holds both for varying reward magnitude and varying reward probability (Davison & McCarthy, 1988). The matching law was originally proposed with perfect matching $\beta = 1$ (Herrnstein, 1961). A large number of studies in various vertebrate species under different experimental conditions observed that β can be somewhat variable, showing slight undermatching ($\beta < 1$) and overmatching ($\beta > 1$), with the former more commonly observed (Baum, 1974; William, 1979; Baum, 1981; Davison, 1991; Baum *et al*, 1999; Lau & Glimcher, 2005; McDowell, 2013). Matching is a robust property which holds over orders of magnitude of reward ratios (up to ~1:500 in pigeons (Baum *et al*, 1999)). The overall robustness of the matching law has led authors to suggest that it reflects intrinsic properties of the vertebrate nervous system (McDowell, 2013).

While previous explanations for the general matching law focused on underlying choice processes (Herrnstein & Prelec, 1991; Soltani & Wang, 2006; Simen & Cohen, 2009), here we show that matching is a robust emergent property of the dopamine system, and that β is an intrinsic property of dopamine neurons that can be directly estimated from neuronal recordings.

To test whether the model provides the matching law, we model the dynamics of the location of a behaving animal as a stochastic process. Let $R(x)$ be the input field, which is the expected reward R as a function of location x. At long time- and length-scales, run-and-tumble motion resembles Brownian motion (Berg, 1993), with a diffusion coefficient $D \approx m^{-1}v^2\tau$, where v is the average run speed, τ is the average run duration, and m is the dimension (we assume that d is close to the adapted level d_0). Brownian motion in the model is biased by longer runs when the agent is moving up the gradient. To account for this, one can add to the diffusion process an advection term that is proportional to the logarithmic gradient: $\chi\nabla \log R(x)$ (Si *et al*, 2012; Dufour *et al*, 2014; Menolascina *et al*, 2017). Taken together, the stochastic dynamics of the agent are approximated by a Langevin equation similar to the classic Keller-Segel equation used to model chemotaxis (Keller & Segel, 1971):

$$dx = \chi\, \nabla \log R(x)\, dt + \sqrt{2D}\, dW \quad [6]$$

where W is an m-dimensional Wiener process (see Supplementary Information 1 for the derivation of Eq. 6). For relatively short runs compared with the adaptation time (sub-second

order), the advection parameter χ, also called chemotactic drift, is given by: $\chi \approx \mathrm{m}^{-1}\mathrm{v}^2\tau \cdot \mu d_0^{-1}$ (Si *et al*, 2012), and thus rises with velocity v, gain μ and mean run duration τ. It is important to note that Eq. 6 holds also for the model variant in which dopamine modulates movement speed (see Supplementary Information 2).

Eq. 6 captures how animal movement depends on the parameters of the dopamine circuit, as well as on movement parameters τ, v. Decreasing the average run duration τ or average movement speed v (as in Parkinson's disease) decreases both diffusivity D and advection χ, resulting in slower effective motion and gradient climbing. Gradient climbing efficiency (chemotactic drift) increases with μd_0^{-1}, which is the gain of dopamine neurons normalized by their baseline activity. Other circuit parameters do not affect movement dynamics.

Eq. 6 is equivalent to the Langevin Monte Carlo algorithm, a common algorithm from statistical physics for sampling probability distributions (Roberts & Tweedie, 1996; Neal, 2011; Girolami & Calderhead, 2011; Dalalyan, 2014). The steady-state distribution can be readily solved, using standard methods of statistical physics, similar to a Boltzmann distribution in a potential field. The motion samples a probability distribution *P(x)* proportional to a power β of the expected-reward distribution:

$$P(x) \propto e^{\beta \log R(x)} = R(x)^{\beta} \quad [7]$$

where the power-law β equals the normalized gain of the dopaminergic neurons: $\beta = \frac{\chi}{D} = \mu d_0^{-1}$. From Eq. 7 we infer that for any two rewards r_1, r_2 the response rates $P(x_1), P(x_2)$ obey the general matching law presented in Eq. 5.

The reward-taxis model therefore predicts operant matching with $\beta = \mu d_0^{-1}$. Thus, β is equal to the average ratio of gain to baseline activity in dopaminergic neurons. As mentioned above, these values can be estimated from the neuronal measurements of Eshel et al. (Eshel *et al*, 2016), $\mu \approx 5$ spikes/s and $d_0 \approx 5$ spikes/s. These values yield $\beta \approx 1$, in agreement with the matching law. Similar parameters are found also in primates (Supplementary Information 3). The agreement is striking since there is no a-priori reason for the gain and baseline to be similar; normalized gain μd_0^{-1} could in principle have a wide range of values including $\mu d_0^{-1} \ll 1$ or $\mu d_0^{-1} \gg 1$.

The matching exponent β only depends on parameters that are intrinsic to the dopamine neurons; β is independent of movement speed v or run duration τ, which may vary depending on animal physiology and the environmental context, as well as on the number of dopaminergic neurons. This may explain the robustness of the matching phenomena across species and

experimental conditions. Taken together, this suggests that the reward-taxis model may provide a physiological mechanism underpinning operant matching.

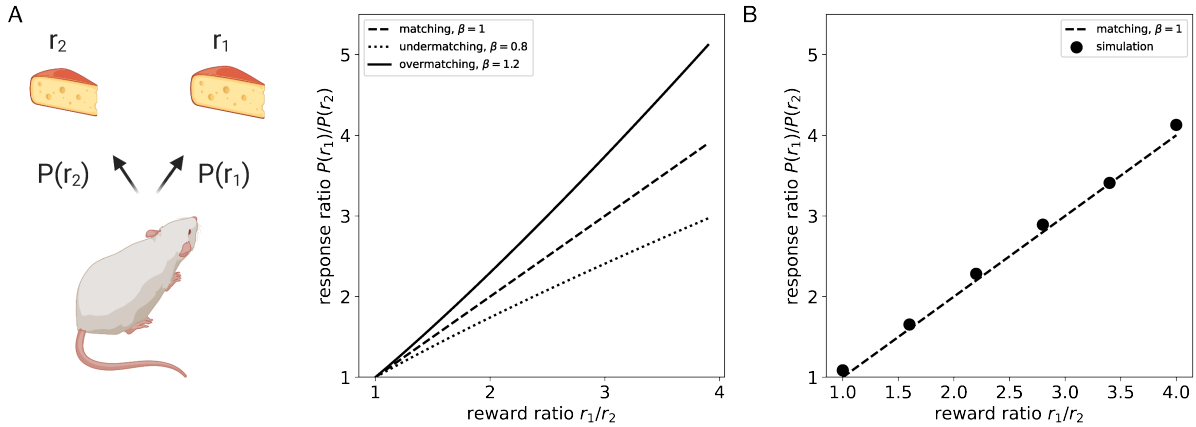


Figure 3. Reward-taxis model provides the generalized matching law. (A) The generalized matching law, amply supported experimentally, is a power-law relation between the frequency of rewards and the frequency of responses $\frac{P(x_1)}{P(x_2)} = \left(\frac{r_1}{r_2}\right)^{\beta}$, r_1, r_2 are rewards at locations x_1, x_2. Perfect matching occurs for $\beta = 1$, while undermatching/overmatching are due to variations in β. Such a power-law relation arises directly from the dynamics of the model where $\beta = \mu d_0^{-1}$. (B) Simulation of the dopamine model for choice between two rewards r_1, r_2. Expected reward is the sum of two Gaussians: $R(x) = r_1 e^{\left(\frac{x-x_1}{b}\right)^2} + r_2 e^{\left(\frac{x-x_2}{b}\right)^2}$ (the exact distribution is not important for matching) with $\tau = 100ms, \mu = 5, d_0 = 5, v = 25cm\ s^{-1}, x_1 = +30cm, x_2 = -30cm, b = 20cm$ ($\beta = \mu d_0^{-1} = 1$, Methods). The model was simulated for different ratios of r_1/r_2, and the response ratio was estimated by the ratio of the time spent $\pm 2.5cm$ from x_1, x_2.

Reward-taxis and pathologies of the dopamine system

Variation and defects in the dopamine system can be classified by their effects on the parameters of the reward-taxis model. Variation in intrinsic neuronal parameters can affect gain μ and baseline firing rate d_0. Such changes are predicted to affect the matching law behavior by changing the exponent β. For example, ADHD is associated both with impaired sensitivity to reinforcement (corresponding to low β) (Kollins *et al*, 1997; Luman *et al*, 2010) and impaired dopaminergic gain (corresponding to low μ) (Tripp & Wickens, 2008; Hauser *et al*, 2016). Reduced gain can also cause reduced sensitivity to reward gradients so that only strong reward gradients produce continuous focused climbing, as shown by work in bacterial chemotaxis (Long *et al*, 2017). Such hypotheses are in principle testable by detailed behavioral experiments and by experimental manipulation of neuronal gain and baseline properties using drugs or genetic tools.

Other disorders can be due to reduction in the number of functional dopaminergic neurons, as in Parkinson's disease, where SNc dopaminergic neurons are lost. Such damage is predicted to change mean run duration τ and/or mean motion vigor v_0. If the damage does not sizably affect

357 the intrinsic properties of surviving neurons, such as gain and baseline, they are not expected
358 to change β in matching law experiments.
359 The analogy to chemotaxis can also be used to explore the role of variability in parameters.
360 Variability can occur over time in the same individual (state), or between individuals (trait). In
361 *E. coli* chemotaxis the basal tumbling rate and adaptation time show large non-genetic
362 variability between bacteria that lasts a generation time (Spudich & Koshland, 1976; Levin *et*
363 *al*, 1998; Levin, 2003; Frankel *et al*, 2014; Keegstra *et al*, 2017; Salek *et al*, 2019). This
364 variation is consequential for gradient climbing performance. Lower basal tumbling frequency
365 improves navigation towards distant targets, whereas high basal tumbling frequency is
366 preferable for nearby targets (Frankel *et al*, 2014). More recently, it was discovered also that
367 pathway gain varies between individual bacteria. Theoretical work indicates that high pathway
368 gain is beneficial for localizing around a single attractant peak, whereas low pathway gain
369 allows efficient crossing between attractant peaks (Karin & Alon, 2021).
370 Mapping these findings to the dopamine model suggests that state and trait variation can affect
371 reward-taxis. Trait-like variation may be due to developmental or genetic factors. State-like
372 variation in parameters, on the other hand, can potentially be implemented by neuromodulators
373 such as epinephrine and serotonin. Movement vigor shows individuality in humans (Reppert
374 *et al*, 2018), which is in some ways analogous to individuality in baseline tumbling frequency.
375 The reward-taxis model therefore provides testable predictions for the effects of such variations
376 on movement and search behavior.
377
378 **Discussion**
379 This study unifies the two main effects of dopamine, encoding reward-derivative and
380 increasing movement vigor, by mapping them to a reward-taxis navigational circuit. The circuit
381 is analogous to the bacterial chemotaxis circuit, where in the dopamine case navigation is along
382 gradients of expected reward. The mapping is based on mathematical analogies at both the
383 physiological and behavioral levels. At the physiological level, experiments on the regulation
384 of dopamine transmission can be parsimoniously explained as fold-change detection (FCD) of
385 expected reward. At the behavioral level, dopamine increases the probability and vigor of
386 movements, thus increasing the duration of correlated motion ("runs") compared with
387 reorientations ("tumbles"). Both aspects map to the well-characterized chemotaxis navigation
388 circuit in bacteria.
389 FCD is a recurring motif in biological sensory systems (Adler & Alon, 2018). Therefore, the
390 model of dopamine transmission as FCD of expected reward is in line with the

391 conceptualization of dopamine neurons as sensory neurons for reward (Watabe-Uchida *et al*,
392 2017). FCD includes the classic Weber's law of sensory systems, which posits that the maximal
393 response to a change in input is normalized by the background level of the signal (Ekman,
394 1959). FCD is more general than Weber's law in that the entire dynamics of the output,
395 including amplitude and duration, is normalized by the background input level. FCD allows
396 the system to function in a scale-invariant manner across several decades of background input
397 (Shoval *et al*, 2010). It also provides a common scale to compare different types of sensory
398 inputs, by referring to their relative (rather than absolute) changes (Hart *et al*, 2013).
399 While the model focused on the average activity of dopaminergic neurons, the proposed
400 mechanism for FCD (inhibition from neighboring GABAergic neurons) may apply at the level
401 of individual dopaminergic neurons or groups of neurons. This raises the possibility of
402 heterogeneity between dopaminergic neurons – different dopaminergic neurons could become
403 adapted to different expected-reward levels at the same time. This would be consistent with a
404 recent study that demonstrated that a single reward can simultaneously elicit positive and
405 negative prediction errors in different neurons (Dabney *et al*, 2020).
406 Our model places vertebrate motion regulation in the wider family of run-and-tumble stochastic
407 navigation circuits, which includes motion regulation in bacteria, algae, and simple animals
408 (Pierce-Shimomura *et al*, 1999; Polin *et al*, 2009; Luo *et al*, 2014; Kirkegaard *et al*, 2016).
409 Reward-taxis was anticipated in the early work on TD learning, where Montague et al. showed
410 that run-and-tumble dynamics driven by reward prediction errors can explain observations on
411 bee foraging (Montague *et al*, 1995). Run-and-tumble navigation with FCD guarantees
412 effective sampling of the rewards distributed in the environment, by implementing a search
413 algorithm (Eq. 6) analogous to the widely used Langevin Monte Carlo (LMC) algorithm for
414 sampling probability distributions (Roberts & Tweedie, 1996; Neal, 2011; Girolami &
415 Calderhead, 2011; Dalalyan, 2014) and for global optimization (Chiang *et al*, 1987; Gelfand &
416 Mitter, 1991; Lee *et al*, 2018; Erdogdu *et al*, 2018; Ma *et al*, 2019; Chen *et al*, 2020). The
417 animal samples a probability distribution given by a power of the distribution of expected
418 rewards. This explains the generalized matching law of operant behavior. Furthermore, run-
419 and-tumble navigation provides benefits beyond the Langevin Monte Carlo algorithm by
420 boosting gradient climbing on sufficiently steep reward gradients due to the positive feedback
421 between behavior and sensing. The positive feedback occurs since running along the gradient
422 provides increasing input that further enhances the run duration (Long *et al*, 2017).
423 The model provides a quantitative and mechanistic explanation of the generalized matching
424 law of operant behavior, with the matching exponent given by the ratio of dopaminergic gain

to basal activity. The logarithmic derivative property is crucial for obtaining the matching law. A non-logarithmic derivative, or absolute responses, do not provide matching (Supplementary Information 3).

The model predicts that manipulating the relative gain of dopamine neurons μd_0^{-1} will change the reward sensitivity parameter β in the matching law. This prediction can be tested by measuring μd_0^{-1} in genetically modified animals where matching behavior is different from wild-type. One such case is mice that are deficient in the cannabinoid type-1 receptor ($CB^{-/-}$), which have β that is lower by ~30% compared with wild-type mice (Sanchis-Segura *et al*, 2004). In agreement with the model prediction, $CB^{-/-}$ mice also have deficient dopaminergic responses relative to baseline (Li *et al*, 2009).

FCD also causes navigation to be invariant (i.e., not affected by) multiplying the input field by a scalar (Shoval *et al*, 2010) – in other words, by multiplying expected rewards across space by a constant factor λ. The FCD model predicts that the entire temporal dynamics of the search process, including the distribution of search times, the distribution of run lengths, etc., are invariant to the scale λ of reward magnitude. In fact, FCD is a necessary and sufficient condition for scale invariance of a search mechanism (Shoval *et al*, 2010). Scale invariance is prevalent across aspects of perception and behavior (Chater & Brown, 1999; Maylor *et al*, 2001; Stewart *et al*, 2006; Hart *et al*, 2018; Han *et al*, 2020). This property may be crucial for the dopamine circuit, since rewards can vary widely in scale and magnitude.

Together with the similarities there are also differences between bacterial chemotaxis and the reward-taxis model for dopamine. The value of β in bacterial chemotaxis is much larger than in the dopamine reward-taxis model, with $\beta > 10$ in *E. coli* (Hu & Tu, 2014; Karin & Alon, 2021) and $\beta \sim 1$ estimated for the dopamine system. The high β value in bacteria indicates a strong preference for higher rewards, akin to an optimization for accumulation near attractant peaks. A value of $\beta \sim 1$ (which results in the matching law) allows a greater range for exploration of submaximal rewards.

While the presentation of reward-taxis in this study focused on spatial movement, its assumptions are general and it may therefore apply to other behavioral systems. We discussed above the possibility that it applies to hippocampal replay. Another potential system is eye movements. Eye movements are modulated by dopamine and impaired in Parkinson's disease (Kori *et al*, 1995; Chan *et al*, 2005; Pretegiani & Optican, 2017), and their vigor is modulated by reward prediction errors (Sedaghat-Nejad *et al*, 2019). Since eye movements are commonly

studied in behavioral experiments such as reward matching, they may be a good candidate to test the reward-taxis model.

The present minimal model does not include several important aspects including goal-directed behavior and planning. These aspects are likely to complement stochastic navigation with more directed movement. Such a combination of navigation mechanisms is evident in simple organisms that employ run-and-tumble navigation. For example, in *C. elegans* thermotaxis, run-and-tumble navigation is combined with biased reorientations in order to navigate towards an optimal temperature range (Luo *et al*, 2014). Formally, while run-and-tumble navigation resembles Langevin-based sampling, directed reorientations are more closely related to gradient descent, which is efficient for local optimization but poor for global optimization (Ma *et al*, 2019; Raginsky *et al*, 2017; Xu *et al*, 2018). Understanding how animals combine stochastic navigation with other behavioral strategies can therefore improve our understanding of the algorithmic basis of animal behavior.

Methods

Model equations and fold-change detection

The equations for dopamine (d) and GABAergic inhibition (g) are provided by:

$$\dot{d} = \omega_d(C + \mu \log R - \alpha g - d) \quad [8]$$

$$\dot{g} = \omega\left(\frac{d}{d_0} - 1\right) \quad [9]$$

For the dopamine equation, ω_d determines the dopamine degradation rate, μ is dopamine gain, R is expected reward (defined in the next Methods section), and α is GABAergic inhibition strength. For the GABAergic inhibition equation, ω determines the adaptation rate and d_0 is the adapted steady-state of dopamine. As is common in FCD circuits, we assume that dopamine dynamics are faster than the dynamics of adaptation due to g (i.e., ω_d is large compared with ω) so we take:

$$d = C + \mu \log R - \alpha g \quad [10]$$

Eqs. 8,9,10 can represent the average activity of individual neurons, or the total activity of many neurons. We therefore used the same equations both to model average individual neuron recordings (as in Figure 1), and to model the effect of dopamine on movement, which is likely to be the sum of the activity of many neurons.

Consider now a constant input $R = R_0$, so that after some time the system reaches steady-state. To find the steady state, we solve Eqs. 8,9, taking $\dot{d} = 0, \dot{g} = 0$, which yields the steady-state solutions $d_{st} = d_0$ and $g_{st} = \alpha^{-1}(C - d_0 + \mu \log R_0)$. The observation that $d_{st} = d_0$ regardless of R_0 and other circuit parameters is an important circuit feature from systems biology known as *exact adaptation* (Barkai & Leibler, 1997; Alon *et al*, 1999; Ma *et al*, 2009; Ferrell Jr, 2016; Alon, 2019). This feature is essential for explaining why dopamine activity returns precisely to baseline after a step increase in expected reward, while GABAergic activity increases in a way that tracks expected reward.

Beyond exact adaptation, the system has an even stronger property of *fold-change detection* (FCD). FCD is defined as dynamics of dopamine (d) in response to an input $\lambda R(t)$ that are independent of λ, starting from initial conditions at steady-state for $\lambda R(0)$. To show this we replace $g = g' + \alpha^{-1}\mu \log \lambda$:

$$\dot{d} = \omega_d(C + \mu \log \lambda R - \alpha g - d) = \omega_d(C + \mu \log R - \alpha g' - d) \quad [11]$$

$$\dot{g}' = \omega\left(\frac{d}{d_0} - 1\right) \quad [12]$$

Eqs. 11, 12 are completely independent of λ, and their steady-state $g'_{st} = \alpha^{-1}(C - d_0 + \mu \log R_0)$ and $d_{st} = d_0$ is also independent of λ. This means that the dynamics of the system have the FCD property. The FCD property is essential for explaining the scale invariance of the dopaminergic responses to rewards in Fig. 1D – the response only depends on the fold-change of expected reward (two-fold change upon reception of reward at p=0.5) but not on reward magnitude.

While Eqs. 8,9,10 provide FCD, they are not the only possible model that provides FCD for this system. In particular, a feed-forward model where expected reward activates g is also possible, i.e.:

$$\dot{d} = \omega_d(d_0 + C + \mu \log R - \alpha g - d) \quad [13]$$

$$\dot{g} = \omega\left(\frac{C + \mu \log R}{\alpha} - g\right) \quad [14]$$

For this circuit, the steady state for a constant input $R = R_0$ is $g_{st} = \frac{\alpha + \mu \log R_0}{\alpha}$ and $d_{st} = d_0$. FCD can also be analogously shown. Given an input $\lambda r(t)$, we can take $g = g' + \alpha^{-1}\mu \log \lambda$, which again provides equations and steady-state that are independent of λ:

$$\dot{d} = \omega_d(d_0 + C + \mu \log \lambda R - \alpha g - d) = \omega_d(d_0 + C + \mu \log R - \alpha g' - d) \quad [15]$$

$$\dot{g}' = \omega\left(\frac{C + \mu \log \lambda R}{\alpha} - g\right) = \omega\left(\frac{C + \mu \log R}{\alpha} - g'\right) \quad [16]$$

Providing FCD. Parameters used in simulations are provided in Table 1.

While this simple log-linear model captures various important experimental observations, it is important to note that it has some clear limitations. One limitation is that both d and g can in principle reach negative values when R is small. Measurements of dopamine responses in monkeys indeed show deviations from sub-linearity for small rewards (Stauffer *et al*, 2014). Future studies may build on improved measurements and better mechanistic characterization of the dopamine circuit to refine this model.

Definition of expected reward and relation between the circuit and TD learning

Here we will define the input to the circuit, which is the logarithmic expected reward $\log R$, and present it in the context of the temporal difference (TD) learning theory of dopamine function (Schultz *et al*, 1997; Sutton & Barto, 1998). We first define the expected temporally discounted sum of future rewards V (also known as the value function in TD learning):

$$V(t_0) = \mathbb{E}\left[\sum_{t=t_0}^{\infty} \gamma^t r(t) dt\right] \quad [17]$$

Where $\gamma < 1$ is a "future discounting" factor and $r(t)$ is the reward received at time *t* into the future (here for simplicity we take discrete time; for equivalent formulation for continuous time, see Doya et al. (Doya, 2000)). It is possible to think of V as a function of the current state *s* of the agent, which may include for example its location in space *x*. This is known as the Markovian setting, where we denote the value function as $V(s)$. The value function plays an important role in decision making - learning the value function is a principal focus of reinforcement learning algorithms (Schultz *et al*, 1997; Sutton & Barto, 1998). However, for our purposes, we assume that V is already learned and can be provided to the circuit as an input. In our model, the input to the circuit for an agent moving into a state *s* at time *t* is defined using the expected reward *R*:

$$R(t,s) = r(t) + V(s) = r(t) + V(t) \quad [18]$$

As an example, consider the setting of Figure 1D, where a reward of size $r = y$ is delivered with probability p at Δt time-units into future: the expected reward would in this case be $R(0) \approx p\gamma^{\Delta t}y$. An actual delivery of the reward would then increase R to $R(\Delta t) \approx y$, so the ratio $\frac{R(\Delta t)}{R(0)} = \frac{1}{p\gamma^{\Delta t}}$ is independent of reward magnitude.

Note that due to discounting and uncertainty, R decays with the distance from a location where a reward is delivered, as in Figure 1E (Gershman, 2014).

We will now show that our model is consistent with the TD learning theory of dopamine function. We will first briefly present the TD learning algorithm. In reinforcement learning, the agent usually does not know V and needs to learn it from experience. This presents a computational problem, since V is an infinite sum over unknown future events. A way to get around this is to update the learned V using dynamic programming (Barto *et al*, 1989). The key insight is that Eq. 17 can be rewritten as:

$$V(t_0) = \mathbb{E}\left[\sum_{t=t_0}^{\infty} \gamma^t r(t)dt\right] = \mathbb{E}[r(t_0)] + \gamma V(t_0 + 1) \quad [19]$$

The above equation implies that V can be estimated iteratively with a simple update rule, which is at the heart of TD learning. If the agent is at state *s* at time *t*, and at state *s'* at time *t+1*, the update rule is:

$$V_{t+1}(s) \leftarrow V_t(s) + \alpha \underbrace{\left(r(t) + \gamma V_t(s') - V_t(s)\right)}_{prediction\ error} \quad [20]$$

Where $V_t(s)$ is the computed estimate of the expected reward at state *s* at time *t*, α is the learning rate, *r*(t) is the reward delivered at time *t* and γ is the discounting factor. There is extensive literature demonstrating correspondence between TD learning and midbrain

dopamine function (reviewed by (Glimcher, 2011)); specifically, experiments show a correspondence between phasic dopamine secretion and the prediction error term of Eq. 20 (Schultz *et al*, 1997; Glimcher, 2011), in the sense that positive or negative firing of dopamine neurons relative to baseline corresponds positive and negative predictions errors in TD models of learning.

The FCD model proposed here is consistent with the correspondence between dopamine function and TD learning. To see this, notice that learning the logarithm of V is equivalent to learning V. Also note from Eq. 19:

$$\log V(t_0) = \log\big(\mathbb{E}[r(t_0)] + \gamma V(t_0+1)\big) \approx \mathbb{E}\big[\log\big(r(t_0) + \gamma V(t_0+1)\big)\big] \quad [21]$$

The last approximation holds when r is either narrowly distributed, or not very large compared with $\gamma V(t_0+1)$. Thus, the following update rule is approximately equivalent to the TD update rule, but for $\log V$:

$$\log V_{t+1}(s) \leftarrow \log V_t(s) + \alpha \underbrace{\big(\log\big(r(t) + \gamma V_t(s')\big) - \log\big(V_t(s)\big)\big)}_{prediction\ error} \quad [22]$$

We note that in the continuous limit, and in the absence of reward, the error term is approximately proportional the logarithmic derivative of the value function. This corresponds to the output of our proposed FCD model for low frequency signals.

The output of the circuit to a delivered reward in a transition from a state s to a state s' is also similar to the above error term:

$$\Delta d = C + \mu \log R(t) - \alpha g(t) - d_0 = \mu\big(\log\big(r(t) + V(s')\big) - \log(V(s)\big) \quad [23]$$

The final equality is due to the fact that prior to reward delivery, GABAergic output adapts to $\alpha^{-1}(C - d_0 + \mu \log V(s))$. The FCD model is therefore compatible with the TD learning theory of dopamine function.

We conclude by noting that since the value that is learned is $\log V$, providing the input to the circuit $\log\big(r(t) + V(t)\big)$ requires a rather complex calculation; however, this can be simplified by using the approximation $\log(r + V) \approx \max(\log r, \log V)$, which can be implemented by neural circuits (Gawne & Martin, 2002; Knoblich *et al*, 2006).

Analysis

The fit of the dopaminergic responses in Figure 1B (including confidence intervals) was performed using the NonlinearModelFit function of Mathematica (version 12.1.1). All other figures and simulations were produced using Python (version 3.8.5). The source code and data to produce all the figures is available at https://github.com/omerka-weizmann/reward_taxis.

Table 1

Parameter	Value (mouse experiments)	Value (primate experiments)
ω_d	50 s^{-1}	100 s^{-1}
ω	15 s^{-1}	30 s^{-1}
C	15 spike s^{-1}	15 spike s^{-1}
μ	6 spike s^{-1}	6 spike s^{-1}
α	0.7	0.7
d_0	5 spike s^{-1}	5 spike s^{-1}

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