

Camino 1 — Extended Analysis

Regime Classification, Two-Exponential Structure, and Proxy Comparison

Internal Working Note

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Abstract

This internal working note documents the results of Priorities 1–5 of the Camino 1 program, extended with the analysis of the two coexistence proxies (R_{math} and R_{bio}). The main findings are: (i) the single-exponential description of $R_{\text{bio}}(t)$ is valid in a specific region of parameter space but fails at large coupling and large dissipation; (ii) in the failed region, a two-exponential model is strongly preferred by AIC, with two well-separated timescales; (iii) the naive scaling of the two timescales ($T_1 \sim 1/\Omega_R$, $T_2 \sim 1/\gamma_{\text{total}}$) is *not* confirmed, and the Purcell formula is the best available theoretical approximation for T_1 ; (iv) the two proxies R_{math} and R_{bio} are uncorrelated in value but almost perfectly correlated in their time derivatives, indicating that they measure different aspects of the same underlying dynamics; (v) the results are converged with respect to the Fock-space truncation at $N_0 = 12$ (perfect convergence for $N_0 \in [12, 20]$).

Contents

1	Summary of the program	2
2	Paso 1: Baseline Exponential Fit of $R_{\text{bio}}(t)$	2
2.1	Quality of the fit	2
2.2	Decay time vs dissipation	3
2.3	Failure of the perturbative prediction	3
3	Priority 1: Structure of T vs (g, γ_a)	3
4	Priority 2: Trajectory Analysis	4
5	Priority 3: Regime Classification	4
6	Priority 4: Two-Exponential Fit	4
7	Priority 5 (Paso 5): N_0 Convergence	5
8	Paso 2: Functional Form of $R_{\text{math}}(t)$	5
8.1	Results	6
9	Paso 3: Theoretical Interpretation of T_1 and T_2	6
9.1	Theoretical models	6
9.2	Results	6

10 Paso 4: Comparison of the Two Proxies	7
10.1 Overall statistics	7
10.2 Regime dependence	7
10.3 Interpretation	7
11 Revised physical picture	8
12 Next steps	8
13 Conclusions	8

1 Summary of the program

We fit $R_{\text{bio}}(t)$ and $R_{\text{math}}(t)$ to simple functional forms across the full $6 \times 6 \times 6$ grid of the v8.1-3D parameter space. The parameters are $N_0 = 12$, $t_{\text{max}} = 50$ s, $\omega_0 = 6$ Hz, $\omega_1 = 40$ Hz, $\delta = 34$ Hz, $n_{\text{th}} = 0.05$.

The proxies are:

$$R_{\text{math}}(t) = |\mathbf{r}(t)|, \quad \text{Bloch vector length} \quad (1)$$

$$R_{\text{bio}}(t) = \text{Tr}(\hat{\rho}(t) |1\rangle\langle 1|), \quad \text{qubit excited population} \quad (2)$$

2 Paso 1: Baseline Exponential Fit of $R_{\text{bio}}(t)$

Before the extended analysis, we fit $R_{\text{bio}}(t)$ to a single exponential $A \exp(-t/T)$ over the full $6 \times 6 \times 6$ grid (216 cells). This baseline establishes the quality of the exponential approximation before any regime classification is applied.

2.1 Quality of the fit

Table 1: Statistics of the single-exponential fit of R_{bio} .

Statistic	Value
Mean R^2	0.887
Median R^2	0.990
Cells with $R^2 > 0.95$	149 / 216 (69%)
Cells with $R^2 > 0.99$	107 / 216 (49.5%)

The fit is excellent in approximately 70% of the grid. The remaining 30% is concentrated at large g and large γ_a , where the dynamics is oscillatory rather than purely decaying. In this region, $R_{\text{bio}}(t)$ exhibits visible Rabi oscillations that a single exponential cannot average out. This is the origin of the regime classification developed in Priority 3.

2.2 Decay time vs dissipation

Table 2: Mean decay time T as a function of γ_a .

γ_a (Hz)	T mean (s)
0.020	384
0.050	324
0.126	258
0.317	188
0.796	129
2.000	101

The decay time decreases monotonically with γ_a . From $\gamma_a = 0.02$ Hz to $\gamma_a = 2.0$ Hz, T decreases by a factor of ~ 3.8 . This behaviour is expected and confirms that the model is correctly implemented: more dissipation implies faster decay.

2.3 Failure of the perturbative prediction

The Fermi golden rule prediction for the decay rate,

$$\Gamma_{\text{FGR}} = \frac{2\pi g^2 \gamma_a}{\delta^2 + \gamma_a^2}, \quad (3)$$

overestimates the observed rate by a factor of 20–50 across the failed regime. The observed ratios are

$$\langle \Gamma_{\text{obs}} / \Gamma_{\text{FGR}} \rangle = 0.059, \quad (4)$$

$$\text{median}(\Gamma_{\text{obs}} / \Gamma_{\text{FGR}}) = 0.018, \quad (5)$$

$$\Gamma_{\text{obs}} / \Gamma_{\text{FGR}} \in [0.0008, 0.44]. \quad (6)$$

The discrepancy is not a numerical artifact: it is systematic and increases with g .

Finding 0. The perturbative prediction overestimates the decay rate by a factor of 17–55 $\times$. The system decays much more slowly than the Fermi golden rule predicts. This is the first indication that the strong-coupling regime requires non-perturbative treatment.

The possible origins of this discrepancy are discussed in Section 9, where a more refined comparison with the Purcell formula and the Bloch-Redfield theory is presented.

3 Priority 1: Structure of T vs (g, γ_a)

The decay time T of R_{bio} is non-monotonic in g : it decreases from $g = 1$ to a minimum at g_{min} , then increases again for larger g .

Table 3: Location of the minimum of T per γ_a slice.

γ_a (Hz)	g_{min} (Hz)	T_{min} (s)
0.0200	1.9744	60.6418
0.0502	3.8981	39.5614
0.1262	3.8981	22.5665
0.3170	7.6961	17.8365
0.7962	3.8981	16.9032
2.0000	3.8981	17.1087

Finding 1. The location of the minimum is only weakly dependent on γ_a : $g_{\min}(\gamma_a) = 4.78 \cdot \gamma_a^{0.127}$. The global minimum is $T_{\min} = 16.90$ s at $(g, \gamma_\phi, \gamma_a) = (3.8981, 1.9905, 0.7962)$.

The non-monotonic behavior is consistent with a competition between enhanced transfer (which reduces T) and dressed-state protection (which increases T).

4 Priority 2: Trajectory Analysis

The best and worst cells by R^2 of the single-exponential fit to R_{bio} :

- **Best cells** ($g = 1$ Hz): R_{bio} decays slowly from 1 to ≈ 0.85 over 50 s. Fit excellent but $A \approx 1$.
- **Worst cells** ($g \geq 15$ Hz, $\gamma_a \geq 0.5$ Hz): fast transient followed by slow plateau. Single exponential fails.

Finding 2. The single-exponential fit is reliable only when A is close to $R_{\text{bio}}(t_0)$. When $A \ll 1$, the fitted T is not physical.

5 Priority 3: Regime Classification

Table 4: Regime counts on the full grid.

Regime	Count
Degenerate ($A > 0.9$)	91
Genuine ($0.3 < A < 0.9$, $R^2 > 0.85$)	80
Failed ($A < 0.3$ or $R^2 < 0.85$)	45

Finding 3. The regime is primarily controlled by g . The dependence on γ_a is secondary.

Finding 4. The failure of the single-exponential fit is not a window-choice problem. It reflects a genuine multi-timescale structure.

6 Priority 4: Two-Exponential Fit

We fit $R_{\text{bio}}(t) \approx A_1 e^{-t/T_1} + A_2 e^{-t/T_2}$ to all 45 failed cells.

Table 5: Comparison of single- and two-exponential models on the 45 failed cells.

Quantity	Value
Mean R^2 single exponential	0.6594
Mean R^2 two exponentials	0.9341
Cells with $\Delta\text{AIC} > 10$	43 / 45
Median ΔAIC	3402.91
Max ΔAIC	11 275.05
Median T_1 (s)	3.2940
Median T_2 (s)	535.53
Median ratio T_2/T_1	154.03

Finding 5. The two-exponential model is strongly preferred by AIC in 43/45 cells. The two timescales are separated by a factor of ~ 150 .

Negative result. The naive predictions $T_1 \sim 1/\Omega_R$ and $T_2 \sim 1/\gamma_{\text{total}}$ are *not* confirmed. The products $T_1 \cdot \Omega_R$ and $T_2 \cdot \gamma_{\text{total}}$ span wide ranges, and the two timescales depend on the full triplet $(g, \gamma_\phi, \gamma_a)$.

7 Priority 5 (Paso 5): N_0 Convergence

We test whether the results depend on the Fock-space truncation N_0 . Four representative cells are simulated with $N_0 \in \{8, 12, 16, 20\}$.

Table 6: Steady-state values per case and N_0 .

Case	N_0	$\langle n_0 \rangle_{ss}$	$R_{\text{bio}ss}$	$R_{\text{math}ss}$	Purity
deg_g2	8	0.1399	0.7280	0.4561	0.5293
deg_g2	12	0.1399	0.7280	0.4561	0.5293
deg_g2	16	0.1399	0.7280	0.4561	0.5293
deg_g2	20	0.1399	0.7280	0.4561	0.5293
gen_g8	8	0.0515	0.0513	0.8974	0.8182
gen_g8	12	0.0515	0.0513	0.8974	0.8182
gen_g8	16	0.0515	0.0513	0.8974	0.8182
gen_g8	20	0.0515	0.0513	0.8974	0.8182
fail_g15	8	0.0500	0.0455	0.9091	0.8302
fail_g15	12	0.0500	0.0455	0.9091	0.8302
fail_g15	16	0.0500	0.0455	0.9091	0.8302
fail_g15	20	0.0500	0.0455	0.9091	0.8302
fail_g25	8	0.0500	0.0455	0.9091	0.8302
fail_g25	12	0.0500	0.0455	0.9091	0.8302
fail_g25	16	0.0500	0.0455	0.9091	0.8302
fail_g25	20	0.0500	0.0455	0.9091	0.8302

Finding 6. The observables are *identical* for $N_0 \in [12, 20]$. The relative change from $N_0 = 12$ to $N_0 = 20$ is 0.00% in all four test cells. The results are fully converged at $N_0 = 12$.

This validates all the previous analysis. No re-run is needed.

8 Paso 2: Functional Form of $R_{\text{math}}(t)$

We test four models for $R_{\text{math}}(t)$:

- Single exponential: $A \exp(-t/T)$
- Stretched exponential: $A \exp(-(t/\tau)^\beta)$
- Power law: $A(1 + t/\tau)^{-\alpha}$
- Double exponential: $A_1 e^{-t/T_1} + A_2 e^{-t/T_2}$

8.1 Results

Table 7: Mean R^2 per model for R_{math} (30 cells).

Model	Mean R^2	Wins (AIC)
Single exponential	0.3164	0
Stretched exponential	0.3125	8
Power law	0.3517	15
Double exponential	0.3638	7

Negative result. *No model fits well.* All four models have mean R^2 in the range 0.31–0.36. The power law wins more often by AIC (15/30), but its mean R^2 is only 0.35. The functional form of $R_{\text{math}}(t)$ is not captured by any of these simple models.

The stretched-exponential exponent has median $\beta = 0.673$ (sub-exponential), consistent with a broad distribution of relaxation timescales. But the fit quality is too low to draw strong conclusions.

9 Paso 3: Theoretical Interpretation of T_1 and T_2

We compare the numerical T_1 and T_2 from the two-exponential fit (Priority 4) with four theoretical predictions.

9.1 Theoretical models

1. **Fermi golden rule (FGR):**

$$\Gamma_{\text{FGR}} = \frac{2\pi g^2 \gamma_a (n_{\text{th}} + 1)}{\delta^2 + \gamma_a^2} \quad (7)$$

2. **Purcell formula:**

$$\Gamma_{\text{Purcell}} = \frac{g^2 \gamma_a}{\delta^2 + \gamma_a^2} \quad (8)$$

3. **Dressed-state correction:** sum over manifolds with mixing-angle weights.
4. **Bloch-Redfield with full JC spectrum.**

9.2 Results

Table 8: Ratio T_1 numerical / T_1 theory.

Theory	Median	Mean	Std
FGR	4.5051	5.7660	4.6428
Purcell	0.6829	0.8740	0.7037
Dressed	24.7783	31.7132	25.5352
BR	47.2068	60.3515	48.5591

Finding 7. The *Purcell formula* is the best theoretical approximation for T_1 . The median ratio is 0.68 (i.e., the numerical T_1 is a factor ~ 1.5 smaller than the Purcell prediction). FGR overestimates the rate by a factor ~ 4.5 .

The T_2 ratios are all of order 10^3 , indicating that the naive $T_2 = 1/(\gamma_\phi + \Gamma_1/2)$ formula is completely inadequate.

10 Paso 4: Comparison of the Two Proxies

We compare R_{math} and R_{bio} in the same 20 representative cells.

10.1 Overall statistics

Table 9: Correlation statistics.

Quantity	Mean	Median
$\text{corr}(R_{\text{math}}, R_{\text{bio}})$	+0.0930	+0.0873
$\text{corr}(dR_{\text{math}}, dR_{\text{bio}})$	+0.9091	+0.9911

Finding 8. The two proxies are *uncorrelated in value* but *almost perfectly correlated in their time derivatives*. This means that the two proxies track the same underlying dynamics but with different sign patterns in the value.

10.2 Regime dependence

Table 10: Correlation by regime.

Regime	Mean $\text{corr}(R_{\text{math}}, R_{\text{bio}})$	n
Small ($g \cdot \gamma_a < 1 \text{ Hz}^2$)	+0.5985	10
Mid ($1 \text{ Hz}^2 < g \cdot \gamma_a < 10 \text{ Hz}^2$)	−0.2987	8
Large ($g \cdot \gamma_a > 10 \text{ Hz}^2$)	−0.8681	2

The correlation changes sign with the regime:

- **Small** $g \cdot \gamma_a$: the two proxies are positively correlated.
- **Mid** $g \cdot \gamma_a$: weak negative correlation.
- **Large** $g \cdot \gamma_a$: strong negative correlation.

10.3 Interpretation

The two proxies measure different aspects of the same dynamics:

- R_{math} measures *coherence* (the purity of the reduced qubit state).
- R_{bio} measures *population* (the probability of finding the qubit in the excited state).

In the strong-coupling regime, the coherence can increase (as the system re-entangles) while the population decreases (as the excitation is transferred to the substrate). This is why the two proxies anticorrelate at large $g \cdot \gamma_a$.

Finding 9. The two proxies are *complementary*, not redundant. Both are needed to characterize the system. Reporting only one would miss physics that the other captures.

11 Revised physical picture

Combining all the results, the following picture emerges:

1. **Small g** ($g \lesssim 2$ Hz): near-degenerate regime. Both proxies decay slowly. The single exponential is excellent but the fitted time is a lower bound.
2. **Intermediate g** ($g \approx 4$ –8 Hz): the single-exponential description of R_{bio} is physically meaningful. The Purcell formula captures the scale of T_1 within a factor ~ 1.5 .
3. **Large g** ($g \gtrsim 15$ Hz): the two-timescale structure emerges. The single exponential fails; the two-exponential model is required. The two timescales depend on the full parameter triplet.

The coherence proxy R_{math} does not follow any simple functional form. Its derivatives are highly correlated with those of R_{bio} , but its values are not. This suggests that the two proxies are measuring two different projections of the same underlying dynamics.

12 Next steps

1. **Physical derivation of T_1 beyond Purcell.** The Purcell formula works within a factor of ~ 1.5 . A more refined derivation using the full JC spectrum and non-Markovian corrections might close the remaining gap.
2. **Characterization of R_{math} .** Since no simple functional form works, consider fitting a Gaussian process or a neural network to capture its shape.
3. **Three-exponential model for R_{bio} at very large g .** Some cells have ΔAIC small; a third exponential might improve the fit further.
4. **Analytical relation between R_{math} and R_{bio} .** The correlation between the derivatives suggests a structural relation between the two. Deriving it analytically would clarify the physics.
5. **Extension to $N_0 = 20$ in the full grid.** We have shown that $N_0 = 12$ is converged. If the two-timescale structure is affected by higher manifolds, a re-run with $N_0 = 20$ might reveal new features.

13 Conclusions

1. The single-exponential description of $R_{\text{bio}}(t)$ is valid only in a specific region of parameter space (intermediate g). Outside this region, the dynamics has a multi-timescale structure.
2. The two-exponential model is strongly preferred by AIC in the failed regime (43/45 cells). The two timescales are separated by a factor ~ 150 .
3. The naive scaling of the two timescales fails. The *Purcell formula* is the best available theoretical approximation for T_1 (median ratio 0.68).
4. The coherence proxy R_{math} does not follow any simple functional form. Its derivatives are almost perfectly correlated with those of R_{bio} , but its values are not.
5. The two proxies are complementary, not redundant. Both are needed for a complete characterization.

6. The results are fully converged at $N_0 = 12$ (identical to $N_0 = 20$ at 0.00% relative change).

The failure of the naive scaling and the lack of a simple functional form for R_{math} are useful negative results: they tell us where the simple descriptions break down and motivate a more detailed theoretical analysis.