INTRODUCTION
Cilia and eukaryotic flagella are highly conserved organelles that project from the surfaces of many cells. The assembly and maintenance of these nearly ubiquitous structures depend on a protein transport system known as intraflagellar transport (IFT).

IFT is a bidirectional movement of multiprotein complexes along the axoneme. Anterograde IFT, driven by kinesin-2, brings cargo proteins from the cell body to the tip of the cilium. At the distal tip, IFT trains are restructured and are moved back to the cell body by cytoplasmic dynein 2 as retrograde IFT.

METHODS
However, it is unknown whether retrograde IFT is disassembled in the cytoplasm or re-enters into flagella as a new anterograde IFT because of the technical difficulty to track individual IFT particles. To clarify the destination of retrograde IFT trains, we established a *Chlamydomonas reinhardtii* strain that expresses a photoconvertible Eos fluorescent protein fused IFT.

RESULTS
We observed that IFT particles were rapidly exchanged between the two flagella, a process we call Interflagellar IFT Transport. We measured IFT particle mixing time between the two flagella and observed that photoconverted particles were equalized within 2-3 minutes. Additionally, we found that only 10-25% of photoconverted fluorescence signal was lost during imaging. This finding suggests that most of the IFT particles are reused and re-enter into the flagella.

MODEL
We propose a simple diffusion based model that predicts an equilibration time matching our observations. In this model, we assume that IFT particles freely diffuse between the basal bodies of two flagella and move at constant speed within the flagellum. This model is parameter free and does not account for IFT exchange with the cytoplasm.